

OM nucleic - nucleic search, using sw model

Run on: September 8, 2004, 04:02:58 ; Search time 17438 Seconds
(without alignments)
13768.318 Million cell updates/sec

Title: US-10-088-467-1
Perfect score: 8040
Sequence: 1 ccgcggcgctgaggcggcgg.....aaataaataaacaaaatgtc 8040

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query				Description
			Match	Length	DB	ID	
	No.	Score					
	1	3583.4	44.6	6117	29	AY421584	AY421584 Homo sapi
	2	2415.4	30.0	5289	29	AY421585	AY421585 Pan trogl
	3	2347.4	29.2	5743	29	AY421586	AY421586 Mus muscu
	4	1903.4	23.7	2065	11	BC029282	BC029282 Homo sapi
	5	965	12.0	6600	29	AY405473	AY405473 Mus muscu
	6	952.2	11.8	6606	29	AY405471	AY405471 Homo sapi
	7	942.8	11.7	6606	29	AY405472	AY405472 Pan trogl
	8	923.2	11.5	1045	13	BX341657	BX341657 BX341657
	9	901.4	11.2	1078	12	BM548310	BM548310 AGENCOURT
	10	901.4	11.2	1201	13	BX374888	BX374888 BX374888
	11	900.4	11.2	964	9	AL525194	AL525194 AL525194
c	12	893.2	11.1	958	9	AL525193	AL525193 AL525193
c	13	886.2	11.0	1201	9	AL540221	AL540221 AL540221
	14	873.2	10.9	1082	13	BX420933	BX420933 BX420933
	15	854	10.6	1201	13	BX376831	BX376831 BX376831
	16	819	10.2	1039	12	BM925723	BM925723 AGENCOURT
	17	796.2	9.9	1066	12	BM907138	BM907138 AGENCOURT
	18	780.8	9.7	1129	12	BM807409	BM807409 AGENCOURT
	19	775.2	9.6	904	13	BQ645609	BQ645609 AGENCOURT
	20	763.4	9.5	1201	13	BX382919	BX382919 BX382919
	21	761.8	9.5	986	12	BI821324	BI821324 603038167
	22	751.4	9.3	1054	12	BM544515	BM544515 AGENCOURT
	23	747	9.3	755	12	BI488407	BI488407 603020905
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	26	740.2	9.2	982	13	BQ720264	BQ720264 AGENCOURT
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	30	718	8.9	1158	12	BM547655	BM547655 AGENCOURT
	31	711	8.8	742	14	CF455392	CF455392 AGENCOURT
	32	690	8.6	879	14	CA454786	CA454786 AGENCOURT
	33	689.6	8.6	791	12	BI195329	BI195329 602944676
c	34	689	8.6	719	14	CA419218	CA419218 UI-H-EZ1-
	35	684	8.5	688	12	BG823114	BG823114 602726452
c	36	684	8.5	715	13	BQ574216	BQ574216 UI-H-EZ1-
	37	682.2	8.5	1201	9	AL540222	AL540222 AL540222
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	39	678.2	8.4	1117	13	BQ067042	BQ067042 AGENCOURT
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	42	672.4	8.4	735	12	BG403849	BG403849 602419692
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ALIGNMENTS

RESULT 1
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 LOCUS AY421584 6117 bp DNA linear GSS 17-DEC-2003
 DEFINITION Homo sapiens ABCA2 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 ACCESSION AY421584
 VERSION AY421584.1 GI:39748443
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 6117)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302
 REFERENCE 2 (bases 1 to 6117)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA
 COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 gene <1..>6117
 /gene="ABCA2"
 /locus_tag="HCM7606"
 ORIGIN
 Query Match 44.6%; Score 3583.4; DB 29; Length 6117;
 Best Local Similarity 60.0%; Pred. No. 0;
 Matches 3597; Conservative 0; Mismatches 2400; Indels 3; Gaps 1;
 Qy 101 TGGGTCCTGGCCTTCGAGATCTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTG 160
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 TGGGTCCTGGCCTTCGAGATCTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTG 60
 Qy 161 CGACAGAAGAAGCCCACCATCTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCCTG 220
 |||||||||||||||||||||||||||| ||||||||||||||||||||
 Db 61 CGACAGAAGAAGCCCACCATCTCCGTGAAGGAAG---CCTTCTACACAGCGGCGCCCCTG 117

Qy	221	ACGTCTGCCGGCATCCTGCCTGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAG	280
Db	118	ACGTCTGCCGGCATCCTGCCTGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAG	177
Qy	281	TTCGGCTTCCTGCAGTACGCCAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGC	340
Db	178	TTCGGCTTCCTGCAGTACGCCAACTCCACNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	237
Qy	341	GTGGTGGAGGAAGGCAACCTGTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAG	400
Db	238	NN	297
Qy	401	GCCCTACGCCAGCATCTGGAGGCCCTCAGTGCGGGCCCGGGCACCTCGGGGAGCCACCTG	460
Db	298	NN	357
Qy	461	GACAGATCCACAGTGTCTTCCTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTC	520
Db	358	NNNNNNNNNNNNNTGTCTTCCTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTC	417
Qy	521	TGGCGTTTCCTGACGCAAACTTGTGCTGCCCCAATAGCACGGCCCAAGCACTCTTGGCC	580
Db	418	TGGCGTTTCCTGACGCAAACTTGTGCTGCCCCAATAGCACGGCCCAAGCACTCTTGGCC	477
Qy	581	GCCCGTGTGGACCCGCCGAGGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGAT	640
Db	478	GCCCGTGTGGACCCGCCGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	537
Qy	641	TCACAGTCTGGCCTCCACAAGGGTCAGGAGCCCTGGAGCCGCTAGGGGGCAATCCCCTG	700
Db	538	NN	597
Qy	701	TTCCGGATGGAGGAGCTGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCG	760
Db	598	NNNNNNNNNNNNNGAGCTGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCG	657
Qy	761	GGCTCGGGGGAGCTGGGCCGGATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAG	820
Db	658	GGCTCGGGGGAGCTGGGCCGGATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAG	717
Qy	821	GGCTACCGGGATGCTGTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGG	880
Db	718	GGCTACCGGGATGCTGTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGG	777
Qy	881	CTGTCTGCTGAGCTCCGGAACCAGCTGGACGTGGCCAAGGTCTCCAGCAGCTGGGCCTG	940
Db	778	CTGTCTGCTGAGCTCCGGAACCAGCTGGACGTGGCCAAGGTCTCCAGCAGCTGGGCCTG	837
Qy	941	GATGCCCCCAACGGCTCGGACTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCG	1000
Db	838	GATGCCCCCAACGGCTCGGACTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCG	897
Qy	1001	CTTCTGGGGGACCTGCTGGATGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGCC	1060
Db	898	CTTCTGGGGGACCTGCTGGATGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGCC	957

Qy	1061	CTGGCCCTGCTACTGCCCCAGGGTGCCTGCACTGGCCGGACCCCCGACCCCCAGCCAGT	1120
Db	958	CTGGCCCTGCTACTGCCCCAGGGTGCCTGCACTGGCCGGACCCCCGACCCCCAGCCAGT	1017
Qy	1121	GGTGCGGGTGGGGCGGCCAATGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACC	1180
Db	1018	GGTGCGGGTGGGGCGGCCAATGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACC	1077
Qy	1181	GCTGAGGAGGGCGCACCCCTCTGCTGCAGCACTGGCCACCCCGACACGCTGCAGGGCCAG	1240
Db	1078	GCTGAGGAGGGCGCACCCCTCTGCTGCAGCACTGGCCACCCCGACACGCTGCAGGGCCAG	1137
Qy	1241	TGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGC	1300
Db	1138	TGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGN	1197
Qy	1301	ACCATTGAACCCGAGGCGCTGCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAG	1360
Db	1198	NN	1257
Qy	1361	GAGCAGCGGAACCTGGGCCTCCTCGTGACCTCATGACCAGCAACCCCAAAATCCTGTAC	1420
Db	1258	NN	1317
Qy	1421	GCGCCTGCGGGCTCTGAGGTCGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTT	1480
Db	1318	NNNGCCAACGAGACTTTTGCTTTT	1377
Qy	1481	GTGGGCAACGTGACTCACTATGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGC	1540
Db	1378	GTGGGCAACGTGACTCACTATGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGC	1437
Qy	1541	TTCTTGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAG	1600
Db	1438	TTCTTGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAG	1497
Qy	1601	CTGCGGCTGCACCCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGA	1660
Db	1498	CTGCGGCTGCACCCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGA	1557
Qy	1661	CAGGACAACTTCTCGCTGCCAGTGGCATGGCCCTCCTGCAGCAGCTGGATAACCATTGAC	1720
Db	1558	CAGGACAACTTCTCGCTGCCAGTGGCATGGCCCTCCTGCAGCAGCTGGATAACCATTGAC	1617
Qy	1721	AACGCGGCTGCGGCTGGATCCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGC	1780
Db	1618	AACGCGGCTGCGGCTGGATCCAGTTCATGTCCAAGNNNNNNNNNNNNNNNNNNNNNNNN	1677
Qy	1781	TTCCCCGACGAGGAGAGCATTGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTC	1840
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Qy	1841	ACTGTTTTTGCCAGTGTGATCTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTG	1900
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Qy	1901	CACTACAAGATCCGCCAGAACTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCC	1960

Db	1798	CACTACAAGATCCGCCAGAACTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCC	1857
Qy	1961	TACTGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGG	2020
Db	1858	TACTGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGG	1917
Qy	2021	ATCCAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAG	2080
Db	1918	ATCCAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAG	1977
Qy	2081	CCAGGCAGCTACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTT	2140
Db	1978	CCAGGCAGCTACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTT	2037
Qy	2141	GTCATTGAGCACATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATG	2200
Db	2038	GTCATTGAGCACATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATG	2097
Qy	2201	ACCATCCAGCACATCGTGGCGGAGAAGGAGCACC GGCTCAAGGAGGTGATGAAGACCATG	2260
Db	2098	ACCATCCAGCACATCGTGGCGGAGAAGGAGCACC GGCTCAAGGAGGTGATGAAGACCATG	2157
Qy	2261	GGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACC GGCTTTGTGCAGCTGTCC	2320
Db	2158	GGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACC GGCTTTGTGCAGCTGTCC	2217
Qy	2321	ATCTCCGTGACAGCACTCACC GCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCAC	2380
Db	2218	ATCTCCGTGACAGCACTCACC GCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCAC	2277
Qy	2381	GTGGTCATCATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTC	2440
Db	2278	GTGGTCATCATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTC	2337
Qy	2441	CTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTAC	2500
Db	2338	CTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTAC	2397
Qy	2501	TTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAG	2560
Db	2398	TTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAG	2457
Qy	2561	ATCACGGCCTTCGAGAAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGC	2620
Db	2458	ATCACGGCCTTCGAGAAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGC	2517
Qy	2621	TCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGC	2680
Db	2518	TCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGC	2577
Qy	2681	CAGTCCCCGGTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTG	2740
Db	2578	CAGTCCCCGGTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTG	2637
Qy	2741	GACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTAC	2800

Db	2638	GACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGNNNNNNNN	2697
Qy	2801	GGGCTGCCCCGGCCCTGGTACTTCCCCTGCAGAAGTCCCTACTGGCTGGGCAGTGGGCGG	2860
Db	2698	NN	2757
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Db	2758	NN	2817
Qy	2921	GAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAG	2980
Db	2818	NNNNACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAG	2877
Qy	2981	GAGCCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGAC	3040
Db	2878	GAGCCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGAC	2937
Qy	3041	GACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCC	3100
Db	2938	GACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCC	2997
Qy	3101	TTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTC	3160
Db	2998	TTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTC	3057
Qy	3161	CCTCCAACGTCGGGTTCGCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAG	3220
Db	3058	CCTCCAACGTCGGGTTCGCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAG	3117
Qy	3221	ATCCGCAAGAACCTGGGCATGTGCCCGCAGCACAATGTGCTCTTTGACCGGCTCACGGTG	3280
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Qy	3281	GAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGA	3340
Db	3178	NN	3237
Qy	3341	GAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAG	3400
Db	3238	NN	3297
Qy	3401	ACATTGTCGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCT	3460
Db	3298	ACATTGTCGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCT	3357
Qy	3461	CGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATC	3520
Db	3358	CGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATC	3417
Qy	3521	TGGGACCTCATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATG	3580
Db	3418	TGGGACCTCATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATG	3477
Qy	3581	GATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGC	3640
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[illegible]

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Qy	4601	GACGCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACC	4660
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Db	4618	NN	4677
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Qy	4841	GCGTCCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCA	4900
Db	4738	NN	4797
Qy	4901	GAAATGTGGACGT CGGC ACCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACC 	4960
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Qy	5081	CTGCTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAAC 	5140
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Qy	5141	GTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGC GGAAGATC 	5200
Db	5038	GTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGC GGAAGATC	5097
Qy	5201	GCGGTGCGCAGGGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACC 	5260
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Qy	5261	TACCTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACCTGCCCAAAGAGCAAGGGCAAC	5320
Db	5158	NN	5217
Qy	5321	CCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTC	5380

ACCESSION AY421585
 VERSION AY421585.1 GI:39748444
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 5289)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 JOURNAL Science 302 (5652), 1960-1963 (2003)
 PUBMED 14671302

REFERENCE 2 (bases 1 to 5289)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 TITLE Direct Submission
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering
 them based on alignment.

FEATURES Location/Qualifiers
 source 1..5289
 /organism="Pan troglodytes"
 /mol_type="genomic DNA"
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ORIGIN

Query Match 30.0%; Score 2415.4; DB 29; Length 5289;
 Best Local Similarity 56.4%; Pred. No. 0;
 Matches 2419; Conservative 0; Mismatches 1871; Indels 0; Gaps 0;

QY 932 CTGGGCCTGGATGCCCCAACGGCTCGGACTCCTCGCCACAGGCGCCACCCACGGAGG 991
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 Db 1 CTGGGCCTGGATGCCCCAACGGCTCGGACTCCTCGCCACAGGCGCCACCCACGGAGG 60

QY 992 CTGCAGGCGCTTCTGGGGGACCTGCTGGATGCCCAGAAGGTTCTGCAGGATGTGGATGTC 1051
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 Db 61 CTGCAGGCGCTTCTGGGGGACCTGCTGGATGCCCAGAAGGTTCTGCAGGATGTGGATGTC 120

QY 1052 CTGTCGGCCCTGGCCCTGCTACTGCCCCAGGGTGCCTGCACTGGCCGGACCCCGGACCC 1111
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 Db 121 CTGTCGGCCCTGGCCCTGCTACTGCCCCAGGGTGCCTGCACTGGCCGGACCCCGGACCC 180

QY 1112 CCAGCCAGTGGTGCGGGTGGGGCGGCCAATGGCACTGGGGCAGGGGCAGTCATGGGCCCC 1171
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 Db 181 CCAGCCAGCGGTGCGGGTGGGGCGGCCAATGGCACTGGGGCAGGGGCAGTCATGGGCCCC 240

QY 1172 AACGCCACCGCTGAGGAGGGCGCACCTCTGCTGCAGCACTGGCCACCCCGGACACGCTG 1231

Db	241	AACGCCACCGCTGAGGAGGGCGCACCTCTGCTGCAGCACTGGCCTCCCCGGACACGCTG	300
Qy	1232	CAGGGCCAGTGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGC	1291
Db	301	CAGGGCCAGTGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGC	360
Qy	1292	AACAACCGCACCATTTGAACCCGAGGCGCTGCGGCCGGGGCAACATGAGCTCCCTGGGCTTC	1351
Db	361	AACAACCGNN	420
Qy	1352	ACGAGCAAGGAGCAGCGGAACCTGGGCCTCCTCGTGCACCTCATGACCAGCAACCCCAA	1411
Db	421	NN	480
Qy	1412	ATCCTGTACGCGCCTGCGGGCTCTGAGGTCGACCGCGTCATCCTCAAGGCCAACGAGACT	1471
Db	481	NNNGCCAACGAGACT	540
Qy	1472	TTTGCTTTTGTGGGCAACGTGACTCACTATGCCAGGTCTGGCTCAACATCTCGGCGGAG	1531
Db	541	TTTGCTTTTGTGGGCAACGTGACTCACTATGCCAGGTCTGGCTCAACATCTCGGCGGAG	600
Qy	1532	ATCCGCAGCTTCCTGGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTAT	1591
Db	601	ATCCGCAGCTTCCTGGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTAT	660
Qy	1592	GTAGCAGAGCTGCGGCTGCACCCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCG	1651
Db	661	GTAGCAGAGCTGCGGCTGCACCCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCG	720
Qy	1652	GCCCTGAGACAGGACAACCTTCTCGCTGCCAGTGGCATGGCCCTCCTGCAGCAGCTGGAT	1711
Db	721	GCCCTGAGACAGGACAACCTTCTCGCTGCCAGTGGCATGGCCCTCCTGCAGCAGCTGGAT	780
Qy	1712	ACCATTGACAACGCGGCCTGCGGCTGGATCCAGTTCATGTCCAAGGTGAGCGTGGACATC	1771
Db	781	ACCATTGACAACGCGGCCTGCGGCTGGATCCAGTTCATGTCCNNNNNNNNNNNNNNNNNN	840
Qy	1772	TTCAAGGGCTTCCCCGACGAGGAGAGCATTTGTCAACTACACCCTCAACCAGGCCTACCAG	1831
Db	841	NN	900
Qy	1832	GACAACGTCAGTGTTTTTGCCAGTGTGATCTTCCAGACCCGGAAGGACGGCTCGCTCCCG	1891
Db	901	NN	960
Qy	1892	CCTCACGTGCACTACAAGATCCGCCAGAACTCCAGCTTCACCGAGAAAACCAACGAGATC	1951
Db	961	NNNNNNNNNNNNNNNNNNNATCCGCCANNACTCCANN TTCACCGNNAAACCAACGAGATC	1020
Qy	1952	CGCCGCGCCTACTGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCCTCTACGGC	2011
Db	1021	CGCCGCGCCTACTGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCCTCTACGGC	1080
Qy	2012	TTTCGTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCACGAC	2071

[illegible]

Qy	2912	GTTCATGGAGGAGGACCAGGCCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGC	2971
Db	1981	NNNAGGAGACCCGTGGC	2040
Qy	2972	ATGGAGGAGGAGCCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAAACTCACCAAGGTC	3031
Db	2041	ATGGAGGAGGAGCCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAAACTCACCAAGGTC	2100
Qy	3032	TACAAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAG	3091
Db	2101	TACAAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAG	2160
Qy	3092	GTGGTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACC	3151
Db	2161	GTGGTCTCCTTCTTGGGCCACAACGGGGCGGGCNNNNNNNNNNNNNNNNTCCATCCTGACC	2220
Qy	3152	GGCCTGTTCCCTCCAACGTCGGGTTCCGCCACCATCTACGGGCACGACATCCGCACGGAG	3211
Db	2221	GGCCTGTTCCCTCCAACGTCGGGTTCCGCCACCATCTACGGGCACGACATCCGCACGNNN	2280
Qy	3212	ATGGATGAGATCCGCAAGAACCTGGGCATGTCCCCGAGCACAATGTGCTCTTTGACCGG	3271
Db	2281	NNGGATGAGATCCGCAANN	2340
Qy	3272	CTCACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAG	3331
Db	2341	NNN	2400
Qy	3332	ATCCGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCA	3391
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Qy	3392	CTGGTGCAGACATTGTCTGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTG	3451
Db	2461	NNNNNNNNNNNNNNNTCTGGGTGGCATNAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTG	2520
Qy	3452	GGCGGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGACCCCTACGCGCGC	3511
Db	2521	GGCGGCTCTCNNNCCATCATCCTGGACGAGCCACGGCGGGCGTGACCCCTNNNNNNNNN	2580
Qy	3512	CGCGCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGCACCATCCTTCTGTCCACC	3571
Db	2581	NNNGCCGCACCATCCTTCTGTCCACC	2640
Qy	3572	CACCACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAG	3631
Db	2641	CACCACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAG	2700
Qy	3632	CTCAAGTGCTGCGGCTCCCCGCTCTTCTCAAGGGCACCTATGGCGACGGGTACCGCCTC	3691
Db	2701	CTCAAGTGCTGCGGCTCCCCGCTCTTCTCAAGGGCACCTATGGCGACGGGTACCGCCTC	2760
Qy	3692	ACGCTGGTCAAGCGGCCCCGCCGAGCCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGC	3751
Db	2761	ACGCTGGTCAAGCGGCCCCGCCGAGCCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGC	2820

Qy	3752	CCCCCAGGTCGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCCAGTTCATCCGC	3811
Db	2821	CCCCCAGGTCGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCCAGTTCATCCGC	2880
Qy	3812	AAGCATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTG	3871
Db	2881	AAGCATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTG	2940
Qy	3872	CCCAGCGAGGCCGCCAAGAAGGGGGCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGC	3931
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Qy	3932	CTGGATGCACTGCACCTCAGCAGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTG TTC	3991
Db	3001	NN	3060
Qy	3992	CTCAAGGTGTCGGAGGAGGATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCC	4051
Db	3061	NN	3120
Qy	4052	AGGAAGGATGTGCTCCCTGGGGCGGAGGGCCCGGCGTCTGGGGAGGGTCACGCTGGCAAT	4111
Db	3121	NN	3180
Qy	4112	CTGGCCCGGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTG	4171
Db	3181	NN	3240
Qy	4172	GGCTCTGCCCCTGGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCC	4231
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Qy	4232	CTCTTTGATAACCCACAGGACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCC	4291
Db	3301	NN	3360
Qy	4292	CTGTGCGAGGGTCGGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAG	4351
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Qy	4352	TTCCACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTC	4411
Db	3421	NN	3480
Qy	4412	TCCCAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTC	4471
Db	3481	NN	3540
Qy	4472	CCGGAGATTGGTGATCTGCCCCGCTGGTCCTGTCACCTTCCCAGTACCACAACCTACACC	4531
Db	3541	NN	3600
Qy	4532	CAGCCCCGTGGCAATTTTCATCCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGG	4591
Db	3601	NN	3660
Qy	4592	CTATCGCCCGACGCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTG	4651

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 5743)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES Location/Qualifiers

source 1. .5743

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gene <1. .>5743

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ORIGIN

Query Match 29.2%; Score 2347.4; DB 29; Length 5743;

Best Local Similarity 51.5%; Pred. No. 0;

Matches 3083; Conservative 0; Mismatches 2539; Indels 369; Gaps 6;

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Qy 161 CGACAGAAGAAGCCCACCATCTCCGTGAAGGAAGTCCCCCTTCTACACAGCGGCGCCCCTG 220

Db 61 CGGCAGAAGAAGCCCACCATCTCTGTGAAGGAAG---CTTCTACACCGCAGCACCGCTG 117

Qy 221 ACGTCTGCCGGCATCCTGCCTGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAG 280

Db 118 ACATCAGCCGGCATCCTGCCCGTCATGCAGTCGCTTTGCCCTGATGGCCAGCGTGATGAG 177

Qy 281 TTCGGCTTCCTGCAGTACGCCAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGC 340

Db 178 TTTGGCTTCCTGCAATATGCCAACTCCACNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 237

Qy 341 GTGGTGAGGAAGGCAACCTGTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAG 400

Db 238 NNN 297

Qy 401 GCCCTACGCCAGCATCTGGAGGCCCTCAGTGCGGGCCCGGGCACCTCGGGGAGCCACCTG 460

Db 298 NNN 357

Qy 461 GACAGATCCACAGTGTCTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTC 520

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Db	418	TGGCGTTTTCCTGATGCAGAACCTGTCACTGCCAACAGCACGGCCCCAAGCCCTCCTAGCT	477
Qy	581	GCCCGTGTGGACCCGCCGAGGTCTACCACCTGCTCTTGGTCCCTCATCTGCCCTGGAT	640
Db	478	GCCCGTGTGGACCTTCCGAGNNN	537
Qy	641	TCACAGTCTGGCCTCCACAAGGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTG	700
Db	538	NN	597
Qy	701	TTCCGGATGGAGGAGCTGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCG	760
Db	598	NNNNNNNNNNNNNGAGCTGCTGCTGGCTCCTGCCCTTTTGAACAGCTCACATGTGCTCCA	657
Qy	761	GGCTCGGGGGAGCTGGGCCGGATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAG	820
Db	658	GTTTCTGGGGAAGTGGGCCGGATTCTTACCATGCCTGAGGGTCATCAGGTAGACCTTCAG	717
Qy	821	GGCTACCGGGATGCTGTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGG	880
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Qy	881	CTGTCTGCTGAGCTCCGGAACCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTG	940
Db	778	TTGGCCGCTGAGCTCAGGAACCAGCTGGACACAGCCAAGATTGCTCAGCAGCTGGGCTTC	837
Qy	941	GATGCCCCCAACGGCTCGGACTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCG	1000
Db	838	GATGTCCCAACGGCTCAGATCCCCAGCCACAGGCACCGTCCCCACAGAGCCTGCCGGCA	897
Qy	1001	CTTCTGGGGGACCTGCTGGATGCCCAGAAGGTTCTGCAGGATGTGGATGTCTGTCTGGCC	1060
Db	898	CTCTTAGGGGACCTGCTGGATGCCCAGAACTTCTGCAGGATGTGGATGTCTTATCAGCC	957
Qy	1061	CTGGCCCTGCTACTGCCCCAGGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGT	1120
Db	958	CTTGCCCTGCTGCTGCCTCAAGGTGCCTGTGCTGGCCAGGCCTCTGCACCTCAAGCCAGC	1017
Qy	1121	GGTGCGGGTGGGGCGGCCAATGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACC	1180
Db	1018	AGCCTGAATGGCCTGGCCAACAGCACCGGGATAGGTGCAAATTCAGGTTCCAACACCACT	1077
Qy	1181	GCTGAGGAGGGCGCACCCCTCTGCTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAG	1240
Db	1078	GTTGAGGAGGGCACCCAGTCACCTGTCAGCCCAGCCTCTCCTGACACTCTGCAAGGGCAG	1137
Qy	1241	TGCTCAGCCTTCGTACAGCTCTGGGCGGGCCTGCAGCCCATCTTGTGTGGCAACAACCGC	1300
Db	1138	TGCTCAGCCTTTGTGCAGCTCTGGGCTGGCTTGCAACCCATCTTGTGTGGCAACAACCGN	1197
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[illegible]

Qy	2201	ACCATCCAGCACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATG	2260
Db	2088	ACCATCCAGCATATTGTGGCAGAGAAAGAGCACAGGCTCAAGGAGGTGATGAAGACCATG	2147
Qy	2261	GGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCC	2320
Db	2148	GGCCTGAACAACGCCGTGCACTGGGTGGCCTGGTTCATCACGGGCTTTGTGCAGCTGTCT	2207
Qy	2321	ATCTCCGTGACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCAC	2380
Db	2208	ATCTCCGTGACAGCTCTGACCGCCATCCTCAAGTACGGCCAGGTGCTCATGCACAGCCAC	2267
Qy	2381	GTGGTCATCATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTC	2440
Db	2268	GTGCTCATTATCTGGCTCTTCCTTGCCGTCTACGCTGTGGCCACTATCATGTTTCTGCTTC	2327
Qy	2441	CTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTAC	2500
Db	2328	CTGGTGTCTGTGCTGTACTCTAAGGCTAAGTTGGCCTCAGCCTGTGGCGGTATCATCTAC	2387
Qy	2501	TTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAG	2560
Db	2388	TTCCTGAGCTACGTTCCTACATGTATGTAGCGATCCGCGAGGAGGTAGCCCATGACAAG	2447
Qy	2561	ATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGC	2620
Db	2448	ATCACTGCCTTCGAGAAGTGCATTGCGTCCCTGATGTCCACAACAGCCTTTGGCCTGGGT	2507
Qy	2621	TCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGC	2680
Db	2508	TCCAAGTACTTTGCACTGTATGAAGTGGCAGGAGTGGGCATCCAGTGGCACACGTTTCAGC	2567
Qy	2681	CAGTCCCCGGTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTG	2740
Db	2568	CAGTCCCCAGTGGGAAGGAGATGACTTCAATCTGCTCCTTGCTGTCACCATGCTTATGGTG	2627
Qy	2741	GACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTAC	2800
Db	2628	GACACGGTGGTCTACGGCGTGCTCACTTGGTACATTGAGGCTGTGCACCCA-----	2678
Qy	2801	GGGCTGCCCCGGCCCTGGTACTTCCCACTGCAGAAGTCTACTGGCTGGGCAGTGGGCGG	2860
Db	2679	-----	2678
Qy	2861	ACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCTATGGAG	2920
Db	2679	-----	2678
Qy	2921	GAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAG	2980
Db	2679	---GACCAGGCCTGTGCCATGGAGAGCCGGCACTTCGAGGAGACCCGCGGCATGGAGGAG	2735
Qy	2981	GAGCCCAACCCACCTGCCTCTGGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGAC	3040
Db	2736	GAGCCCAACCCACCTGCCCTTGGTCGTCTGTGTGGACAAGCTCACCAAGGTCTATAAGAAT	2795

Qy	3041	GACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCTC	3100
Db	2796	GACAAGAAGATGGCCTTAAACAAACTGAGCCTCAATCTGTATGAGAATCAGGTGGTCTCTC	2855
Qy	3101	TTCTTGGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTC	3160
Db	2856	TTCTTAGGCCACAACGGGGCCGGCAAGACCACGACCATGTCGATCCTGACTGGACTGTTC	2915
Qy	3161	CCTCCAACGTCGGGTTCGCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAG	3220
Db	2916	CCACCCACGTCGGGCTCAGCCACTATCTATGGGCACGACATCCGCACCGAGATGGATGAG	2975
Qy	3221	ATCCGCAAGAACCTGGGCATGTGCCCGCAGCACAAATGTGCTCTTTGACCGGCTCACGGTG	3280
Db	2976	ATCCGCAAGAACCTGGGCATGTGCC-----	3001
Qy	3281	GAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGA	3340
Db	3002	-----	3001
Qy	3341	GAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAG	3400
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Qy	3401	ACATTGTGCGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCT	3460
Db	3020	ACGTTGTCTGGAGGCATGAAGCGCAAGCTTTCGGTAGCCATTGCCTTTGTGGGTGGCTCT	3079
Qy	3461	CGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATC	3520
Db	3080	AGAGCCATTATCTTAGACGAGCCACGGCTGGCGTGGACCCCTATGCTCGCCGTGCCATC	3139
Qy	3521	TGGGACCTCATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATG	3580
Db	3140	TGGGACCTCATCTGAAGTACAAGCCGGGCCGCACTATCCTCCTGTCTACCCATCACATG	3199
Qy	3581	GATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGC	3640
Db	3200	GATGAGGCTGACCTGCTGGGGGATCGCATTGCCATCATCTCCCATGGGAAGCTCAAATGC	3259
Qy	3641	TGCGGCTCCCCGCTCTTCCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTC	3700
Db	3260	TGTGGCTCTCCCCTCTTCCTCAAGGGAGCCTATGGCGATGGGTACCGCCTCACATTGGTC	3319
Qy	3701	AAGCGGCCCGCCGAGCCGGGGGGCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGT	3760
Db	3320	AAGCAGCCTGCAGAACCTGGCACCTCCCAAGAGCCAGGGCTGGCTTCCAGCCCCTCAGGT	3379
Qy	3761	CGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTG	3820
Db	3380	TGTCCTCGGCTGAGCAGCTGCTCGGAGCCGCAAGTGTCCAGTTCATCCGCAAGCATGTG	3439
Qy	3821	GCCTCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAG	3880
Db	3440	GCTTCCTCCCTGCTGGTCTCAGACACGAGACCGAGCTCTCCTACATCCTGCCCAGCGAG	3499
Qy	3881	GCCGCCAAGAAGGGGGCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCA	3940

Db	3500	GCCGTCAAGAAGGGGGCCTTCGAGCGCCTCTTTTCAGCAACTGGAACACAGCCTGGATGCG	3559
Qy	3941	CTGCACCTCAGCAGCTTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCCCTCAAGGTG	4000
Db	3560	CTCCATCT-----	3567
Qy	4001	TCGGAGGAGGATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGAT	4060
Db	3568	-----GATGTGAAGGAGTCCCGBAAGGAT	3591
Qy	4061	GTGCTCCCTGGGGCGGAGGGCCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCCG	4120
Db	3592	GTGCTGCCTGGGGCAGAGGGCCTGACAGCTGTGGGGGGTCAAGCTGGCAACCTGGCTCGG	3651
Qy	4121	TGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCC	4180
Db	3652	TGCTCAGAGCTGGCACAGTCACAGGCATCGCTGCAGTCTGCATCCTCTGTGGGCTCTGCC	3711
Qy	4181	CGTGGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGAT	4240
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Qy	4241	AACCCACAGGACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGG	4300
Db	3772	AACTTGCAGGACCCAGACAATGTCAGCTTACAAGNNNNNNNNNNNNNNNNNNNNNNNNNNN	3831
Qy	4301	GTCGGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGG	4360
Db	3832	NN	3891
Qy	4361	CTGCTGGTCAAACGCTTCCACTGCGCCCCGCCGCAACTCCAAGGCACTCTTCTCCAGATC	4420
Db	3892	NN	3951
Qy	4421	TTGCTGCCAGCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATT	4480
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Qy	4601	GACGCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGGGGGTGGGTGCCACC	4660
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Qy	4721	GAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAG	4780

[illegible]

[illegible]

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
 Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
 Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
 Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
 Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
 Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
 Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
 Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 22388257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 2065)
 AUTHORS Strausberg,R.
 TITLE Direct Submission
 JOURNAL Submitted (01-MAY-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Baylor College of Medicine Human Genome
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 50 Row: a Column: 5
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 15451835
 This clone has the following problem: no polyA-tail.

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ORIGIN

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 Matches 1989; Conservative 0; Mismatches 1; Indels 75; Gaps 1;

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Db	1441	 GAACCTGGGCCTCCTCGTGACCTCATGACCAGCAACCCCCAAAATCCTGTACGCGCCTGC	1500
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RESULT 5

AY405473

LOCUS AY405473 6600 bp DNA linear GSS 16-DEC-2003

DEFINITION Mus musculus ABCA1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY405473

VERSION AY405473.1 GI:39761447

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 6600)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 6600)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering

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Qy      1865  CAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAACTCC 1924
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Qy 4076 GAGGGCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCCGGTGCTCGGAGCTGACC 4135
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Qy 4196 GCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCA 4255
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Qy 4316 CGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGC 4375
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AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
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TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES Location/Qualifiers
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ORIGIN

Query Match 11.8%; Score 952.2; DB 29; Length 6606;
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Matches 2748; Conservative 0; Mismatches 2411; Indels 249; Gaps 21;

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Qy      2039 CGCGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAG 2098

Db      1621 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1680

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Qy 5336 ATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTG 5395
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Db 4705 ATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGCTCTG 4764

Qy 5396 CTGCAGGGCAC---GGATGTCTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTG 5452
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Db 4765 ATGACCACATCAGTGGATGTCCTTGTGTCCATCTGTGTCATCTTTGCAATGTCCTTCGTC 4824

Qy 5453 CCGGCCAGCTTCGTTGTCTTCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAG 5512
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Db 4825 CCAGCCAGCTTTGTCTGATTCCTGATCCAGGAGCGGGTCAGCAAAGCAAAACACCTGCAG 4884

Qy 5513 TTTGTCAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTC 5572
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Db 4885 TTCATCAGTGGAGTGAAGCCTGTCACTACTGGCTCTCTAATTTTGTCTGGGATATGTGC 4944

Qy 5573 AACTACCTGGTCCCCGCTACCTGCTGTGTCATCATCCTGTTGTGTTTCGACCTGCCGGCC 5632
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Db 4945 AATTACGTTGTCCCTGCCCACTGGTCATTATCATCTTCATCTGCTTCCAGCAGAAGTCC 5004

Qy	5633	TACACGTCGCCCACCAACTTCCCTGCCGTCCCTCTCCCTCTTCCTGCTCTATGGGTGGTCC	5692
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Qy	5693	ATCACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTG	5752
Db	5065	ATCACACCTCTCATGTACCCAGCCTCCTTGTGTTCAGATCCCCAGCACAGCCTATGTG	5124
Qy	5753	TTCCTCATTTGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTA	5812
Db	5125	GTGCTCACCAGCGTGAACCTCTTCATTGGCATTAAATGGCAGCGTGGCCACCTTTGTGCTG	5184
Qy	5813	CAGCTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTC	5872
Db	5185	GAGCTGTTC---ACCGACAATAAGCTGAATAATATCAATGATATCCTGAAGTCCGTGTTC	5241
Qy	5873	CTCATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTAC	5932
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Qy	5933	ATCAACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGG	5992
Db	5302	ATGGCTGATGCCCTGGAAAGGTTGGGGAGAATCGCTTGT---GTCACCATATCTTGG	5358
Qy	5993	GACATTGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTG	6052
Db	5359	GACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGGGTGGTGTTCCTCCTCATT	5418
Qy	6053	ACCATCATGTGCCAGTACAACCTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAG	6112
Db	5419	ACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCCAGACCTGTAAATGCAAAGCTATCT	5478
Qy	6113	CCTGTG---GAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGAC	6169
Db	5479	CCTCTGAATGATGAAGATGAAGATGTGAGGCGGGAAAGACAGAGAATTCTTGATGGTGA	5538
Qy	6170	GCCGACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATT	6229
Db	5539	GGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATATA-----TAGAAGG	5589
Qy	6230	GGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGG	6289
Db	5590	AAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCATTCTCCTGGTGAGTGCTTTGGG	5649
Qy	6290	CTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAG	6349
Db	5650	CTCCTGGGAGTTAATGGGGCTGGAAAATCATCAACTTTCAAGATGTTAACAGGAGATACC	5709
Qy	6350	AGCACGACGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAG	6409
Db	5710	ACTGTTACCAGAGGAGATGCTTTCCTTAACAANNNNNTATCTTATCAAACATCCATGAA	5769
Qy	6410	GTGCAGCAGAGCCTCGGCTACTGCCCAGTGACGCGCTGTTGACGAGCTCACGGCC	6469
Db	5770	GTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTGTTGACTGGG	5829

Qy 6470 CGGGAGCACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGG 6529
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 Db 6010 CCTGTGGTGTTTCTGGATGAACCCACCACAGGCATGGATCCCAAAGGCCCGGCGTTCTTG 6069

Qy 6710 TGGAACTCATCTCGACCTCATCAAGACAGGGCGTTCAAGTGGTGCTGACATCACACAGC 6769
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 Db 6070 TGGAAATTGTGCCCTAAGTGTGTCAAGGAGGGGAGATCAGTAGTGCTTACATCTCATAGT 6129

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 Db 6130 ATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGAAGGTTCAAG 6189

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 Db 6310 CCTGGAAGTGTCTAAAAGAGAAACACCGGAACATGCTACAATACCAGCTTCCATCTTCA 6369

Qy 7007 CACATCTCGCTGGCCCAGGTGTTCAAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATC 7066
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 Db 6370 TTATCTTCTCTGGCCAGGATATTCAGCATCCTCTCCCAGAGCAAAAAGCGACTCCACATA 6429

Qy 7067 GAGGACTACTCGGTCAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAG 7126
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 Db 6430 GAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACTTTGCCAAGGAC 6489

Qy 7127 CAGAGTGA 7134
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 Db 6490 CAAAGTGA 6497

RESULT 7

AY405472

LOCUS AY405472 6606 bp DNA linear GSS 16-DEC-2003

DEFINITION Pan troglodytes ABCA1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY405472

VERSION AY405472.1 GI:39761446

KEYWORDS GSS.

[illegible]

[illegible]

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Qy	2999	CTGGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTG	3058
Db	2509	CTGGGCGTGTCCATTGAGAACCTGGTAAAAGTCTACCGAGATGGGATGAAGGTGGCTGTN	2568
Qy	3059	AACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGG	3118
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Qy	3119	GCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTC	3178
Db	2629	GCGGGGAAGACGACCANNNGTCAATCCTGACCGGGTTGTTCCCCCGACCTCGGGCACC	2688
Qy	3179	GCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGC	3238
Db	2689	GCCTACATCCTGGGAAAAGACATTGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGG	2748
Qy	3239	ATGTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTC	3298
Db	2749	GTCTGTCCCAGCATAACGTGCTGTTTGACNNGCTGACTGTGGAAGAACACATCTGGTTC	2808
Qy	3299	TACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATC	3358
Db	2809	TATGCCCCGCTTGAAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATGGCC	2868
Qy	3359	GAGGACCTGG--AGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGC	3415
Db	2869	CTGGATGTTGGTTTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTCAGGTGGA	2928
Qy	3416	ATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTG	3475
Db	2929	ATGCAGAGAAAAGCTATCTGTGGCCTTGGCCTTTGTGCGGGGATCTAAGGTTGTCAATTCTG	2988
Qy	3476	GACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTG	3535
Db	2989	GATGAACCCACAGCTGGTGTGGACCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTG	3048
Qy	3536	AAGTACAAGCCAGGCCGCACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTG	3595
Db	3049	AAATACCGACAAGGCCGCACCATTTATTCTCTCTACACACCACATGGATGAAGCGGACATC	3108
Qy	3596	CTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTC	3655
Db	3109	CTGGGGGACAGGATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCCTG	3168
Qy	3656	TTCCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCGAG	3715
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[illegible]

[illegible]

Qy 5453 CCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAG 5512
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Qy 5513 TTTGTCAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTC 5572
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 Db 5125 GTGCTCACCAGCGTGAACCTCTTCATTGGCATTAAATGGCAGCGTGGCCACCTTTGTGCTG 5184

Qy 5813 CAGCTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTC 5872
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 Db 5185 GAGCTGTTC---ACCGACAATAAGCTGAATAATATCAATGATATCCTGAAGTCTGTGTTC 5241

Qy 5873 CTCATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTAC 5932
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Qy 5933 ATCAACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGG 5992
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Qy 6053 ACCATCATGTGCCAGTACAACCTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAG 6112
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 Db 5422 NNN 5481

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Qy 6173 GACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGC 6232
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Qy 6233 CGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCTGCGAGTGCTTCGGGCTC 6292
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 Db 5593 CGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCATTCTCCTGGTGAGTGCTTTGGGCTC 5652

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Db	5713	GTTACCNNAGGAGATGCTTTCCTTAACAANNNNNTATCTTATCAAACATCCATGAAGTA	5772
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Db	5773	CATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTGTTGACTGGGAGA	5832
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Db	5833	GAACACGTGGAGTTCCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAAGTTGGCAAGGTT	5892
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Qy	6713	AACCTCATCCTCGACCTCATCAAGACAGGGCGTTTCAAGTGGTGCTGACATCACACAGCATG	6772
Db	6073	AATTGTGCCCTAAGTGTGTCAAGGAGGGGAGATCAGTAGTGCTTACATCTCATAGTATG	6132
Qy	6773	GAGGAGTGCAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGC	6832
Db	6133	GAAGAATGTGAAGCTCTTGCACCTAGGATGGCAATCATGGTCAATGGAAGGTTGAGGTGC	6192
Qy	6833	CTGGGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGG	6892
Db	6193	CTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGGAGATGGTTATACAATAGTTGTACGA	6252
Qy	6893	A---CCAAGAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCG	6949
Db	6253	ATAGCAGGGTCCAACCCGACCTGAAGCCTGTCCAGGATTTCTTTGGACTTGCAATTCCT	6312
Qy	6950	GAAGCCATGCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCAC	7009
Db	6313	GGAAGTGTTCCTAAAAGAGAAACACCGGAACATGCTACAATACCAGCTTCCATCTTCATTA	6372
Qy	7010	ATCTCGCTGGCCAGGTGTTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAG	7069
Db	6373	TCTTCTCTGGCCAGGATATTCAGCATCCTCTCCAGAGCAAAAAGCGACTCCACATAGAA	6432
Qy	7070	GACTACTCGGTCAGCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAG	7129
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Qy	7130	AGTGA 7134	

Db 6493 AGTGA 6497

RESULT 8

BX341657

LOCUS BX341657 1045 bp mRNA linear EST 01-MAY-2003

DEFINITION BX341657 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens cDNA clone CS0DK003YD11 5-PRIME, mRNA sequence.

ACCESSION BX341657

VERSION BX341657.1 GI:30313005

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1045)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5334.f For more information about this cluster, see

<http://www.genoscope.cns.fr/>

cgi-bin/cluster.cgi?seq=CS0DK003CB06QP1&cluster=5334.f. Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DK003CB06QP1.

FEATURES	Location/Qualifiers
----------	---------------------

source

1. .1045

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/mol type="mRNA"
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/clone="CS0DK003YD11"
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/cell line="HELA"
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/clone lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 11.5%; Score 923.2; DB 13; Length 1045;

Best Local Similarity 95.3%; Pred. No. 6.5e-133;

Matches 955; Conservative 23; Mismatches 21; Indels 3; Gaps 3;

QY 907 GGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGACTCCTC 966

Db 41 GTACCGGTCCGGAATTCCCGGGATGCTGGGCCTGGATGCCCCAACGGCTCGGACTCCTC 100

QY 967 GCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGATGCCCA 1026
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Db 101 GCCACAGG-SCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGATGCCCA 159

Qy	1027	GAAGGTTCTGCAGGATGTGGATGTCTGTCTGGCCCTGGCCCTGCTACTGCCCCAGGGTGC	1086
Db	160	GAAGGTTCTGCAGGATGTGGATGTCTGTCTGGCCCTGGCCCTGCTACTGCCCCAGGGTGC	219
Qy	1087	CTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAATGGCAC	1146
Db	220	CTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAATGGCAC	279
Qy	1147	TGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTCTGCTGC	1206
Db	280	TGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTCTGCTGC	339
Qy	1207	AGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCTCTGGGC	1266
Db	340	AGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCTCTGGGC	399
Qy	1267	CGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCTGCGGCG	1326
Db	400	CGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCTGCGGCG	459
Qy	1327	GGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCTCCTCGT	1386
Db	460	GGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCTCCTCGT	519
Qy	1387	GCACCTCATGACCAGCAACCCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGTCGACCG	1446
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Qy	1447	CGTCATCCTCAAGGCCAACGAGACTTTTGGCTTTTGTGGGCAACGTGACTCACTATGCCCCA	1506
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Qy	1507	GGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCTGCAGCA	1566
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Qy	1567	ACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCCGAGGCACTGAA	1626
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Qy	1627	CCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACTTCTCGCTGCCCAGTGG	1686
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Db	760	CCTGTCAMTGGAWRAGCTGCCGCCGGCCCTGAGACARGACAAMTTCTCGCTGCCCAATGG	819
Qy	1687	CATGGCCCTCCTGCAGCAGCTGGATAACCATTGACAACGCGGCCTGCGGCTGGATCCAGTT	1746
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Qy	1747	CATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCATTGTCAA	1806
		: : : :	
Db	879	CATGTCCAAGGTGAGCGTGGACATCTTCAARGGSTTCCCCGACGAGGAGAGCATTRTMAA	938
Qy	1807	CTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGGCAGTGTGATCTTCCA	1866
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Db	939	MTAAACCCTCAAACARGCCTAMCAGGACAAMGTCACTGTTTTTKSCAGTGTGATCWTCCA	998

QY 7 CGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCTGCTGCT 66

Db	21	CGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCTGCTGCT	80
Qy	67	CTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGATCTTCAT	126
Db	81	CTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGATCTTCAT	140
Qy	127	CCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCATCTCCGT	186
Db	141	CCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCATCTCCGT	200
Qy	187	GAAGGAAGTCCCCTTCTACACAGCGGCGCCCTGACGTCTGCCGGCATCCTGCCTGTCAT	246
Db	201	GAAGGAAGTCTCCTTCTACACAGCGGCGCCCTGACGTCTGCCGGCATCCTGCCTGTCAT	260
Qy	247	GCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGCCAACTC	306
Db	261	GCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGCCAACTC	320
Qy	307	CACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCTGTTTGA	366
Db	321	CACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCTGTTTGA	380
Qy	367	CCCAGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGAGGCCCT	426
Db	381	CCCAGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGAGGCCCT	440
Qy	427	CAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTCCTTCTC	486
Db	441	CAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTCCTTCTC	500
Qy	487	TCTGGACTCGGTGGCCAGAAAACCGCAGGAGCTCTGGCGTTTCCTGACGCAAACTTGTC	546
Db	501	TCTGGACTCGGTGGCCAGAAAACCGCAGGAGCTCTGGCGTTTCCTGACGCAAACTTGTC	560
Qy	547	GCTGCCCAATAGCACGGCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCGAGGTCTA	606
Db	561	GCTGCCCAATAGCACGGCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCGAGGTCTA	620
Qy	607	CCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAAGGGTCA	666
Db	621	CCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAAGGGTCA	680
Qy	667	GGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCTGCTGGC	726
Db	681	GGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCTGCTGGC	740
Qy	727	TCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCGGATCCT	786
Db	741	TCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCGGATCCT	800
Qy	787	CACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTGCAGTGG	846
Db	801	CACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTGCAGTGG	860
Qy	847	GCAGGCTGCTGCGCGTGCCAGGCGCTTCTCT-GGGCTGTCTGCTGAGCTCCG-GAACCAG	904
Db	861	GCAGGGTGCTGCGCGTGCCAGGCGCTTCTCTGGGGCTGTCTGCTGAGCTCCGCGAACCAC	920

Qy 905 CTGGACGTGGCC-AAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCCAACGGCT--CGGAC 961
 ||| ||| |||| |||| ||||| || ||||| ||||| ||| ||| ||||
 Db 921 CTGAACGGGGCCAAAGGCCTCCCACCACCTGGGCCTGGATGCCCCCAACGGTTCGGGAC 980

Qy 962 TCCTCGCCACAGGCGCCACCCCCAC 986
 ||||| |||| | | | |||| |
 Db 981 TCCTCCCCACCAGGGGCCACCCCC 1005

RESULT 10

BX374888

LOCUS BX374888 1201 bp mRNA linear EST 08-MAY-2003

DEFINITION BX374888 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 cDNA clone CS0DC004YF05 5-PRIME, mRNA sequence.

ACCESSION BX374888

VERSION BX374888.1 GI:30448362

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1201)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 5334.f For
 more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0DC004CC03QP1&cluster=5334.f](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DC004CC03QP1&cluster=5334.f). Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DC004CC03QP1.

FEATURES

source

Location/Qualifiers

1. .1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DC004YF05"

/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 11.2%; Score 901.4; DB 13; Length 1201;

Best Local Similarity 91.9%; Pred. No. 1.6e-129;

Matches 971; Conservative 30; Mismatches 46; Indels 10; Gaps 5;

Qy 4834 CTCGCCAGCGTCCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCACCGC 4893

Db	65	CTCGCCAGCGTCCCCGGATGAGGACCTGCAGGCCTGGRACGTCTCCCTGCCGCCACCGC	124
Qy	4894	TGGGCCAGAAATGTGGACGTCGGCACCCCTCCCTGCCCGCGCCTGGTACGGGAGCCCGTCCG	4953
Db	125	TGGGCCAGAAATGTGGACGTCGGCACCCCTCCCTGCCCGCGCCTGGTACGGGAGCCCGTCCG	184
Qy	4954	CTGCACCTGCTCTGCGCAGGGCACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCC	5013
Db	185	CTGCACCTGCTCTGCGCAGGGCACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCC	244
Qy	5014	GCCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTC	5073
Db	245	G-CCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTC	303
Qy	5074	TGAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTT	5133
Db	304	TKAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGSCATCACCTT	363
Qy	5134	TGGAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCG	5193
Db	364	TGGRAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCG	423
Qy	5194	GAAGATCGCGGTGCGCAGGGCTGCCAGGTTTTCTACAACAACAAGGGCTATCACAGCAT	5253
Db	424	GAAGATCGCGGKGCGCAGGGSTGCCAGGTTTTCTACAACAACAAGGGSTATCACAGCAT	483
Qy	5254	GCCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACCTGCCAAGAGCAA	5313
Db	484	GCCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACCTGCCAAGAGCAA	543
Qy	5314	GGGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGC	5373
Db	544	GGGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGC	603
Qy	5374	CAGCCTCTCCCTGGATTACCTGCTGCAGGGCACGGATGTCGTCATCGCCATCTTCATCAT	5433
Db	604	CCASCTCTCCCTGGATTACCTGCTGCAGGGCACGGRTGTGTGTCATCGCCATCTTCATCAT	663
Qy	5434	CGTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCAC	5493
Db	664	CGTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCAC	723
Qy	5494	CAAGGCCAAGCATCTGCAGTTTGTGAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAA	5553
Db	724	CAAGGCCAAGCACCTGCAGTTTGTGAGCGGCTGCRACCCCATCATCTACTGGCTGGCGAA	783
Qy	5554	CTACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCTGCTGTGTATCATCCTGTT	5613
Db	784	CTACGTGTGGGACAWGCTCAACTACCTGGTCCCCGCTACCTGCTGTGTATCATCCTGTT	843
Qy	5614	TGTGTTTCGACCTGCCGGCCTACACGTCGCCCCACCAACTTCCCTGCCGTCTCTCCCTCTT	5673
Db	844	TGTGTTTCGACCTGCCGGCCTACACGTCGCCCCACCAACTTCCCTGCCGTCTCTCCCTCTT	903
Qy	5674	CCTGCTCTATGGGTGGTCCATCACGCCCCATCATGTACCCGGCCTCCTTCTGGTTTCGAGGT	5733

Db 904 TTTTCTYTATGGGTGG-GCAWCACGCCCATCAWGTACCCGGCCTCCYTCTGGKTCGAGGT 962

QY 5734 CCCCAGCTCCGCCTACGTGTTTCCTCATTGTGCATCAATCTCTTCATCGGCATCACCGCCAC 5793
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Db 963 CCCCAGCTCCGCCTACGTGTTTCCTCATTGTGCATCAATCTCTTCATCGGSATCACCG-CAC 1021

QY 5794 CGTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAG 5853
 |||||||||:||||:|: || :| || | | ||||||| :| :|

Db 1022 CGTGGCCACYTTTCYKGYACAGMCTTCGASACGAC----AAGGACTGAAGGTGKTAMA--- 1074

QY 5854 TTACCTGAAAAGCTGCTTCCTCATTTTCCCAACTAC 5890
 | |||||||||:||||| ||| || : || :|

Db 1075 GTGACTGAAAAGCKGCTTCTCATTTTCCAMTACAMC 1111

RESULT 11
 AL525194

LOCUS AL525194 964 bp mRNA linear EST 22-MAY-2003

DEFINITION AL525194 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 cDNA clone CS0DC005YF02 5-PRIME, mRNA sequence.

ACCESSION AL525194

VERSION AL525194.2 GI:31043449

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 964)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 13, 2001 this sequence version replaced gi:12788687.
 Contact: Genoscope

Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5334.f For
 more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0DC005DC01QP1&cluster=5334.f](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DC005DC01QP1&cluster=5334.f). Contact :
 Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DC005DC01QP1.

FEATURES

source

Location/Qualifiers

1. .964

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DC005YF02"

/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 11.2%; Score 900.4; DB 9; Length 964;
Best Local Similarity 99.2%; Pred. No. 2.2e-129;
Matches 915; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy	5784	TCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGGACCTGAAGG	5843
Db	44		
	44	TCCCGGGATCCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGGACCTGAAGG	103
Qy	5844	TTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTGGGCCACG	5903
Db	104		
	104	TTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTGGGCCACG	163
Qy	5904	GGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATTGGCCAGT	5963
Db	164		
	164	GGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATTGGCCAGT	223
Qy	5964	TTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGGTGGCCATGG	6023
Db	224		
	224	TTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGGTGGCCATGG	283
Qy	6024	CGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTTCCTGCGGC	6083
Db	284		
	284	CGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTTCCTGCGGC	343
Qy	6084	GGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTGGCCAGTG	6143
Db	344		
	344	GGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTGGCCAGTG	403
Qy	6144	AGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAGAACCTGA	6203
Db	404		
	404	AGCGGCAGCAAGTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAGAACCTGA	463
Qy	6204	CCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGG	6263
Db	464		
	464	CCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGG	523
Qy	6264	GTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCA	6323
Db	524		
	524	GTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCA	583
Qy	6324	CCTTCAAGATGCTGACCGGCACGAGAGCACGACGGGGGGCGAGGCCTTCGTCAATGGAC	6383
Db	584		
	584	CCTTCAAGATGCTGACCGGCACGAGAGCACGACGGGGGGCGAGGCCTTCGTCAATGGAC	643
Qy	6384	ACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCGAGTGTG	6443
Db	644		
	644	ACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCGAGTGTG	703
Qy	6444	ACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCTGCAGCTGTACACGCGGCTGCGTG	6503
Db	704		
	704	ACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCTGCAGCTGTACACGCGGCTGCGTG	763
Qy	6504	GGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGA	6563
Db	764		
	764	GGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGA	823

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Qy      6564 CCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCA 6623
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Db      824 CCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAA-CTCTCCA 882

Qy      6624 CGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCACCACAGGCA 6683
          |||||||||||||||||||||||||||||||||||||||||||||||
Db      883 CGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCACCACAGGCA 942

Qy      6684 TGGACCCCAAGGCCCGGCGCTT 6705
          ||||||||||||||||||
Db      943 TGGACCCCAAGGCCCGGCGCTT 964

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RESULT 12

AL525193/c

LOCUS AL525193 958 bp mRNA linear EST 22-MAY-2003

DEFINITION AL525193 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DC005YF02 3-PRIME, mRNA sequence.

ACCESSION AL525193

VERSION AL525193.2 GI:31043448

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 958)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 13, 2001 this sequence version replaced gi:12788686.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5334.f For more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0DC005DC01NP1&cluster=5334.f](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DC005DC01NP1&cluster=5334.f). Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DC005DC01NP1.

FEATURES

source

Location/Qualifiers

1. .958

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DC005YF02"

/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match

11.1%; Score 893.2; DB 9; Length 958;

Best Local Similarity 97.9%; Pred. No. 2.8e-128;
Matches 923; Conservative 12; Mismatches 5; Indels 3; Gaps 3;

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Qy      7050 CTGGCGTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACACTGGACAATGTGTTCG 7109
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Db      958 YTGGCGTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACACTGGACAATGTGTTCG 899

Qy      7110 TGAACTTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGCCGCCATCCG 7169
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      898 TGAACTTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGCCGCCATCCG 839

Qy      7170 CACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGG 7229
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      838 CACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGG 779

Qy      7230 AGCTCCGGGCACTTGTGGCAGACGAGCCCGAGGACCTGGACACGGAGGACGAGGGCCTCA 7289
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      778 AGCTCCGGGCACTTGTGGCAGACGAGCCCGAGGACCTGGACACGGAGGACGAGGGCCTCA 719

Qy      7290 TCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCCTTCAACACGGACACGCTCTGCTGACCAC 7349
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      718 TCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCCTTCAACACGGACACGCTCTGCTGACCAC 659

Qy      7350 CCAGAGCTGGGCCAGGGAGGACACGCTCCACTGACCACCCAGAGCTGGGCCAGGGACTCA 7409
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      658 CCAGAGCTGGGCCAGGGAGGACACGCTCCACTGACCACCCAGAGCTGGGCCAGGGACTCA 599

Qy      7410 ACAATGGGGACAGAAGTCCCCCAGTGCCTGCCAGGGCCTGGAGTGGAGGTTCAGGACCAA 7469
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      598 ACAATGGGGACAGAAGTCCCCCAGTGCCTGCCAGGGCCTGGAGTGGAGGTTCAGGACCAA 539

Qy      7470 GGGGCTTCTGGTCCTCCAGCCCCGTACTCGGCCATGCCCTGCGGTCACTGCGGTTGCCG 7529
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Db      538 GGGGCTTCTGGTCCTCCAGCCCCGTACTCGGCCATGCCCTGCGGTCACTGCGGTTGCCG 479

Qy      7530 CCCCTAATTGTGCCAAAGGCTGACCCGGCCCCGGGCTGCGTACACCCTTGCCCTGCTTTGC 7589
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      478 CCCCTAATTGTGCCAAAGGCTGACCCGGCCCCGGGCTGCGTACACCCTTGCCCTGCTTTGC 419

Qy      7590 CTTAAAGCCTCGGGGTCTGCCCCGGCCCCCTCGCCCCCTGCCTGGCACTGCTCACCGCCCAAG 7649
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      418 CTTAAAGCCTCGGGGTCTGCCCCGGCCCCCTCGCCCCCTGCCTGGCACTGCTCACCGCCCAAG 359

Qy      7650 GCGACGCCGGCTGGACCAGGCACTGCTGGCCTTTCTCCTGCCCGGCCTCGGAACCAGCTT 7709
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      358 GCGACGCCGGCTGGACCAGGCACTGCTGGCCTTTCTCCTGCCCGGCCTCGGAACCAGCTT 299

Qy      7710 TTCTCTCTTACGATGAAGGCTGATGCCGAGAGCGGGCTGTGGGCGGAGCTGGGTCACTCC 7769
          ||||:||||||||||||||||||||||||||||||||||||||||||:|||
Db      298 TTCTHTCTTACGATGAAGGCTGATGCCGAGAGCGGGCTGTGGGCGGAGCTGGGTCACTCC 239

Qy      7770 CGTATTTATTTTGCTTTGAGAAGAGGCTCCTCTGGCCCTGCTCTCCTGCAGGGAGGTGGC 7829
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      238 CGTATTTATTTTGCTTTGAGAAGAGGCTCCTCTGGCCCTGCTCTCCTGCAGGGAGGTGGC 179

Qy      7830 TGTCCCGCGGGAAGCCATCAGCTTGGGCCAGCTGGCAGGTGGCAGGAATGGAGAAGCTGA 7889
          ||| | |||||||||||||||||||||:|||||||||||||||||||
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Db 178 TGT-CTGCGGGAAGCCATCAGCTTGGGCCARCTGGCAGGTGGCAGGAATGGAGAAGCTGA 120

Qy 7890 CCCTGCTGGCCAGGCAAGGGGCCAGACC-CCCCCAACCCCCAGCTGCCATCGCTCTCCC 7948
 ||||| ||||||||||||||||:||||| |||||||||||||||||||||

Db 119 CCCTGNTGGCCAGGCAAGGGGCSAGACCGCCCCCAACCCCCAGCTGCCATCGCTCTCCC 60

Qy 7949 ACCCAGCTTGGCCCCCTGCCCCGCCACCTCCCTGGGAGCCGGG 7991
 |||||||| |||||||||| ||:||||||| |||:::|

Db 59 ACCCAGCTT-GCCCCCTGCCACCMACCTCCCTTGGADMMDK 18

RESULT 13

AL540221/c

LOCUS AL540221 1201 bp mRNA linear EST 31-MAY-2003

DEFINITION AL540221 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 CS0DF032Y004 3-PRIME, mRNA sequence.

ACCESSION AL540221

VERSION AL540221.2 GI:31264782

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1201)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 15, 2001 this sequence version replaced gi:12870176.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 5334.f For more information about this cluster, see

<http://www.genoscope.cns.fr/>

cgi-bin/cluster.cgi?seq=CS0DF032BH02NP1&cluster=5334.f. Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DF032BH02NP1.

FEATURES

source

Location/Qualifiers

1. .1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DF032Y004"

/tissue_type="FETAL BRAIN"

/dev_stage="fetal"

/clone_lib="Homo sapiens FETAL BRAIN"

/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Query Match

11.0%; Score 886.2; DB 9; Length 1201;

Matches 959; Conservative 16; Mismatches 25; Indels 8; Gaps 6;

Qy	7006	GCACATCTCGCTGGCCCAGGTGTTTCAGCAAGATGGAGCAGGTGCTCTGGCGTGCTGGGCAT	7065
Db	1003	GSACACATTTGGTTGCCAGGTTTCASCMAGATGGAGCAGGTGTYTGGCGTG-TTGGCAT	945
Qy	7066	CGAGGACTACTCGGTTCAGCCAGACCACACTGGACAATGTGTTCGTGAACCTTTGCCAAGAA	7125
Db	944	SGAGGACTACTC-GTCAGCCAGACCACACTGGACAATGTGTTCGT-AACTTTGCCAAGAA	887
Qy	7126	GCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCT	7185
Db	886	GCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCT	827
Qy	7186	CGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGT	7245
Db	826	CGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGT	767
Qy	7246	GGCAGACGAGCCCGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGA	7305
Db	766	GGCAGACGAGCCCGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGA	707
Qy	7306	GCGGGCCCCAGCTGTCTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGGCCAGG	7365
Db	706	GCGGGCCCCAGCTGTCTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGGCCAGG	647
Qy	7366	GAGGACACGCTCCACTGACCACCCAGAGCTGGGGCCAGGGACTCAACAATGGGGACAGAAG	7425
Db	646	GAGGACACGCTCCACTGACCACCCAGAGCTGGGGCCAGGGACTCAACAATGGGRACAGAAG	587
Qy	7426	TCCCCCAGTGCCTGCCAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTC	7485
Db	586	TCCCCCAGTGCCTGCCAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGRGCTTCTGGTCCTC	527
Qy	7486	CAGCCCCCTGTACTCGGCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAA	7545
Db	526	CAGCCCCCTGTACTCGGCCATG-CCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAA	468
Qy	7546	AGGCTGACCCGGCCCCGGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGT	7605
Db	467	AGGCTGACCCGGCCCCGGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGT	408
Qy	7606	CTGCCCCGGCCCCCTCGCCCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGAC	7665
Db	407	CTGCCCCGGCCCCCTCGCCCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGAC	348
Qy	7666	CAGGCACTGCTGGCCTTTCTCCTGCCCGGCTCGGAACCAAGCTTTTCTCTCTTACGATGA	7725
Db	347	CAGGCACTGCTGSCCTTTCTCCTSCCGGCTCGGAACCAAGCTTTTCTCTCTTACGATGA	288
Qy	7726	AGGCTGATGCCGAGAGCGGGCTGTGGGCGGAGCTGGGTCACTCCCGTATTTATTTTGCTT	7785
Db	287	AGGCTGATGCCGAGAGCGGGCTGTGGGCGGAGCTGGGTCACTCCCGTATTTATTTTGCTT	228
Qy	7786	TGAGAAGAGGCTCCTCTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCC	7845

Db 227 TGAGAAGAGGCTCCTCTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCC 168

Qy 7846 ATCAGCTTGGGCCAGCTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCA 7905
 |||

Db 167 ATCAGCTTGGGCCAGCTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCA 108

Qy 7906 AGGGGCCAGACCCCCCCCCAACCCCCAGCTGCCAT---CGCTCTCCACCCAGCTTGGCCC 7962
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Db 107 AGGGCCCMCCCCCCCCAACCCCMGCTGCCANTCGCTCTCCMCCCACGCTCTSSCCC 48

Qy 7963 CCTGCCCCGCCACCTCCCTGGGAGCCGGGCCTGTACATAGCGCACAGA 8010
 |||

Db 47 CCTGCCCCGCCACCTCCCTGGGAGCC-GGCSTGTACATAGCGCACAGA 1

RESULT 14

BX420933

LOCUS BX420933 1082 bp mRNA linear EST 13-MAY-2003

DEFINITION BX420933 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 CS0DF036YI11 5-PRIME, mRNA sequence.

ACCESSION BX420933

VERSION BX420933.1 GI:30638255

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1082)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 5334.f For
 more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0DF036AE06QP1&cluster=5334.f](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF036AE06QP1&cluster=5334.f). Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DF036AE06QP1.

FEATURES

source

Location/Qualifiers

1. .1082

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DF036YI11"

/tissue_type="FETAL BRAIN"

/dev_stage="fetal"

/clone_lib="Homo sapiens FETAL BRAIN"

/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Query Match 10.9%; Score 873.2; DB 13; Length 1082;
 Best Local Similarity 95.6%; Pred. No. 3.7e-125;
 Matches 937; Conservative 21; Mismatches 14; Indels 8; Gaps 6;

Qy	1	CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT	60
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Db	108	CCGCGGCGCTGAGGARGCGGA-CGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT	166
Qy	61	GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGAT	120
Db	167	GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGAT	226
Qy	121	CTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT	180
		:	
Db	227	CTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGARGCCCACCAT	286
Qy	181	CTCCGTGAAGGAAGTCCCCCTTCTACACAGCGGCGCCCCCTGACGTCTGCCGGCATCCTGCC	240
Db	287	CTCCGTGAAGGAAG---CCTTCTACACAGCGGCGCCCCCTGACGTCTGCCGGCATCCTGCC	343
Qy	241	TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGC	300
		:	
Db	344	TGTAATGCAATCGCTGTGCCCCGACGGCCAGCRAGACGAGTTCGGCTTCCTGCAGTACGC	403
Qy	301	CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT	360
Db	404	CAACTCCACGGTCACGCAGCTGCTTGAACGCCTGGACCGCGTGGTGGAGGAAGGCAACCT	463
Qy	361	GTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA	420
		:	
Db	464	GTTTAACCCAGCGCGGCCAGCCTGGGCTCAAAGCTCGARGCCCTACGCCAGCATCTGGA	523
Qy	421	GGCCCTCAGTGCGGGCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC	480
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Db	524	GGCCCTCAATRCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC	583
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Db	584	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCA-GAGCTCTGGCGTTTCCTGACGCAAAA	642
Qy	541	CTTGTCGCTGCCCAATAGCACGGCCCAAGCACTCTTGCCGCCCCGTGTGGACCCGCCCGA	600
		:	
Db	643	MTTGTCGCTGCCCAATAGCACGGCCCAAGCACTCTTGCCGCCCCGTATGGACCCGCCCGA	702
Qy	601	GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	660
		: :	
Db	703	AGTCTACCACCTGCWCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	762
Qy	661	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	720
		:	
Db	763	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTWCCGGATGGAGGAGCTGCT	822
Qy	721	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	780
		:	
Db	823	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGGGCTGGGSCG	882

Qy 781 GATCCTCACTGTGCCTG-AGAGTCAGAAGGGAGCCCTGCAGGGCTA-CCGGGATGCTGTC 838
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 Db 883 GAWCCTCACTGTGCCTGAAAAATMARAAGGRAGCCCTGCAGGGCTACCCGGRATGCTGTC 942
 Qy 839 TGCAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGG 898
 ||||||||||||||||:||||||||||||||:|||||||||||||||
 Db 943 TGCAGTGGGCAGGCTGCTGCRCGTGCCAGGCGCTTCTCTRGGCTGTCTGCTGAGCTCCGG 1002
 Qy 899 AACCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCG 958
 ||||||||:|||||||||||:| ||||||| |||||||||
 Db 1003 AACCAGCTGGRCGTGGCCAAGGTCTCCMM-CAGCTGGGGCTGGATGCCCCAACGGCTCG 1061
 Qy 959 GACTCCTCGCCACAGGCGCC 978
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 Db 1062 GACTCCTCGCMACAAGGGCC 1081

RESULT 15

BX376831

LOCUS BX376831 1201 bp mRNA linear EST 08-MAY-2003

DEFINITION BX376831 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens cDNA clone CS0DD006YF01 5-PRIME, mRNA sequence.

ACCESSION BX376831

VERSION BX376831.1 GI:30458506

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1201)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5334.f For more information about this cluster, see

[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DD006CC01QP1&cluster=5334.f)

[cgi-bin/cluster.cgi?seq=CS0DD006CC01QP1&cluster=5334.f](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DD006CC01QP1&cluster=5334.f). Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DD006CC01QP1.

FEATURES

source

Location/Qualifiers

1. .1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DD006YF01"

/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 10.6%; Score 854; DB 13; Length 1201;
Best Local Similarity 84.3%; Pred. No. 3.7e-122;
Matches 959; Conservative 90; Mismatches 76; Indels 12; Gaps 10;

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Qy      1 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 60
          |||
Db      67 CCGCGGCGCTGAGGCGGCGGA-SGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCCGCT 125

Qy      61 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGAT 120
          |||
Db     126 GCTGCTCTGGMAGMVCCTGACGCTCAMACGCCGGAGCCCGTGGGTCTTGGCCTTCGCGMT 185

Qy     121 CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 180
          |||
Db     186 CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGACAGAAGCCCACCAT 245

Qy     181 CTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCTGACGTCTGCCGGCATCCTGCC 240
          |||
Db     246 CTCCGTGAAGGAAG---CCTTCTACACAGCGGCGCCCTGACGTCTGCCGGCATCCTGCC 302

Qy     241 TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGC 300
          |||
Db     303 TGTCATGCCATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTCGGCTTCCTGCCGTCCGC 362

Qy     301 CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCA-ACC 359
          |||
Db     363 CAACCCACGGTCACGCCGCCGCTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCACACC 422

Qy     360 TGTTTGACCCA-GCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTG 418
          |||
Db     423 TGTTTGACCCACGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGMATCTG 482

Qy     419 GAGGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCT 478
          |||
Db     483 GAGGCCCTCAGTGCGGGCCCCGGGCACCTMGGGGAGCCACCTGGACAGATTACAGTKTYT 542

Qy     479 TCCTTCTCTCTGGACTCGGTGGCCAGAAACCCGAGGAGCTCTGGCGTTTCCTGACGCAA 538
          |||
Db     543 TCCTTCTCTCTGGACTYGGTGGCCAGAAACCCGCA-GAGCACTRGCGTTTCCTGACGCAA 601

Qy     539 AACTTGTGCTGCCAATAGCACGGCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCC 598
          |||
Db     602 AAMTTGTGCGWCMCAATAGCACGGCCCAAGCACTCTTGCCCGCMCGTDTGGACCCGCCC 661

Qy     599 GAGGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCAC 658
          |||
Db     662 GAGGTCTAMMACCTGCTCTTTGGTCCCTCATCTGCMCTGGATTYACAGTYTGRCTCCAC 721

Qy     659 -AAGGGTCAGGAGCCCTGGAGCCGCTA-GGGGGCAATCCCCTGTTCCGGATGGAGGAGC 716
          |||
Db     722 AAAGGGTYAGGAGCCCTGGAGCCGCTWGGGGGGCAATCCCCTKTTCCGGATGGAGGAGC 781

Qy     717 TGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGG 776
          |||
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Db	782	AGCTGMWGGMTCCCTGCCCCACCTGGAGCAGCACACCTGCAMGCCGGGCGWCGGGGGGAGMWGG	841
Qy	777	GCCGGATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCT-ACCGGGATGCT	835
		: : : :	
Db	842	GCCGRATYCTCACTGTCCTTARAATTAGAAGGGAGCCCTGCAGGGCTWACCGGGATGCT	901
Qy	836	GTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTC	895
		: :	
Db	902	GTTTKCAGTTRGCAGGCTGCTGCGCGTTCCAGRCGCTTTTWTGGCTKWTTTMYGAGCCC	961
Qy	896	CGGAACCAGCTGGACGTGGCCAAGGTCTCCAGCAGCTGGGCCTGGATGCCCCCAACGGC	955
Db	962	CGGAACCAGCTGGACGTGKCCAAGGTCTYCCAGCAGCCGGGCCTTGAWTKCCCCAAMGGG	1021
Qy	956	TCGGACTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTG	1015
		: : : :	
Db	1022	TYGGAMTTCTYGCMAAGG-GCCCAMCCCMCGGRGGCTGCRGGGSYTTTKGGGGACYTC	1080
Qy	1016	CTGGATGCCCAGAAGGTCTGCAGGATGTGGATGTCCTGTGCGCCCTGGCCCTGCTACTG	1075
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Db	1081	YTGGAAMAAAAAGATTTTAAAGRAWWATGRWTTYTTTTGGCCCTKSCCYT-CTWCWT	1139
Qy	1076	CCCCAGGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGG	1132
Db	1140	CCCCARGGKNCYTTCCYTKSCCGACCCCCGDYTYCMMCMATTTKTVGGRDGGGGGS	1196

Search completed: September 8, 2004, 18:14:43
Job time : 17497 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 8, 2004, 02:25:51 ; Search time 29577 Seconds
(without alignments)
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Title: US-10-088-467-1
Perfect score: 8040
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: gb_ov:*
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7: gb_ph:*
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9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
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20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
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25: em_pl:*
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27: em_sts:*

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 34: em_htg_pln:*
 35: em_htg_rod:*
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 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
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 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	8040	100.0	8056	6	AX522071	AX522071 Sequence
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3	8036.4	100.0	8269	6	BD140900	BD140900 Human and
4	8036.4	100.0	8269	6	BD140901	BD140901 Human and
5	8032	99.9	8195	6	AX235951	AX235951 Sequence
6	7529.2	93.6	7610	6	AX405561	AX405561 Sequence
7	7482	93.1	7482	9	AF327657	AF327657 Homo sapi
8	7301.8	90.8	7305	6	AX235953	AX235953 Sequence
9	6686.8	83.2	6792	6	AX088337	AX088337 Sequence
10	6011	74.8	6011	9	AB028985	AB028985 Homo sapi
11	5915.4	73.6	6006	6	AX088339	AX088339 Sequence
12	5810	72.3	8040	6	BD140902	BD140902 Human and
13	5810	72.3	8040	6	BD140903	BD140903 Human and
14	5810	72.3	8040	10	AB037937	AB037937 Rattus no
15	5636.2	70.1	7629	10	MMABC2	X75927 Mus musculu
16	5536.8	68.9	5540	6	AX709974	AX709974 Sequence
17	3438.2	42.8	4914	10	AK129274	AK129274 Mus muscu
18	3299.4	41.0	3320	9	BC008755	BC008755 Homo sapi
19	3223	40.1	3327	9	HSM805201	AL833967 Homo sapi
20	1819	22.6	1836	9	HSM802591	AL162060 Homo sapi
21	1009	12.5	7878	10	MMABC1	X75926 Mus musculu
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23	991.4	12.3	7323	6	BD234203	BD234203 ATP-bindi
24	991.4	12.3	7323	9	HSAF000148	AF000148 Homo sapi
25	986.6	12.3	6786	9	AB055982	AB055982 Homo sapi
26	986.6	12.3	7860	6	AR393480	AR393480 Sequence
27	986.6	12.3	7860	6	AX092594	AX092594 Sequence
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29	986.4	12.3	6880	6	AX253450	AX253450 Sequence
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34	986.4	12.3	9741	6	AX127830	AX127830 Sequence
35	986.4	12.3	9741	6	AX139817	AX139817 Sequence
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38	986.4	12.3	9854	6	AX139818	AX139818 Sequence
39	985.6	12.3	9593	6	AX059976	AX059976 Sequence
40	985	12.3	10442	6	AX060713	AX060713 Sequence
41	985	12.3	10442	6	AX060892	AX060892 Sequence
42	985	12.3	10442	9	AF285167	AF285167 Homo sapi
43	985	12.3	10474	6	AX060721	AX060721 Sequence
44	985	12.3	10474	6	AX060900	AX060900 Sequence
45	983.4	12.2	10474	6	AX060719	AX060719 Sequence

ALIGNMENTS

RESULT 1

AX522071

LOCUS AX522071 8056 bp DNA linear PAT 24-OCT-2002

DEFINITION Sequence 3 from Patent WO02064781.

ACCESSION AX522071

VERSION AX522071.1 GI:24410961

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Reiner,P.B., Connop,B.P. and Pollard,M.

TITLE Regulation of amyloid precursor protein expression by modification
of abc transporter expression or activity

JOURNAL Patent: WO 02064781-A 3 22-AUG-2002;
Active Pass Pharmaceuticals, Inc. (CA)

FEATURES

source

Location/Qualifiers

1. .8056

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 8040; DB 6; Length 8056;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 8040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT	60
Db	17	CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT	76
QY	61	GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGAT	120
Db	77	GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGAT	136
QY	121	CTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT	180
Db	137	CTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT	196

Qy	181	CTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCCTGACGTCTGCCGGCATCCTGCC	240
Db	197	CTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCCTGACGTCTGCCGGCATCCTGCC	256
Qy	241	TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGC	300
Db	257	TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGC	316
Qy	301	CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT	360
Db	317	CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT	376
Qy	361	GTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA	420
Db	377	GTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA	436
Qy	421	GGCCCTCAGTGCGGGCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC	480
Db	437	GGCCCTCAGTGCGGGCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC	496
Qy	481	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA	540
Db	497	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA	556
Qy	541	CTTGTCGCTGCCCAATAGCACGGCCCAAGCACTCTTGCCGCCCCGTGTGGACCCGCCCGA	600
Db	557	CTTGTCGCTGCCCAATAGCACGGCCCAAGCACTCTTGCCGCCCCGTGTGGACCCGCCCGA	616
Qy	601	GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	660
Db	617	GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	676
Qy	661	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	720
Db	677	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	736
Qy	721	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	780
Db	737	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	796
Qy	781	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	840
Db	797	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	856
Qy	841	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	900
Db	857	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	916
Qy	901	CCAGCTGGACGTGGCCAAGGTCTCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	960
Db	917	CCAGCTGGACGTGGCCAAGGTCTCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	976
Qy	961	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1020
Db	977	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1036
Qy	1021	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGGCCCTGGCCCTGCTACTGCCCCA	1080

Db	1037	 TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTCGGCCCTGGCCCTGCTACTGCCCCA	1096
Qy	1081	GGGTGCCTGCACTGGCCGGACCCCGGACCCCAAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Db	1097	GGGTGCCTGCACTGGCCGGACCCCGGACCCCAAGCCAGTGGTGCGGGTGGGGCGGCCAA	1156
Qy	1141	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCTC	1200
Db	1157	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCTC	1216
Qy	1201	TGCTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
Db	1217	TGCTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1276
Qy	1261	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTAACCCGAGGCGCT	1320
Db	1277	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTAACCCGAGGCGCT	1336
Qy	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380
Db	1337	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1396
Qy	1381	CCTCGTGCACCTCATGACCAGCAACCCCAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
Db	1397	CCTCGTGCACCTCATGACCAGCAACCCCAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1456
Qy	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1500
Db	1457	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1516
Qy	1501	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1517	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1576
Qy	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620
Db	1577	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1636
Qy	1621	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1680
Db	1637	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1696
Qy	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATAACCATTGACAACGCGGCCTGCGGCTGGAT	1740
Db	1697	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATAACCATTGACAACGCGGCCTGCGGCTGGAT	1756
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1800
Db	1757	CCAGTTCATGTCCAAGGTGAGCGTGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1816
Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1860
Db	1817	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1876
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1920

Db	1877	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1936
Qy	1921	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1980
Db	1937	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1996
Qy	1981	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Db	1997	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2056
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Db	2057	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2116
Qy	2101	GTTCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2160
Db	2117	GTTCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2176
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Db	2177	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2236
Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280
Db	2237	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2296
Qy	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2340
Db	2297	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2356
Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2400
Db	2357	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2416
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2460
Db	2417	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2476
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Db	2477	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2536
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
Db	2537	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2596
Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640
Db	2597	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2656
Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2700
Db	2657	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2716
Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760
Db	2717	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2776

Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2777	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2836
Qy	2821	CTTCCCCTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2837	CTTCCCCTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2896
Qy	2881	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCTATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2897	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCTATGGAGGAGGACCAGGCCTGTGCCAT	2956
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3000
Db	2957	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3016
Qy	3001	GGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3017	GGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3076
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3077	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3136
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCG	3180
Db	3137	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCG	3196
Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3197	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3256
Qy	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3257	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3316
Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3317	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3376
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3420
Db	3377	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3436
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3480
Db	3437	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3496
Qy	3481	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3540
Db	3497	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3556
Qy	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3557	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3616

Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3617	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3676
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3720
Db	3677	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3736
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTG	3780
Db	3737	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTG	3796
Qy	3781	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3797	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3856
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3857	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3916
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3917	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3976
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTTCCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4020
Db	3977	GCTGATGGACACGACCCTGGAGGAAGTGTTTCCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4036
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4037	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4096
Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4097	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4156
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4200
Db	4157	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4216
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4217	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4276
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAA	4320
Db	4277	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAA	4336
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4337	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4396
Qy	4381	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4397	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4456
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500

Db	4457	 CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4516
Qy	4501	CCTGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4517	 CCTGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4576
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCT	4620
Db	4577	 CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCT	4636
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4637	 CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4696
Qy	4681	CAACGGCTCGCTGGGGCCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4697	 CAACGGCTCGCTGGGGCCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4756
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4757	 TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4816
Qy	4801	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4860
Db	4817	 CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4876
Qy	4861	GCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCGGCACC	4920
Db	4877	 GCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCGGCACC	4936
Qy	4921	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	4980
Db	4937	 CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	4996
Qy	4981	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5040
Db	4997	 CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5056
Qy	5041	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5100
Db	5057	 CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5116
Qy	5101	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5160
Db	5117	 CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5176
Qy	5161	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCCA	5220
Db	5177	 CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCCA	5236
Qy	5221	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5280
Db	5237	 GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5296
Qy	5281	CGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5340

Db	5297	CGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5356
Qy	5341	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5400
Db	5357	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5416
Qy	5401	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5460
Db	5417	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5476
Qy	5461	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAG	5520
Db	5477	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAG	5536
Qy	5521	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5580
Db	5537	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5596
Qy	5581	GGTCCCCGCTACCTGCTGTGTATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTC	5640
Db	5597	GGTCCCCGCTACCTGCTGTGTATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTC	5656
Qy	5641	GCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCC	5700
Db	5657	GCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCC	5716
Qy	5701	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCTCAT	5760
Db	5717	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCTCAT	5776
Qy	5761	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5820
Db	5777	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5836
Qy	5821	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5880
Db	5837	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5896
Qy	5881	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5940
Db	5897	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5956
Qy	5941	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGGGACATTGT	6000
Db	5957	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGGGACATTGT	6016
Qy	6001	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6060
Db	6017	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6076
Qy	6061	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6120
Db	6077	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6136
Qy	6121	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6180
Db	6137	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6196

Qy	6181	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6240
Db	6197	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6256
Qy	6241	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCCT	6300
Db	6257	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCCT	6316
Qy	6301	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6360
Db	6317	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6376
Qy	6361	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6420
Db	6377	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6436
Qy	6421	CCTCGGCTACTGCCCCGAGTGACGCGCTGTTGACGAGCTCACGGCCCGGGAGCACCT	6480
Db	6437	CCTCGGCTACTGCCCCGAGTGACGCGCTGTTGACGAGCTCACGGCCCGGGAGCACCT	6496
Qy	6481	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6540
Db	6497	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6556
Qy	6541	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6600
Db	6557	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6616
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Qy	6661	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6720
Db	6677	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6736
Qy	6721	CCTCGACCTCATCAAGACAGGGCGTTTCAAGTGGTGTGACATCACACAGCATGGAGGAGTG	6780
Db	6737	CCTCGACCTCATCAAGACAGGGCGTTTCAAGTGGTGTGACATCACACAGCATGGAGGAGTG	6796
Qy	6781	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6840
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Qy	7201	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA	7260
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Qy	7321	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7380
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Qy	7621	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7680
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RESULT 2

AF178941

LOCUS AF178941 8056 bp mRNA linear PRI 04-MAY-2001

DEFINITION Homo sapiens ATP-binding cassette sub-family A member 2 (ABCA2)
mRNA, complete cds.

ACCESSION AF178941

VERSION AF178941.1 GI:9957466

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 8056)

AUTHORS Vulevic,B., Chen,Z., Boyd,J.T., Davis,W. Jr., Walsh,E.S.,
Belinsky,M.G. and Tew,K.D.

TITLE Cloning and characterization of human adenosine
5'-triphosphate-binding cassette, sub-family A, transporter 2
(ABCA2)

JOURNAL Cancer Res. 61 (8), 3339-3347 (2001)

MEDLINE 21205831

PUBMED 11309290

REFERENCE 2 (bases 1 to 8056)

AUTHORS Vulevic,B., Chen,Z., Walsh,E.S. and Tew,K.D.

TITLE Direct Submission

JOURNAL Submitted (19-AUG-1999) Pharmacology, Fox Chase Cancer Center, 7701
Burholme avenue, Philadelphia, PA 19111, USA

FEATURES Location/Qualifiers

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/chromosome="9"
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ORIGIN

Query Match 100.0%; Score 8040; DB 9; Length 8056;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGAGCCCGTGGGTCCTGGCCTTCGAGAT	120
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Db	137	 CTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT	196
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Qy	301	CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT	360
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Qy	361	GTTTGACCCAGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA	420
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Qy	481	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA	540
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Qy	661	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	720
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Qy	721	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	780
Db	737	 GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	796
Qy	781	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	840
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Qy	841	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	900
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Qy	901	CCAGCTGGACGTGGCCAAGGTCTCCAGCAGCTGGGCCTGGATGCCCCCAACGGCTCGGA	960
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Db	977	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1036
Qy	1021	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGGCCCTGGCCCTGCTACTGCCCCA	1080
Db	1037	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGGCCCTGGCCCTGCTACTGCCCCA	1096
Qy	1081	GGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
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Qy	1141	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1200
Db	1157	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1216
Qy	1201	TGCTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
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Qy	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380
Db	1337	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1396
Qy	1381	CCTCGTGACCTCATGACCAGCAACCCCAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
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Qy	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1500
Db	1457	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1516
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Qy	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620
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Db	1637	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1696
Qy	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGAT	1740
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Qy	1921	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1980
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Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
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Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
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Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGA	2700
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Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
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Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3420
Db	3377	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3436
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCTGGACGA	3480
Db	3437	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCTGGACGA	3496
Qy	3481	GCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCTGAAGTA	3540
Db	3497	GCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCTGAAGTA	3556
Qy	3541	CAAGCCAGGCCGCACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600

Db	3557	 CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3616
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCGCTCTTCCT	3660
Db	3617	 GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCGCTCTTCCT	3676
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3720
Db	3677	 CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3736
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTG	3780
Db	3737	 GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTG	3796
Qy	3781	CTCCGAGCTCCAGGTGTCCAGTTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3797	 CTCCGAGCTCCAGGTGTCCAGTTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3856
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3857	 AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3916
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3917	 CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3976
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTTCCTCAAGGTGTGCGAGGAGGATCAGTCGCT	4020
Db	3977	 GCTGATGGACACGACCCTGGAGGAAGTGTTTCCTCAAGGTGTGCGAGGAGGATCAGTCGCT	4036
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4037	 GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4096
Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4097	 CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4156
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4200
Db	4157	 GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4216
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4217	 CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4276
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAA	4320
Db	4277	 TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAA	4336
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4337	 GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4396
Qy	4381	CTGCGCCCGCCGCAACTCCAAGGCACCTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440

Db	4397	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4456
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4457	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4516
Qy	4501	CCTGTACCTTCCCAGTACCACAACTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4517	CCTGTACCTTCCCAGTACCACAACTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4576
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCT	4620
Db	4577	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCT	4636
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4637	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4696
Qy	4681	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4697	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4756
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4757	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4816
Qy	4801	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4860
Db	4817	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4876
Qy	4861	GCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCCGCACC	4920
Db	4877	GCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCCGCACC	4936
Qy	4921	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	4980
Db	4937	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	4996
Qy	4981	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACC CGCCCCAGATGCGGGTGGTACAGGCGA	5040
Db	4997	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACC CGCCCCAGATGCGGGTGGTACAGGCGA	5056
Qy	5041	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5100
Db	5057	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5116
Qy	5101	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5160
Db	5117	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5176
Qy	5161	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5220
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Qy	5221	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5280
Db	5237	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5296

Qy	5281	CGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5340
Db	5297	CGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5356
Qy	5341	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5400
Db	5357	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5416
Qy	5401	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5460
Db	5417	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5476
Qy	5461	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGCA	5520
Db	5477	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGCA	5536
Qy	5521	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5580
Db	5537	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5596
Qy	5581	GGTCCCCGCTACCTGCTGTGTGTCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTC	5640
Db	5597	GGTCCCCGCTACCTGCTGTGTGTCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTC	5656
Qy	5641	GCCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCC	5700
Db	5657	GCCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCC	5716
Qy	5701	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTTCCTCAT	5760
Db	5717	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTTCCTCAT	5776
Qy	5761	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCTGCTACAGCTCTT	5820
Db	5777	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCTGCTACAGCTCTT	5836
Qy	5821	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5880
Db	5837	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5896
Qy	5881	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5940
Db	5897	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5956
Qy	5941	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGGGACATTGT	6000
Db	5957	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGGGACATTGT	6016
Qy	6001	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCTCCTGACCATCAT	6060
Db	6017	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCTCCTGACCATCAT	6076
Qy	6061	GTGCCAGTACAACCTTCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6120
Db	6077	GTGCCAGTACAACCTTCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6136

Qy	6121	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6180
Db	6137	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6196
Qy	6181	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6240
Db	6197	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6256
Qy	6241	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6300
Db	6257	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6316
Qy	6301	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6360
Db	6317	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6376
Qy	6361	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6420
Db	6377	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6436
Qy	6421	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCGGGAGCACCT	6480
Db	6437	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCGGGAGCACCT	6496
Qy	6481	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6540
Db	6497	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6556
Qy	6541	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6600
Db	6557	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6616
Qy	6601	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTT	6660
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Qy	6661	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6720
Db	6677	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6736
Qy	6721	CCTCGACCTCATCAAGACAGGGCGTTTCAAGTGGTGCTGACATCACACAGCATGGAGGAGTG	6780
Db	6737	CCTCGACCTCATCAAGACAGGGCGTTTCAAGTGGTGCTGACATCACACAGCATGGAGGAGTG	6796
Qy	6781	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6840
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Qy	6841	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6900
Db	6857	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6916
Qy	6901	CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6960
Db	6917	CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6976
Qy	6961	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7020

Db	6977	 CAAGGAGCGGCACCAACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7036
Qy	7021	CCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7080
Db	7037	CCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7096
Qy	7081	CAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT	7140
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Qy	7141	GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7200
Db	7157	GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7216
Qy	7201	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA	7260
Db	7217	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA	7276
Qy	7261	GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7320
Db	7277	GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7336
Qy	7321	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7380
Db	7337	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7396
Qy	7381	TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGC	7440
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Qy	7441	CAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCG	7500
Db	7457	CAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCG	7516
Qy	7501	GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCC	7560
Db	7517	GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCC	7576
Qy	7561	GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCCCTCG	7620
Db	7577	GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCCCTCG	7636
Qy	7621	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7680
Db	7637	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7696
Qy	7681	TTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA	7740
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Qy	7741	GCGGGCTGTGGGCGGAGCTGGGTTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCT	7800
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Qy	7801	CTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAG	7860

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RESULT 3

BD140900

LOCUS BD140900 8269 bp DNA linear PAT 18-SEP-2002

DEFINITION Human and rat ABCA2 gene.

ACCESSION BD140900

VERSION BD140900.1 GI:23235845

KEYWORDS WO 0208424-A/1.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 8269)

AUTHORS Inagaki,N.

TITLE Human and rat ABCA2 gene

JOURNAL Patent: WO 0208424-A 1 31-JAN-2002;

BANYU PHARMACEUTICAL CO LTD,NOBUYA INAGAKI

COMMENT OS Homo sapiens (human)

PN WO 0208424-A/1

PD 31-JAN-2002

PF 26-JUL-2001 WO 2001JP006457

PR 26-JUL-2000 JP 00P 225462

PI NOBUYA INAGAKI

PC

C12N15/12,C07K14/47,C12N1/15,C12N1/19,C12N1/21,C12N5/00,G01N33/ 68,

PC G01N33/15,G01N33/50

CC Human and rat ABCA2 gene

FH Key Location/Qualifiers

FT source 1. .8269

FT /organism='Homo sapiens (human)'. .

FEATURES Location/Qualifiers

source 1. .8269

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 8036.4; DB 6; Length 8269;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 8037; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	278	 TGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCCCTGGCCTTCGAGATCT	337
Qy	123	TCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCATCT	182
Db	338	 TCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCATCT	397
Qy	183	CCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCCTGACGTCTGCCGGCATCCTGCCTG	242
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Qy	303	ACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCTGT	362
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Qy	363	TTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGAGG	422
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Qy	423	CCCTCAGTGCGGGCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTCCT	482
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Qy	543	TGTCGCTGCCCAATAGCACGGCCCAAGCACTCTTGGCCGCCCGTGTGGACCCGCCGAGG	602
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Qy	603	TCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAAGG	662
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Qy	663	GTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCTGC	722
Db	878	 GTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCTGC	937
Qy	723	TGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCGGA	782
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Qy	783	TCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTGCA	842
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Db	1058	GTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAACC	1117
Qy	903	AGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGACT	962
Db	1118	AGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGACT	1177
Qy	963	CCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGATG	1022
Db	1178	CCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGATG	1237
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Db	1238	CCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGGCCCTGGCCCTGCTACTGCCCCAGG	1297
Qy	1083	GTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAATG	1142
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Qy	1263	GGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTAACCCGAGGCGCTGC	1322
Db	1478	GGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTAACCCGAGGCGCTGC	1537
Qy	1323	GGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCTCC	1382
Db	1538	GGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCTCC	1597
Qy	1383	TCGTGCACCTCATGACCAGCAACCCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGTCG	1442
Db	1598	TCGTGCACCTCATGACCAGCAACCCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGTCG	1657
Qy	1443	ACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTATG	1502
Db	1658	ACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTATG	1717
Qy	1503	CCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCTGC	1562
Db	1718	CCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCTGC	1777
Qy	1563	AGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGCAC	1622
Db	1778	AGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGCAC	1837
Qy	1623	TGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCCCCA	1682
Db	1838	TGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCCCCA	1897
Qy	1683	GTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGATCC	1742
Db	1898	GTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGATCC	1957

Qy	1743	AGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCATTG	1802
Db	1958	AGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCATTG	2017
Qy	1803	TCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGATCT	1862
Db	2018	TCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGATCT	2077
Qy	1863	TCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAACT	1922
Db	2078	TCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAACT	2137
Qy	1923	CCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAATA	1982
Db	2138	CCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAATA	2197
Qy	1983	CTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCGCG	2042
Db	2198	CTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCGCG	2257
Qy	2043	CCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGATGT	2102
Db	2258	CCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGATGT	2317
Qy	2103	TCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTGATTGAGCACATGATGCCGC	2162
Db	2318	TCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTGATTGAGCACATGATGCCGC	2377
Qy	2163	TGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGCGG	2222
Db	2378	TGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGCGG	2437
Qy	2223	AGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCACT	2282
Db	2438	AGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCACT	2497
Qy	2283	GGGTGGCCTGGTTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCACCG	2342
Db	2498	GGGTGGCCTGGTTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCACCG	2557
Qy	2343	CCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTTCC	2402
Db	2558	CCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTTCC	2617
Qy	2403	TGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTCCA	2462
Db	2618	TGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTCCA	2677
Qy	2463	AGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTACA	2522
Db	2678	AGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTACA	2737
Qy	2523	TGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTGCA	2582
Db	2738	TGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTGCA	2797

Qy	2583	TCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTATG	2642
Db	2798	TCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTATG	2857
Qy	2643	AGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGACG	2702
Db	2858	AGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGACG	2917
Qy	2703	ACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCATCC	2762
Db	2918	ACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCATCC	2977
Qy	2763	TCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTACT	2822
Db	2978	TCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTACT	3037
Qy	2823	TCCCACTGCAGAAGTCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAGCT	2882
Db	3038	TCCCACTGCAGAAGTCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAGCT	3097
Qy	2883	GGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGTGCCATGG	2942
Db	3098	GGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGTGCCATGG	3157
Qy	2943	AGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCTGG	3002
Db	3158	AGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCTGG	3217
Qy	3003	TTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAACA	3062
Db	3218	TTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAACA	3277
Qy	3063	AGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGCGG	3122
Db	3278	AGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGCGG	3337
Qy	3123	GCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCCGCCA	3182
Db	3338	GCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCCGCCA	3397
Qy	3183	CCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCATGT	3242
Db	3398	CCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCATGT	3457
Qy	3243	GCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTACT	3302
Db	3458	GCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTACT	3517
Qy	3303	CACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGAGG	3362
Db	3518	CACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGAGG	3577
Qy	3363	ACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAAGC	3422
Db	3578	ACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAAGC	3637
Qy	3423	GCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGAGC	3482

Db	3638	 GCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGAGC	3697
Qy	3483	CCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTACA	3542
Db	3698	 CCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTACA	3757
Qy	3543	AGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGGGG	3602
Db	3758	 AGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGGGG	3817
Qy	3603	ACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCTCA	3662
Db	3818	 ACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCTCA	3877
Qy	3663	AGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGGGG	3722
Db	3878	 AGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGGGG	3937
Qy	3723	GCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGGCCCCGCTGAGCAGCTGCT	3782
Db	3938	 GCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGGCCCCGCTGAGCAGCTGCT	3997
Qy	3783	CCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTCAG	3842
Db	3998	 CCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTCAG	4057
Qy	3843	ACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTTCG	3902
Db	4058	 ACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTTCG	4117
Qy	3903	AGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGGGC	3962
Db	4118	 AGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGGGC	4177
Qy	3963	TGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTGCGAGGAGGATCAGTCGCTGG	4022
Db	4178	 TGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTGCGAGGAGGATCAGTCGCTGG	4237
Qy	4023	AGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGGCC	4082
Db	4238	 AGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGGCC	4297
Qy	4083	CGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTCGC	4142
Db	4298	 CGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTCGC	4357
Qy	4143	AGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGGCT	4202
Db	4358	 AGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGGCT	4417
Qy	4203	ACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAATG	4262
Db	4418	 ACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAATG	4477
Qy	4263	TCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAAGC	4322

Db	4478	TCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTGGGCCAGGGCAGCCGCAAGC	4537
Qy	4323	TGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCACT	4382
Db	4538	TGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCACT	4597
Qy	4383	GCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGTCT	4442
Db	4598	GCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGTCT	4657
Qy	4443	GCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGTCC	4502
Db	4658	GCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGTCC	4717
Qy	4503	TGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGCCA	4562
Db	4718	TGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGCCA	4777
Qy	4563	ACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCTCG	4622
Db	4778	ACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCTCG	4837
Qy	4623	TGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGCCA	4682
Db	4838	TGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGCCA	4897
Qy	4683	ACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGCTC	4742
Db	4898	ACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGCTC	4957
Qy	4743	GGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTTTCG	4802
Db	4958	GGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTTTCG	5017
Qy	4803	TGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCTGC	4862
Db	5018	TGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCTGC	5077
Qy	4863	AGGCCTGGAACGTCTCCCTGCCGCCCCACCGCTGGGCCAGAAATGTGGACGTCGGCACCCCT	4922
Db	5078	AGGCCTGGAACGTCTCCCTGCCGCCCCACCGCTGGGCCAGAAATGTGGACGTCGGCACCCCT	5137
Qy	4923	CCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GGCT	4982
Db	5138	CCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GGCT	5197
Qy	4983	TCTCCTGCCCCAGCAGTGTGGGCGGGCACC CGCCCCAGATGCGGGTGGTACAGGCGACA	5042
Db	5198	TCTCCTGCCCCAGCAGTGTGGGCGGGCACC CGCCCCAGATGCGGGTGGTACAGGCGACA	5257
Qy	5043	TCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTACCTCCGACCGCT	5102
Db	5258	TCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTACCTCCGACCGCT	5317
Qy	5103	TCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGCCT	5162
Db	5318	TCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGCCT	5377

Qy	5163	CATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCAGG	5222
Db	5378	CATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCAGG	5437
Qy	5223	TTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAACG	5282
Db	5438	TTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAACG	5497
Qy	5283	CCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCACCG	5342
Db	5498	CCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCACCG	5557
Qy	5343	TCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGG	5402
Db	5558	TCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGG	5617
Qy	5403	GCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCT	5462
Db	5618	GCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCT	5677
Qy	5463	TCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGACGG	5522
Db	5678	TCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGACGG	5737
Qy	5523	GCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCTGG	5582
Db	5738	GCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCTGG	5797
Qy	5583	TCCCCGCTACCTGCTGTGTATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTCGC	5642
Db	5798	TCCCCGCTACCTGCTGTGTATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTCGC	5857
Qy	5643	CCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCCCA	5702
Db	5858	CCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCCCA	5917
Qy	5703	TCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCATTG	5762
Db	5918	TCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCATTG	5977
Qy	5763	TCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCTGCTACAGCTCTTCG	5822
Db	5978	TCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCTGCTACAGCTCTTCG	6037
Qy	5823	AGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCC	5882
Db	6038	AGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCC	6097
Qy	5883	CCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGT	5942
Db	6098	CCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGT	6157
Qy	5943	ACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCA	6002
Db	6158	ACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCA	6217

Qy	6003	CCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGT	6062
Db	6218	CCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGT	6277
Qy	6063	GCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGG	6122
Db	6278	GCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGG	6337
Qy	6123	ATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACA	6182
Db	6338	ATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACA	6397
Qy	6183	TGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGG	6242
Db	6398	TGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGG	6457
Qy	6243	CCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCA	6302
Db	6458	CCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCA	6517
Qy	6303	ACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCACGAGAGCACGACGGGGG	6362
Db	6518	ACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCACGAGAGCACGACGGGGG	6577
Qy	6363	GCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCC	6422
Db	6578	GCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCC	6637
Qy	6423	TCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCCGGGAGCACCTGC	6482
Db	6638	TCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCCGGGAGCACCTGC	6697
Qy	6483	AGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGG	6542
Db	6698	AGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGG	6757
Qy	6543	CTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCG	6602
Db	6758	CTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCG	6817
Qy	6603	GCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTTCC	6662
Db	6818	GCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTTCC	6877
Qy	6663	TGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCC	6722
Db	6878	TGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCC	6937
Qy	6723	TCGACCTCATCAAGACAGGGCGTTTCAAGTGGTGTGACATCACACAGCATGGAGGAGTGCG	6782
Db	6938	TCGACCTCATCAAGACAGGGCGTTTCAAGTGGTGTGACATCACACAGCATGGAGGAGTGCG	6997
Qy	6783	AGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCA	6842
Db	6998	AGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCA	7057
Qy	6843	TCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCA	6902

Db	7058	TCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCA	7117
Qy	6903	GCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCA	6962
Db	7118	GCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCA	7177
Qy	6963	AGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCC	7022
Db	7178	AGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCC	7237
Qy	7023	AGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTCA	7082
Db	7238	AGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTCA	7297
Qy	7083	GCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGACAACCTGG	7142
Db	7298	GCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGACAACCTGG	7357
Qy	7143	AGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCC	7202
Db	7358	AGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCC	7417
Qy	7203	TGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGAGG	7262
Db	7418	TGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGAGG	7477
Qy	7263	ACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCCT	7322
Db	7478	ACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCCT	7537
Qy	7323	TCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTG	7382
Db	7538	TCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTG	7597
Qy	7383	ACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCAGTGCCTGCCA	7442
Db	7598	ACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCAGTGCCTGCCA	7657
Qy	7443	GGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCCTGTACTCGGC	7502
Db	7658	GGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCCTGTACTCGGC	7717
Qy	7503	CATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCCCGG	7562
Db	7718	CATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCCCGG	7777
Qy	7563	GCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCCGGCCCCCTCGCC	7622
Db	7778	GCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCCGGCCCCCTCGCC	7837
Qy	7623	CCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCCTT	7682
Db	7838	CCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCCTT	7897
Qy	7683	TCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGAGC	7742
		TCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGAGC	

Db 7898 TCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGAGC 7957

Qy 7743 GGGCTGTGGGCGGAGCTGGGTTCAGTCCCGTATTTATTTTGGCTTTGAGAAGAGGCTCCTCT 7802
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Db 8078 GGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCCC 8137

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Qy 7983 GGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAAAATGTC 8040
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Db 8198 GGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAAAATGTC 8255

RESULT 4

BD140901

LOCUS BD140901 8269 bp DNA linear PAT 18-SEP-2002

DEFINITION Human and rat ABCA2 gene.

ACCESSION BD140901

VERSION BD140901.1 GI:23235846

KEYWORDS WO 0208424-A/2.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 8269)

AUTHORS Inagaki, N.

TITLE Human and rat ABCA2 gene

JOURNAL Patent: WO 0208424-A 2 31-JAN-2002;
 BANYU PHARMACEUTICAL CO LTD, NOBUYA INAGAKI

COMMENT OS Homo sapiens (human)

PN WO 0208424-A/2

PD 31-JAN-2002

PF 26-JUL-2001 WO 2001JP006457

PR 26-JUL-2000 JP 00P 225462

PI NOBUYA INAGAKI

PC

C12N15/12, C07K14/47, C12N1/15, C12N1/19, C12N1/21, C12N5/00, G01N33/ PC
 68,

PC G01N33/15, G01N33/50

CC Human and rat ABCA2 gene

FH Key Location/Qualifiers

FT source 1. .8269

FT /organism='Homo sapiens (human)'.

FEATURES Location/Qualifiers

source 1. .8269

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 8036.4; DB 6; Length 8269;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8037; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      3 GCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCTGC 62
        |||
Db     218 GCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCTGC 277

Qy     63 TGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGATCT 122
        |||
Db     278 TGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGATCT 337

Qy    123 TCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCATCT 182
        |||
Db    338 TCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCATCT 397

Qy    183 CCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCCTGACGTCTGCCGGCATCCTGCCTG 242
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Db    398 CCGTGAAGGAAGTCTCCTTCTACACAGCGGCGCCCCTGACGTCTGCCGGCATCCTGCCTG 457

Qy    243 TCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTTCGGCTTCCTGCAGTACGCCA 302
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Qy    303 ACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCTGT 362
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Db    518 ACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCTGT 577

Qy    363 TTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGAGG 422
        |||
Db    578 TTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGAGG 637

Qy    423 CCCTCAGTGCGGGCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTCCT 482
        |||
Db    638 CCCTCAGTGCGGGCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTCCT 697

Qy    483 TCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAACT 542
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Qy    543 TGTCGCTGCCCCAATAGCACGGCCCAAGCACTCTTGGCCGCCCCTGTGGACCCGCCCAGG 602
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Qy    603 TCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAAGG 662
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Qy    663 GTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCTGC 722
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Qy    723 TGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCGGA 782
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Db	938	TGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCGGA	997
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Db	998	TCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTGCA	1057
Qy	843	GTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAACC	902
Db	1058	GTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAACC	1117
Qy	903	AGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGACT	962
Db	1118	AGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGACT	1177
Qy	963	CCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGATG	1022
Db	1178	CCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGATG	1237
Qy	1023	CCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGCCCTGGCCCTGCTACTGCCCCAGG	1082
Db	1238	CCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGCCCTGGCCCTGCTACTGCCCCAGG	1297
Qy	1083	GTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAATG	1142
Db	1298	GTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAATG	1357
Qy	1143	GCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTCTG	1202
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Qy	1203	CTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCTCT	1262
Db	1418	CTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCTCT	1477
Qy	1263	GGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCTGC	1322
Db	1478	GGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCTGC	1537
Qy	1323	GGCGGGGCAACATGAGCTCCCTGGGCTTACGAGCAAGGAGCAGCGGAACCTGGGCCTCC	1382
Db	1538	GGCGGGGCAACATGAGCTCCCTGGGCTTACGAGCAAGGAGCAGCGGAACCTGGGCCTCC	1597
Qy	1383	TCGTGCACCTCATGACCAGCAACCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGTCG	1442
Db	1598	TCGTGCACCTCATGACCAGCAACCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGTCG	1657
Qy	1443	ACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTATG	1502
Db	1658	ACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTATG	1717
Qy	1503	CCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCTGC	1562
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Qy	1563	AGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGCAC	1622
Db	1778	AGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGCAC	1837

Qy	1623	TGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACTTCTCGCTGCCCCA	1682
Db	1838	TGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACTTCTCGCTGCCCCA	1897
Qy	1683	GTGGCATGGCCCTCCTGCAGCAGCTGGATAACCATTGACAACGCGGCCTGCGGCTGGATCC	1742
Db	1898	GTGGCATGGCCCTCCTGCAGCAGCTGGATAACCATTGACAACGCGGCCTGCGGCTGGATCC	1957
Qy	1743	AGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCATTG	1802
Db	1958	AGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCATTG	2017
Qy	1803	TCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGATCT	1862
Db	2018	TCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGATCT	2077
Qy	1863	TCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAACT	1922
Db	2078	TCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAACT	2137
Qy	1923	CCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAATA	1982
Db	2138	CCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAATA	2197
Qy	1983	CTGGCGGCCGCTTCTACTTCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCGCG	2042
Db	2198	CTGGCGGCCGCTTCTACTTCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCGCG	2257
Qy	2043	CCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGATGT	2102
Db	2258	CCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGATGT	2317
Qy	2103	TCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCCGC	2162
Db	2318	TCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCCGC	2377
Qy	2163	TGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGCGG	2222
Db	2378	TGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGCGG	2437
Qy	2223	AGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCACT	2282
Db	2438	AGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCACT	2497
Qy	2283	GGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCACCG	2342
Db	2498	GGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCACCG	2557
Qy	2343	CCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTTCC	2402
Db	2558	CCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTTCC	2617
Qy	2403	TGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTCCA	2462
Db	2618	TGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTCCA	2677

Qy	2463	AGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTACA	2522
Db	2678	AGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTACA	2737
Qy	2523	TGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTGCA	2582
Db	2738	TGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTGCA	2797
Qy	2583	TCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTATG	2642
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Qy	2643	AGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGACG	2702
Db	2858	AGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGACG	2917
Qy	2703	ACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCATCC	2762
Db	2918	ACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCATCC	2977
Qy	2763	TCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTACT	2822
Db	2978	TCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTACT	3037
Qy	2823	TCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAGCT	2882
Db	3038	TCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAGCT	3097
Qy	2883	GGCCGTGGGCACGCACCCCCCGCCTCAGTGTCTATGGAGGAGGACCAGGCCTGTGCCATGG	2942
Db	3098	GGCCGTGGGCACGCACCCCCCGCCTCAGTGTCTATGGAGGAGGACCAGGCCTGTGCCATGG	3157
Qy	2943	AGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCTGG	3002
Db	3158	AGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCTGG	3217
Qy	3003	TTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAACA	3062
Db	3218	TTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAACA	3277
Qy	3063	AGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGCGG	3122
Db	3278	AGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGCGG	3337
Qy	3123	GCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCCA	3182
Db	3338	GCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCCA	3397
Qy	3183	CCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCATGT	3242
Db	3398	CCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCATGT	3457
Qy	3243	GCCCGCAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTACT	3302
Db	3458	GCCCGCAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTACT	3517
Qy	3303	CACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGAGG	3362

Db	3518	 CACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGAGG	3577
Qy	3363	ACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAAGC	3422
Db	3578	 ACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAAGC	3637
Qy	3423	GCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGAGC	3482
Db	3638	 GCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGAGC	3697
Qy	3483	CCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTACA	3542
Db	3698	 CCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTACA	3757
Qy	3543	AGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGGGG	3602
Db	3758	 AGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGGGG	3817
Qy	3603	ACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCTCA	3662
Db	3818	 ACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCTCA	3877
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Db	3878	 AGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGGGG	3937
Qy	3723	GCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTGCT	3782
Db	3938	 GCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTGCT	3997
Qy	3783	CCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTCAG	3842
Db	3998	 CCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTCAG	4057
Qy	3843	ACACAAGCACGGAGCTCTCCTACATCCTGCCAGCGAGGCCGCCAAGAAGGGGGCTTTCG	3902
Db	4058	 ACACAAGCACGGAGCTCTCCTACATCCTGCCAGCGAGGCCGCCAAGAAGGGGGCTTTCG	4117
Qy	3903	AGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGGGC	3962
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Qy	3963	TGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTCGGAGGAGGATCAGTCGCTGG	4022
Db	4178	 TGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTCGGAGGAGGATCAGTCGCTGG	4237
Qy	4023	AGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGGCC	4082
Db	4238	 AGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGGCC	4297
Qy	4083	CGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTCGC	4142
Db	4298	 CGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTCGC	4357
Qy	4143	AGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCGTGGCGACGAGGGAGCTGGCT	4202

Db	4358	AGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGGCT	4417
Qy	4203	ACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAATG	4262
Db	4418	ACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAATG	4477
Qy	4263	TCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAAGC	4322
Db	4478	TCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAAGC	4537
Qy	4323	TGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCACT	4382
Db	4538	TGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCACT	4597
Qy	4383	GCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGTCT	4442
Db	4598	GCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGTCT	4657
Qy	4443	GCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGTCC	4502
Db	4658	GCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGTCC	4717
Qy	4503	TGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGCCA	4562
Db	4718	TGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGCCA	4777
Qy	4563	ACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCAGCAGCTCG	4622
Db	4778	ACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCAGCAGCTCG	4837
Qy	4623	TGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGCCA	4682
Db	4838	TGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGCCA	4897
Qy	4683	ACGGCTCGCTGGGGCCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGCTC	4742
Db	4898	ACGGCTCGCTGGGGCCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGCTC	4957
Qy	4743	GGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTTTCG	4802
Db	4958	GGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTTTCG	5017
Qy	4803	TGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCTGC	4862
Db	5018	TGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCTGC	5077
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Db	5078	AGGCCTGGAACGTCTCCCTGCCGCCCCACCGCTGGGCCAGAAATGTGGACGTGGCACCCCT	5137
Qy	4923	CCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACCGGCT	4982
Db	5138	CCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACCGGCT	5197
Qy	4983	TCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGACA	5042
Db	5198	TCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGACA	5257

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Qy	5103	TCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGCCT	5162
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Qy	5163	CATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCAGG	5222
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Qy	5223	TTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAACG	5282
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Qy	5283	CCATCCTGCGTGCCAACCTGCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCACCG	5342
Db	5498	CCATCCTGCGTGCCAACCTGCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCACCG	5557
Qy	5343	TCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGG	5402
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Qy	5403	GCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCT	5462
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Qy	5463	TCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAGCG	5522
Db	5678	TCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAGCG	5737
Qy	5523	GCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCTGG	5582
Db	5738	GCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCTGG	5797
Qy	5583	TCCCCGCTACCTGCTGTGTGTCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTCGC	5642
Db	5798	TCCCCGCTACCTGCTGTGTGTCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTCGC	5857
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Db	5858	CCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCCCA	5917
Qy	5703	TCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCTTCATTG	5762
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Qy	5763	TCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCTGCTACAGCTCTTCG	5822
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RESULT 5

AX235951

LOCUS AX235951 8195 bp DNA linear PAT 26-SEP-2001

DEFINITION Sequence 7 from Patent WO0164875.

ACCESSION AX235951

VERSION AX235951.1 GI:15795822

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Glucksmann,M.A.

TITLE Human transporter genes and proteins encoded thereby

JOURNAL Patent: WO 0164875-A 7 07-SEP-2001; Millennium Pharmaceuticals, Inc. (US)

FEATURES Location/Qualifiers

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ORIGIN

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Query Match          99.9%;  Score 8032;  DB 6;  Length 8195;
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Matches 8035;  Conservative 0;  Mismatches 5;  Indels 0;  Gaps 0;

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Db	2798	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2857
Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2858	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2917
Qy	2821	CTTCCCCTGCAGAAGTCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2918	CTTCCCCTGCAGAAGTCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2977
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Db	2978	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCATGGAGGAGGACCAGGCCTGTGCCAT	3037
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3000
Db	3038	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3097
Qy	3001	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3098	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3157
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3158	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3217
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCG	3180
Db	3218	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCG	3277
Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3278	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3337
Qy	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3338	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3397
Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3398	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3457
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTGCGGTGGCATGAA	3420
Db	3458	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTGCGGTGGCATGAA	3517
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3480
Db	3518	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3577
Qy	3481	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3540
Db	3578	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3637

Qy	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3638	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3697
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3698	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3757
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3720
Db	3758	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3817
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTG	3780
Db	3818	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTG	3877
Qy	3781	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3878	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3937
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3938	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3997
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3998	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	4057
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTCCCTCAAGGTGTGCGAGGAGGATCAGTCGCT	4020
Db	4058	GCTGATGGACACGACCCTGGAGGAAGTGTTCCCTCAAGGTGTGCGAGGAGGATCAGTCGCT	4117
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4118	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4177
Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4178	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4237
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Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4418	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4477

Qy	4381	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4478	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4537
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4538	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4597
Qy	4501	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4598	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4657
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCT	4620
Db	4658	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCT	4717
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4718	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4777
Qy	4681	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4778	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4837
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4838	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4897
Qy	4801	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4860
Db	4898	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4957
Qy	4861	GCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCCGCACC	4920
Db	4958	GCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCCGCACC	5017
Qy	4921	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	4980
Db	5018	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	5077
Qy	4981	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5040
Db	5078	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5137
Qy	5041	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5100
Db	5138	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5197
Qy	5101	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5160
Db	5198	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5257
Qy	5161	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5220
Db	5258	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5317
Qy	5221	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTCAACAA	5280

Db	5318	 GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5377
Qy	5281	CGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5340
Db	5378	 CGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5437
Qy	5341	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5400
Db	5438	 CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5497
Qy	5401	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5460
Db	5498	 GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5557
Qy	5461	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAG	5520
Db	5558	 CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAG	5617
Qy	5521	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5580
Db	5618	 CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5677
Qy	5581	GGTCCCCGCTACCTGCTGTGTGCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTC	5640
Db	5678	 GGTCCCCGCTACCTGCTGTGTGCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTC	5737
Qy	5641	GCCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCC	5700
Db	5738	 GCCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCC	5797
Qy	5701	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCTCAT	5760
Db	5798	 CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCTCAT	5857
Qy	5761	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5820
Db	5858	 TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5917
Qy	5821	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5880
Db	5918	 CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5977
Qy	5881	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5940
Db	5978	 CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	6037
Qy	5941	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGGGACATTGT	6000
Db	6038	 GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGGGACATTGT	6097
Qy	6001	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6060
Db	6098	 CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6157
Qy	6061	GTGCCAGTACAACCTTCCTGCGGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6120

Db	6158	GTGCCAGTACAACCTTCCTGCGGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6217
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Qy	6241	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6300
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Qy	6361	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6420
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Db	6878	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6937
Qy	6841	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCAGGACCAAGAG	6900
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Qy	6901	CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6960
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Qy	7261	GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7320
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Qy	7321	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7380
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Qy	7561	GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCCCTCG	7620
Db	7658	GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCCCTCG	7717
Qy	7621	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7680
Db	7718	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7777
Qy	7681	TTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA	7740
Db	7778	TTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA	7837
Qy	7741	GCGGGCTGTGGGCGGAGCTGGGTCACTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCT	7800
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RESULT 6

AX405561

LOCUS AX405561 7610 bp DNA linear PAT 14-JUN-2002

DEFINITION Sequence 28 from Patent WO0222684.

ACCESSION AX405561

VERSION AX405561.1 GI:21438586

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Lee,E.A., Yue,H., Lal,P.G., Walia,N.K., Baughn,M.R., Warren,B.A., Lee,S., Sanjanwala,M.S., Yao,M.G., Ramkumar,J., Thornton,M., Gandhi,A.R., Policky,J.L., Elliott,V.S., Arvizu,C., Raumann,B.E., Bruns,C.M., Naini,A., Hafalia,A.J., Nguyen,D.B., Xu,Y., Lu,D.A., Ison,C.H., Griffin,J.A., Reddy,R.M. and Burford,N.

TITLE Transporters and ion channels

JOURNAL Patent: WO 0222684-A 28 21-MAR-2002; Incyte Genomics, Inc. (US)

FEATURES Location/Qualifiers

source 1. .7610
 /organism="Homo sapiens"
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 /note="Incyte ID No: 7078207CB1"

ORIGIN

Query Match 93.6%; Score 7529.2; DB 6; Length 7610;
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Qy	421	GGCCCTCAGTGCGGGCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC	480
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Qy	541	CTTGTCGCTGCCCCAATAGCACGGCCCAAGCACTCTTGGCCGCCCGTGTGGACCCGCCCGA	600
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Db	797	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	856
Qy	781	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	840
Db	857	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	916
Qy	841	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	900
Db	917	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	976
Qy	901	CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	960
Db	977	CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	1036
Qy	961	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1020

Db	1037	 CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1096
Qy	1021	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTCGGCCCTGGCCCTGCTACTGCCCCA	1080
Db	1097	 TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTCGGCCCTGGCCCTGCTACTGCCCCA	1156
Qy	1081	GGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Db	1157	 GGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1216
Qy	1141	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1200
Db	1217	 TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1276
Qy	1201	TGCTGCAGCACTGGCCACCCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
Db	1277	 TGCTGCAGCACTGGCCACCCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1336
Qy	1261	CTGGGCGGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTAACCCGAGGCGCT	1320
Db	1337	 CTGGGCGGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTAACCCGAGGCGCT	1396
Qy	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380
Db	1397	 GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1456
Qy	1381	CCTCGTGCACCTCATGACCAGCAACCCCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
Db	1457	 CCTCGTGCACCTCATGACCAGCAACCCCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1516
Qy	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1500
Db	1517	 CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1576
Qy	1501	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1577	 TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1636
Qy	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620
Db	1637	 GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1696
Qy	1621	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1680
Db	1697	 ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1756
Qy	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATAACCATTGACAACGCGGCCTGCGGCTGGAT	1740
Db	1757	 CAGTGGCATGGCCCTCCTGCAGCAGCTGGATAACCATTGACAACGCGGCCTGCGGCTGGAT	1816
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1800
Db	1817	 CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1876
Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCAGTGTGTTTTTGCCAGTGTGAT	1860

Db	1877	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTC	ACTGTTTTT	GCCAGTGTGAT	1936
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA			1920
Db	1937	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA			1996
Qy	1921	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA			1980
Db	1997	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA			2056
Qy	1981	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG			2040
Db	2057	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG			2116
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT			2100
Db	2117	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT			2176
Qy	2101	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTGATTGAGCACATGATGCC			2160
Db	2177	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTGATTGAGCACATGATGCC			2236
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC			2220
Db	2237	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC			2296
Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA			2280
Db	2297	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA			2356
Qy	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC			2340
Db	2357	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC			2416
Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT			2400
Db	2417	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT			2476
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC			2460
Db	2477	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC			2536
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA			2520
Db	2537	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA			2596
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG			2580
Db	2597	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG			2656
Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA			2640
Db	2657	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA			2716
Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA			2700
Db	2717	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA			2776

Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760
Db	2777	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2836
Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2837	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2896
Qy	2821	CTTCCCCTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2897	CTTCCCCTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2956
Qy	2881	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCTATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2957	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCTATGGAGGAGGACCAGGCCTGTGCCAT	3016
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3000
Db	3017	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3076
Qy	3001	GGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3077	GGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3136
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3137	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3196
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCGC	3180
Db	3197	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCGC	3256
Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3257	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3316
Qy	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3317	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3376
Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3377	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3436
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3420
Db	3437	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3496
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3480
Db	3497	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3556
Qy	3481	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3540
Db	3557	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3616

Qy	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3617	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3676
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3677	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3736
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3720
Db	3737	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3796
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTG	3780
Db	3797	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTG	3856
Qy	3781	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3857	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3916
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3917	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3976
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3977	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	4036
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTGCGAGGAGGATCAGTCGCT	4020
Db	4037	GCTGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTGCGAGGAGGATCAGTCGCT	4096
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4097	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4156
Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4157	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4216
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4200
Db	4217	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4276
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4277	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4336
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTGGGCCAGGGCAGCCGCAA	4320
Db	4337	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTGGGCCAGGGCAGCCGCAA	4396
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4397	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4456
Qy	4381	CTGCGCCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440

Db	4457	 CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4516
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4517	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4576
Qy	4501	CCTGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4577	CCTGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4636
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCT	4620
Db	4637	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCT	4696
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4697	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4756
Qy	4681	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4757	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4816
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4817	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4876
Qy	4801	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4860
Db	4877	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4936
Qy	4861	GCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCCGCACC	4920
Db	4937	GCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCCGCACC	4996
Qy	4921	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACCGG	4980
Db	4997	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACCGG	5056
Qy	4981	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5040
Db	5057	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5116
Qy	5041	CATCCTGACCGACATCACGGGCCACAATGTCTCTGAGTACCTGCTCTTACCTCCGACCG	5100
Db	5117	CATCCTGACCGACATCACGGGCCACAATGTCTCTGAGTACCTGCTCTTACCTCCGACCG	5176
Qy	5101	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5160
Db	5177	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5236
Qy	5161	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5220
Db	5237	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5296
Qy	5221	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTCAACAA	5280

Db	5297	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTCAACAA	5356
Qy	5281	CGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5340
Db	5357	CGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5416
Qy	5341	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5400
Db	5417	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5476
Qy	5401	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5460
Db	5477	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5536
Qy	5461	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTTCAG	5520
Db	5537	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTTCAG	5596
Qy	5521	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5580
Db	5597	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5656
Qy	5581	GGTCCCCGCTACCTGCTGTGTTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTC	5640
Db	5657	GGTCCCCGCTACCTGCTGTGTTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTC	5716
Qy	5641	GCCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCC	5700
Db	5717	GCCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCC	5776
Qy	5701	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTTCCTCAT	5760
Db	5777	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTTCCTCAT	5836
Qy	5761	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5820
Db	5837	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5896
Qy	5821	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5880
Db	5897	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5956
Qy	5881	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5940
Db	5957	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	6016
Qy	5941	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGT	6000
Db	6017	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGT	6076
Qy	6001	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6060
Db	6077	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6136
Qy	6061	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6120
Db	6137	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6196

Qy	6121	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6180
Db	6197	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6256
Qy	6181	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGBAAGATTGGCCGTATCCT	6240
Db	6257	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGBAAGATTGGCCGTATCCT	6316
Qy	6241	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6300
Db	6317	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6376
Qy	6301	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6360
Db	6377	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6436
Qy	6361	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6420
Db	6437	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6496
Qy	6421	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCCGGGAGCACCT	6480
Db	6497	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCCGGGAGCACCT	6556
Qy	6481	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6540
Db	6557	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6616
Qy	6541	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6600
Db	6617	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6676
Qy	6601	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTT	6660
Db	6677	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTT	6736
Qy	6661	CCTGGACGAGCCCACCACAGGCATGGACCCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6720
Db	6737	CCTGGACGAGCCCACCACAGGCATGGACCCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6796
Qy	6721	CCTCGACCTCATCAAGACAGGGCGTTTCAAGTGGTGCTGACATCACACAGCATGGAGGAGTG	6780
Db	6797	CCTCGACCTCATCAAGACAGGGCGTTTCAAGTGGTGCTGACATCACACAGCATGGAGGAGTG	6856
Qy	6781	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6840
Db	6857	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6916
Qy	6841	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6900
Db	6917	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6976
Qy	6901	CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6960
Db	6977	CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	7036

Qy 6961 CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC 7020
 |||
 Db 7037 CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC 7096
 Qy 7021 CCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT 7080
 |||
 Db 7097 CCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT 7156
 Qy 7081 CAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT 7140
 |||
 Db 7157 CAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT 7216
 Qy 7141 GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG 7200
 |||
 Db 7217 GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG 7276
 Qy 7201 CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA 7260
 |||
 Db 7277 CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA 7336
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RESULT 7

AF327657

LOCUS AF327657 7482 bp mRNA linear PRI 01-MAR-2001

DEFINITION Homo sapiens ABC transporter ABCA2 (ABCA2) mRNA, complete cds.

ACCESSION AF327657

VERSION AF327657.1 GI:13173185

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 7482)

AUTHORS Kaminski,W.E., Piehler,A., Pullmann,K., Porsch-Ozcurumez,M.,
 Duong,C., Bared,G.M., Buchler,C. and Schmitz,G.

TITLE Complete coding sequence, promoter region, and genomic structure of
 the human ABCA2 gene and evidence for sterol-dependent regulation

in macrophages

JOURNAL Biochem. Biophys. Res. Commun. 281 (1), 249-258 (2001)

MEDLINE 21092814

PUBMED 11178988

REFERENCE 2 (bases 1 to 7482)

AUTHORS Kaminski,W.E.

TITLE Direct Submission

JOURNAL Submitted (12-DEC-2000) Institute for Clinical Chemistry and Laboratory Medicine, University of Regensburg, FJS Allee 11, Regensburg 93042, Germany

FEATURES Location/Qualifiers

source 1. .7482

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ORIGIN

Query Match 93.1%; Score 7482; DB 9; Length 7482;
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Matches 7482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	601	TCTGCCCTGGATTACAGTCTGGCCTCCACAAGGGTCAGGAGCCCTGGAGCCGCCTAGGG	660
Qy	689	GGCAATCCCCTGTTCCGGATGGAGGAGCTGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTC	748
Db	661	GGCAATCCCCTGTTCCGGATGGAGGAGCTGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTC	720
Qy	749	ACCTGCACGCCGGGCTCGGGGGAGCTGGGCCGGATCCTCACTGTGCCTGAGAGTCAGAAG	808
Db	721	ACCTGCACGCCGGGCTCGGGGGAGCTGGGCCGGATCCTCACTGTGCCTGAGAGTCAGAAG	780
Qy	809	GGAGCCCTGCAGGGCTACCGGGATGCTGTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGG	868
Db	781	GGAGCCCTGCAGGGCTACCGGGATGCTGTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGG	840
Qy	869	CGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAACCAGCTGGACGTGGCCAAGGTCTCCAG	928
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Db	1021	GTCCTGTCGGCCCTGGCCCTGCTACTGCCCCAGGGTGCCTGCACTGGCCGGACCCCCGGA	1080
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Db	1141	CCCAACGCCACCGCTGAGGAGGGCGCACCTCTGCTGCAGCACTGGCCACCCCGGACACG	1200
Qy	1229	CTGCAGGGCCAGTGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGT	1288
Db	1201	CTGCAGGGCCAGTGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGT	1260
Qy	1289	GGCAACAACCGCACCATTTGAACCCGAGGCGCTGCGGCGGGGCAACATGAGCTCCCTGGGC	1348
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Qy	1349	TTCACGAGCAAGGAGCAGCGGAACCTGGGCCTCCTCGTGCACCTCATGACCAGCAACCCC	1408
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Qy	1409	AAAATCCTGTACGCGCCTGCGGGCTCTGAGGTGCACCGCGTCATCCTCAAGGCCAACGAG	1468
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Db	1981	 GGCTTCGTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCAC	2040
Qy	2069	GACGTGGTGGAGCCAGGCAGCTACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGAT	2128
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Qy	2189	TCCGTGGCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTG	2248
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Qy	3149	ACCGGCCTGTTCCCTCCAACGTGCGGTTCCGCCACCATCTACGGGCACGACATCCGCACG	3208
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Qy	3209	GAGATGGATGAGATCCGCAAGAACCTGGGCATGTGCCCCGAGCACAATGTGCTCTTTGAC	3268
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Qy	3269	CGGCTCACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAG	3328
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Db	3361	TCACTGGTGCAGACATTGTCGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTC	3420
Qy	3449	GTGGGCGGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCG	3508
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Qy	3569	ACCCACCACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGG	3628
Db	3541	ACCCACCACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGG	3600
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Qy	3869	CTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTTCGAGCGCCTCTTCAGCACCTGGAGCGC	3928
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Qy	4589	CGGCTATCGCCCGACGCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGG	4648
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Qy	4649	GTGGGTGCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCACGTTGAAC	4708
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Qy	4709	CTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAG	4768
Db	4681	CTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAG	4740
Qy	4769	TCCTTCACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCGCCCCA	4828
Db	4741	TCCTTCACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCGCCCCA	4800
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Db	4861	 ACCGCTGGGCCAGAAATGTGGACGTCGGCACCCCTCCCTGCCGCGCCTGGTACGGGAGCCC	4920
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Db	4921	 GTCCGCTGCACCTGCTCTGCGCAGGGCACC GGCTTCTCCTGCCCCAGCAGTGTGGGCGGG	4980
Qy	5009	CACCCGCCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACATCACCGGCCACAAT	5068
Db	4981	 CACCCGCCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACATCACCGGCCACAAT	5040
Qy	5069	GTCTCTGAGTACCTGCTCTTACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATC	5128
Db	5041	 GTCTCTGAGTACCTGCTCTTACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATC	5100
Qy	5129	ACCTTTGGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATG	5188
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Qy	5189	GTGCGGAAGATCGCGGTGCGCAGGGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCAC	5248
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Qy	5249	AGCATGCCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACCTGCCCAAG	5308
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Db	5281	 AGCAAGGGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACC	5340
Qy	5369	AGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGGGCAGGATGTCGTCATCGCCATCTTC	5428
Db	5341	 AGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGGGCAGGATGTCGTCATCGCCATCTTC	5400
Qy	5429	ATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAG	5488
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Qy	5669	CTCTTCCTGCTCTATGGGTGGTCCATCAGCCCCATCATGTACCGGCCTCCTTCTGGTTC	5728
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Qy	6209	GTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTG	6268
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Qy	7229	GAGCTCCGGGCACTTGTGGCAGACGAGCCGAGGACCTGGACACGGAGGACGAGGGCCTC	7288
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RESULT 8

AX235953

LOCUS AX235953 7305 bp DNA linear PAT 26-SEP-2001

DEFINITION Sequence 9 from Patent WO0164875.

ACCESSION AX235953

VERSION AX235953.1 GI:15795824

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Glucksmann,M.A.

TITLE Human transporter genes and proteins encoded thereby

JOURNAL Patent: WO 0164875-A 9 07-SEP-2001;
 Millennium Pharmaceuticals, Inc. (US)

FEATURES

Location/Qualifiers
 source 1. .7305
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 /db_xref="taxon:9606"

ORIGIN

Query Match 90.8%; Score 7301.8; DB 6; Length 7305;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 7303; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 95 AGCCCGTGGGTCTTGGCCTTCGAGATCTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTG 154
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 Db 61 AGCCCGTGGGTCTTGGCCTTCGAGATCTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTG 120

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Qy	1535	CGCAGCTTCCTGGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTATGTA	1594
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Qy	1595	GCAGAGCTGCGGCTGCACCCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCGGCC	1654
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Qy	1655	CTGAGACAGGACAACTTCTCGCTGCCCAGTGGCATGGCCCTCCTGCAGCAGCTGGATACC	1714
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Qy	1775	AAGGGCTTCCCCGACGAGGAGAGCATTGTCAACTACACCCTCAACCAGGCCTACCAGGAC	1834
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Qy	1895	CACGTGCACTACAAGATCCGCCAGAACTCCAGCTTCACCGAGAAAACCAACGAGATCCGC	1954
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Qy	1955	CGCGCCTACTGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCCTCTACGGCTTC	2014
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Qy	2075	GTGGAGCCAGGCAGCTACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTC	2134
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Qy	2135	CTGTTTGTCAATTGAGCACATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTG	2194
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Qy	2195	GCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAG	2254
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Qy	2255	ACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAG	2314
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Qy	2435	TGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATC	2494
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Qy	2495	ATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCAT	2554
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Qy	2555	GATAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGT	2614
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Qy	3215	GATGAGATCCGCAAGAACCTGGGCATGTGCCCAGCACAATGTGCTCTTTGACCGGCTC	3274
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Qy	5075	GAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTT	5134
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RESULT 9

AX088337

LOCUS AX088337 6792 bp DNA linear PAT 17-MAR-2001

DEFINITION Sequence 1 from Patent WO0114414.

ACCESSION AX088337

VERSION AX088337.1 GI:13397233

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS le Bihan, S., Wilson, C. and Charest, D.L.

TITLE Human abc2 transporter and uses thereof

JOURNAL Patent: WO 0114414-A 1 01-MAR-2001;

Activepass Pharmaceuticals, Inc. (CA)

FEATURES

Location/Qualifiers

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CDS

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ORIGIN

Query Match 83.2%; Score 6686.8; DB 6; Length 6792;
 Best Local Similarity 99.3%; Pred. No. 0;
 Matches 6748; Conservative 9; Mismatches 33; Indels 7; Gaps 4;

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Db	1081	TCCGTGACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTG	1140
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Qy	2444	GTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTC	2503
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Qy	2684	TCCCCGGTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGAC	2743
Db	1438	TCCCCGGTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGAC	1497
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Db	1498	GCCGTGGTCTATGGCATCCTCMCGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGG	1557
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Db	1558	CTGCCCCGGCCCTGGTACTTCCCCTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACA	1617
Qy	2864	GAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCTATGGAGGAG	2923
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Qy	2924	GACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAG	2983
Db	1678	GACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAG	1737
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Db	1738	CCCACCCACCTGCCTCTGGTTGTCTKCGTGGACAACTCACCAAGGTCTACAAGGACGAC	1797
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Qy	3164	CCAACGTCGGGTTCGCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATC	3223
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Db	1978	CGCAAGAAC--GGGCATGTGCCC-CAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAG	2034
Qy	3284	GAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAG	3343
Db	2035	GAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCCCAGAGAG	2094
Qy	3344	ATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACA	3403
Db	2095	ATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACA	2154
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Qy	3524	GACCTCATCCTGAAGTACAAGCCAGGCCGCACCATCCTTCTGTCCACCCACCACATGGAT	3583
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Qy	3584	GAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGC	3643
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Qy	4184	GGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAAC	4243
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Qy	4244	CCACAGGACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTC	4303
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Qy	4304	GGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTG	4363
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Db	3115	 CTGGTCAAACGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTG	3174
Qy	4424	CTGCCAGCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGT	4483
Db	3175	 CTGCCAGCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGT	3234
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Qy	4544	AATTTTCATCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCCGAC	4603
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Qy	4604	GCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGC	4663
Db	3355	 GCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGC	3414
Qy	4664	GTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAG	4723
Db	3415	 GTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAG	3474
Qy	4724	TCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGG	4783
Db	3475	 TCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGG	3534
Qy	4784	CTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCG	4843
Db	3535	 CTGCCACTGTCAAATTTTCGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCG	3594
Qy	4844	TCCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCACCGCTGGGCCAGAA	4903
Db	3595	 TCCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCACCGCTGGGCCAGAA	3654
Qy	4904	ATGTGGACGTGCGCACCCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGC	4963
Db	3655	 ATGTGGACGTGCGCACCCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGC	3714
Qy	4964	TCTGCGCAGGGCACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATG	5023
Db	3715	 TCTGCGCAGGGCACCGGCTTCTCCTGCCCCAACAGTGTGGGCGGGCACCCGCCCCAGATG	3774
Qy	5024	CGGGTGGTCACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTG	5083
Db	3775	 CGGGTGGTCACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTG	3834
Qy	5084	CTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTC	5143
Db	3835	 CTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTC	3894
Qy	5144	CTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCG	5203
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Db	3955	TGCGCCAGGGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTAC	4014
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Qy	5444	TCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAG	5503
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Qy	5984	TTCGAGTGGGACATTGTCAACCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGC	6043
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RESULT 10

AB028985

LOCUS AB028985 6011 bp mRNA linear PRI 10-MAY-2002

DEFINITION Homo sapiens mRNA for KIAA1062 protein, partial cds.

ACCESSION AB028985

VERSION AB028985.2 GI:20521747

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Kikuno,R., Nagase,T., Ishikawa,K., Hirosawa,M., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.

TITLE Prediction of the coding sequences of unidentified human genes. XIV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro

JOURNAL DNA Res. 6 (3), 197-205 (1999)

MEDLINE 99397452

PUBMED 10470851

REFERENCE 2 (bases 1 to 6011)

AUTHORS Ohara,O., Nagase,T. and Kikuno,R.

TITLE Direct Submission

JOURNAL Submitted (17-JUN-1999) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)

COMMENT On May 9, 2002 this sequence version replaced gi:5689460.

FEATURES

source

Location/Qualifiers

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/Note="This sequence was obtained by subcloning of the DNA
fragments derived from two cDNA clones (1 - 2387 was
derived from hg03338 and 2388 - 6011 was derived from
hj03579)."
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gene 1. .6011

CDS <1. .5316

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ORIGIN

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Query Match          74.8%;  Score 6011;  DB 9;  Length 6011;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 6011;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Db      1 ATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGC 60

Qy      2090 TACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAG 2149
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Db      61 TACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAG 120
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Qy	2150	CACATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAG	2209
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Qy	2210	CACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAAC	2269
Db	181	CACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAAC	240
Qy	2270	AACGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTG	2329
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Qy	2330	ACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATC	2389
Db	301	ACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATC	360
Qy	2390	ATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCT	2449
Db	361	ATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCT	420
Qy	2450	GTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGC	2509
Db	421	GTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGC	480
Qy	2510	TACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCC	2569
Db	481	TACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCC	540
Qy	2570	TTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTAC	2629
Db	541	TTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTAC	600
Qy	2630	TTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCG	2689
Db	601	TTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCG	660
Qy	2690	GTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTACCATGCTGATGGTGGACGCCGTG	2749
Db	661	GTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTACCATGCTGATGGTGGACGCCGTG	720
Qy	2750	GTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCC	2809
Db	721	GTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCC	780
Qy	2810	CGGCCCTGGTACTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCC	2869
Db	781	CGGCCCTGGTACTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCC	840
Qy	2870	TGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTGATGGAGGAGGACCAG	2929
Db	841	TGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTGATGGAGGAGGACCAG	900
Qy	2930	GCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACC	2989
Db	901	GCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACC	960
Qy	2990	CACCTGCCTCTGGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAG	3049

Db	961	 CACCTGCCTCTGGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAG	1020
Qy	3050	CTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGC	3109
Db	1021	 CTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGC	1080
Qy	3110	CACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACG	3169
Db	1081	 CACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACG	1140
Qy	3170	TCGGGTTCCGCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAG	3229
Db	1141	 TCGGGTTCCGCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAG	1200
Qy	3230	AACCTGGGCATGTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACAC	3289
Db	1201	 AACCTGGGCATGTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACAC	1260
Qy	3290	CTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGAC	3349
Db	1261	 CTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGAC	1320
Qy	3350	AAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCTG	3409
Db	1321	 AAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCTG	1380
Qy	3410	GGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATC	3469
Db	1381	 GGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATC	1440
Qy	3470	ATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTC	3529
Db	1441	 ATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTC	1500
Qy	3530	ATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCT	3589
Db	1501	 ATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCT	1560
Qy	3590	GACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCC	3649
Db	1561	 GACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCC	1620
Qy	3650	CCGCTCTTCCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCC	3709
Db	1621	 CCGCTCTTCCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCC	1680
Qy	3710	GCCGAGCCGGGGGGGGCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGGCCCCG	3769
Db	1681	 GCCGAGCCGGGGGGGGCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGGCCCCG	1740
Qy	3770	CTGAGCAGCTGCTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGC	3829
Db	1741	 CTGAGCAGCTGCTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGC	1800
Qy	3830	CTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAG	3889

Db	1801	CTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAG	1860
Qy	3890	AAGGGGGCTTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTC	3949
Db	1861	AAGGGGGCTTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTC	1920
Qy	3950	AGCAGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTCGGAGGAG	4009
Db	1921	AGCAGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTCGGAGGAG	1980
Qy	4010	GATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCT	4069
Db	1981	GATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCT	2040
Qy	4070	GGGGCGGAGGGCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAG	4129
Db	2041	GGGGCGGAGGGCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAG	2100
Qy	4130	CTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCGTGGCGAC	4189
Db	2101	CTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCGTGGCGAC	2160
Qy	4190	GAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAG	4249
Db	2161	GAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAG	2220
Qy	4250	GACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTCGGCCAG	4309
Db	2221	GACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTCGGCCAG	2280
Qy	4310	GGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTC	4369
Db	2281	GGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTC	2340
Qy	4370	AAACGCTTCCACTGCGCCCCGCCGCAACTCCAAGGCACTCTTCTCCAGATCTTGCTGCCA	4429
Db	2341	AAACGCTTCCACTGCGCCCCGCCGCAACTCCAAGGCACTCTTCTCCAGATCTTGCTGCCA	2400
Qy	4430	GCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTG	4489
Db	2401	GCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTG	2460
Qy	4490	CCCCCGCTGGTCTGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTC	4549
Db	2461	CCCCCGCTGGTCTGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTC	2520
Qy	4550	ATCCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCCAGGCCAGC	4609
Db	2521	ATCCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCCAGGCCAGC	2580
Qy	4610	CCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTC	4669
Db	2581	CCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTC	2640
Qy	4670	AAGTCTCCCGCCAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGC	4729
Db	2641	AAGTCTCCCGCCAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGC	2700

Qy	4730	CTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCA	4789
Db	2701	CTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCA	2760
Qy	4790	CTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCCGCCCATCTGACTCGCCAGCGTCCCCG	4849
Db	2761	CTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCCGCCCATCTGACTCGCCAGCGTCCCCG	2820
Qy	4850	GATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGG	4909
Db	2821	GATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGG	2880
Qy	4910	ACGTCGGCACCCCTCCCTGCCGCGCCTGGTACGGGAGCCCCTCCGCTGCACCTGCTCTGCG	4969
Db	2881	ACGTCGGCACCCCTCCCTGCCGCGCCTGGTACGGGAGCCCCTCCGCTGCACCTGCTCTGCG	2940
Qy	4970	CAGGGCACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTG	5029
Db	2941	CAGGGCACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTG	3000
Qy	5030	GTCACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTC	5089
Db	3001	GTCACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTC	3060
Qy	5090	ACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAG	5149
Db	3061	ACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAG	3120
Qy	5150	TCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGC	5209
Db	3121	TCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGC	3180
Qy	5210	AGGGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAAC	5269
Db	3181	AGGGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAAC	3240
Qy	5270	AGCCTCAACAACGCCATCCTGCGTGCCAACTGCCCAAGAGCAAGGGCAACCCGGCGGCT	5329
Db	3241	AGCCTCAACAACGCCATCCTGCGTGCCAACTGCCCAAGAGCAAGGGCAACCCGGCGGCT	3300
Qy	5330	TACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGAT	5389
Db	3301	TACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGAT	3360
Qy	5390	TACCTGCTGCAGGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTC	5449
Db	3361	TACCTGCTGCAGGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTC	3420
Qy	5450	GTGCCGGCCAGCTTCGTGTGCTTCTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTG	5509
Db	3421	GTGCCGGCCAGCTTCGTGTGCTTCTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTG	3480
Qy	5510	CAGTTTGTGACGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATG	5569
Db	3481	CAGTTTGTGACGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATG	3540

Qy	5570	CTCAACTACCTGGTCCCCGCTACCTGCTGTGTGCATCATCCTGTTTGTGTTTCGACCTGCCG	5629
Db	3541	CTCAACTACCTGGTCCCCGCTACCTGCTGTGTGCATCATCCTGTTTGTGTTTCGACCTGCCG	3600
Qy	5630	GCCTACACGTGCGCCACCAACTTCCCTGCCGTCCTCTCCCTCTTCCTGCTCTATGGGTGG	5689
Db	3601	GCCTACACGTGCGCCACCAACTTCCCTGCCGTCCTCTCCCTCTTCCTGCTCTATGGGTGG	3660
Qy	5690	TCCATCACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTAC	5749
Db	3661	TCCATCACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTAC	3720
Qy	5750	GTGTTCCCTCATTGTGCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTG	5809
Db	3721	GTGTTCCCTCATTGTGCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTG	3780
Qy	5810	CTACAGCTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGC	5869
Db	3781	CTACAGCTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGC	3840
Qy	5870	TTCCTCATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAG	5929
Db	3841	TTCCTCATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAG	3900
Qy	5930	TACATCAACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAG	5989
Db	3901	TACATCAACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAG	3960
Qy	5990	TGGGACATTGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTC	6049
Db	3961	TGGGACATTGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTC	4020
Qy	6050	CTGACCATCATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACC	6109
Db	4021	CTGACCATCATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACC	4080
Qy	6110	AAGCCTGTGGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGAC	6169
Db	4081	AAGCCTGTGGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGAC	4140
Qy	6170	GCCGACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATT	6229
Db	4141	GCCGACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATT	4200
Qy	6230	GGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGG	6289
Db	4201	GGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGG	4260
Qy	6290	CTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAG	6349
Db	4261	CTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAG	4320
Qy	6350	AGCACGACGGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAG	6409
Db	4321	AGCACGACGGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAG	4380
Qy	6410	GTGCAGCAGAGCCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTTCGACGAGCTCACGGCC	6469

Db	4381	 GTGCAGCAGAGCCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTTCGACGAGCTCACGGCC	4440
Qy	6470	CGGGAGCACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGG	6529
Db	4441	 CGGGAGCACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGG	4500
Qy	6530	GTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGC	6589
Db	4501	 GTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGC	4560
Qy	6590	ACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTTGGGTACCCA	6649
Db	4561	 ACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTTGGGTACCCA	4620
Qy	6650	GCCTTCATCTTCCTGGACGAGCCACCACAGGCATGGACCCCAAGGCCGGCGCTTCCTC	6709
Db	4621	 GCCTTCATCTTCCTGGACGAGCCACCACAGGCATGGACCCCAAGGCCGGCGCTTCCTC	4680
Qy	6710	TGGAACCTCATCCTCGACCTCATCAAGACAGGGCGTTCAGTGGTGCTGACATCACACAGC	6769
Db	4681	 TGGAACCTCATCCTCGACCTCATCAAGACAGGGCGTTCAGTGGTGCTGACATCACACAGC	4740
Qy	6770	ATGGAGGAGTGCAGGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGG	6829
Db	4741	 ATGGAGGAGTGCAGGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGG	4800
Qy	6830	TGCCTGGGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTG	6889
Db	4801	 TGCCTGGGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTG	4860
Qy	6890	CGGACCAAGAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCG	6949
Db	4861	 CGGACCAAGAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCG	4920
Qy	6950	GAAGCCATGCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCAC	7009
Db	4921	 GAAGCCATGCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCAC	4980
Qy	7010	ATCTCGCTGGCCCAGGTGTTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAG	7069
Db	4981	 ATCTCGCTGGCCCAGGTGTTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAG	5040
Qy	7070	GACTACTCGGTCAGCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAG	7129
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Qy	7130	AGTGACAACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGC	7189
Db	5101	 AGTGACAACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGC	5160
Qy	7190	TGCTTGCTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACCTTGTGGCA	7249
Db	5161	 TGCTTGCTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACCTTGTGGCA	5220
Qy	7250	GACGAGCCCGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGG	7309

Db	5221	GACGAGCCCGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGG	5280
Qy	7310	GCCCAGCTGTCCTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGG	7369
Db	5281	GCCCAGCTGTCCTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGG	5340
Qy	7370	ACACGCTCCACTGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCC	7429
Db	5341	ACACGCTCCACTGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCC	5400
Qy	7430	CCAGTGCCTGCCAGGGCCTGGAGTGGAGGTTCAGGACCAAGGGGCTTCTGGTCCTCCAGC	7489
Db	5401	CCAGTGCCTGCCAGGGCCTGGAGTGGAGGTTCAGGACCAAGGGGCTTCTGGTCCTCCAGC	5460
Qy	7490	CCCTGTACTCGGCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAAAGGC	7549
Db	5461	CCCTGTACTCGGCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAAAGGC	5520
Qy	7550	TGACCCGGCCCCGGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGC	7609
Db	5521	TGACCCGGCCCCGGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGC	5580
Qy	7610	CCGGCCCCCTCGCCCCCTGCCTGGCACTGCTCACCGCCCCAAGGCGACGCCGGCTGGACCAGG	7669
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LOCUS AX088339 6006 bp DNA linear PAT 17-MAR-2001
 DEFINITION Sequence 3 from Patent WO0114414.
 ACCESSION AX088339
 VERSION AX088339.1 GI:13397235
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS le Bihan,S., Wilson,C. and Charest,D.L.
 TITLE Human abc2 transporter and uses thereof
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ORIGIN

Query Match 73.6%; Score 5915.4; DB 6; Length 6006;
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 Matches 5965; Conservative 9; Mismatches 32; Indels 6; Gaps 3;

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Db	3115	ACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTTCCCCCGCTGGTCTGTACCTTCC	3174
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Qy	4694	GGGCCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGAC	4753
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Qy	6134	GTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATT	6193
Db	4795	GTGGCCAGTGAGCGGCAGCGGGTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATT	4854
Qy	6194	GAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGC	6253
Db	4855	GAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGC	4914
Qy	6254	CTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGC	6313
Db	4915	CTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGC	4974
Qy	6314	AAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTC	6373

Db	4975	 AAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTC	5034
Qy	6374	GTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGC	6433
Db	5035	 GTCAATGGACACAGCGTGCTGAAGGAGCTGCHCCAGGTGCAGCAGAGCCTCGGCTACTGC	5094
Qy	6434	CCGCAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCTGCAGCTGTACACG	6493
Db	5095	 CCGCAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCTGCAGCTGTACACG	5154
Qy	6494	CGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAG	6553
Db	5155	 CGGCTNCGTGGGATCYCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAG	5214
Qy	6554	CTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGG	6613
Db	5215	 CTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGG	5274
Qy	6614	AAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCC	6673
Db	5275	 AAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCC	5334
Qy	6674	ACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCCTCGACCTCATC	6733
Db	5335	 ACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCCTTGACCTCATC	5394
Qy	6734	AAGACAGGGCGTTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGC	6793
Db	5395	 AAGACAGGGCGTTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGC	5454
Qy	6794	ACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTG	6853
Db	5455	 ACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTG	5514
Qy	6854	AAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTG	6913
Db	5515	 AAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTG	5574
Qy	6914	AAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCAC	6973
Db	5575	 AAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCAC	5634
Qy	6974	CACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAGC	7033
Db	5635	 CACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAGC	5694
Qy	7034	AAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACA	7093
Db	5695	 AAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACA	5754
Qy	7094	CTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAG	7153
Db	5755	 CTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAG	5814
Qy	7154	ACGGAGCCGCCATCCGCACTGCAGTCCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCC	7213

Db 5815 ACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCC 5874
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 Db 5875 CGGTCTGCCCCACGGAGCTCCGGGCACCTTGTGGCAGACGAGCCCGAGGACCTGGACACG 5934
 Qy 7274 GAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCAGCTGTCCTTCAACACGGAC 7333
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 Db 5935 GAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCAGCTGTCCTTCAACACGGAC 5994
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RESULT 12

BD140902

LOCUS BD140902 8040 bp DNA linear PAT 18-SEP-2002

DEFINITION Human and rat ABCA2 gene.

ACCESSION BD140902

VERSION BD140902.1 GI:23235847

KEYWORDS WO 0208424-A/3.

SOURCE Rattus sp.

ORGANISM Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 8040)

AUTHORS Inagaki,N.

TITLE Human and rat ABCA2 gene

JOURNAL Patent: WO 0208424-A 3 31-JAN-2002;
BANYU PHARMACEUTICAL CO LTD,NOBUYA INAGAKI

COMMENT OS Rattus sp. (rat)

PN WO 0208424-A/3

PD 31-JAN-2002

PF 26-JUL-2001 WO 2001JP006457

PR 26-JUL-2000 JP 00P 225462

PI NOBUYA INAGAKI

PC

C12N15/12,C07K14/47,C12N1/15,C12N1/19,C12N1/21,C12N5/00,G01N33/ 68, PC

PC G01N33/15,G01N33/50

CC Human and rat ABCA2 gene

FH Key Location/Qualifiers

FT source 1. .8040

FT /organism='Rattus sp. (rat)'.

FEATURES Location/Qualifiers

source 1. .8040

/organism="Rattus sp."

/mol_type="genomic DNA"

/db_xref="taxon:10118"

ORIGIN

Query Match 72.3%; Score 5810; DB 6; Length 8040;

Best Local Similarity 84.0%; Pred. No. 0;

Matches 6768; Conservative 0; Mismatches 1205; Indels 85; Gaps 15;

Qy 1 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 60
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 Db 34 CCGCGGCGCTGAGGCGGCGGAGCGCGGCCCGGCCATGGGCTTCCTGCACCAGCTGCAGCT 93

Qy 61 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTGGCCTTCGAGAT 120
 |||
 Db 94 GCTGCTCTGGAAGAACGTGACGCTGAAGCGCCGGAGCCCGTGGGTCTGGCCTTCGAGAT 153

Qy 121 CTTTCATCCCCCTGGTGTCTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 180
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 Db 154 CTTTCATCCCCCTTGTCTCTTCTTCATCCTGTTGGGACTGCGGCAGAAGAAGCCCACCAT 213

Qy 181 CTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCTGACGTCTGCCGGCATCCTGCC 240
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 Db 214 CTCTGTGAAGGAAG---CTTTCTACACGGCAGCACCGCTGACATCGGCCGGCATCCTGCC 270

Qy 241 TGTTCATGCAATCGCTGTGCCCGGACGGCCAGCGAGACGAGTTCCGGCTTCCTGCAGTACGC 300
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 Db 271 TGTTCATGCAGTCGCTTTGCCCTGATGGCCAGCGTGATGAGTTTGGCTTCCTGCAGTATGC 330

Qy 301 CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT 360
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 Db 331 CAACTCCACGGTCACCCAGCTTCTGGAACGCCTCAACCGTGTAGTGAAGAGAGCAACTT 390

Qy 361 GTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA 420
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 Db 391 GTTTGACCCAGAGCGACCTAGCCTGGGCTCAGAGCTTGAGGCACTGCACCAACGTCTGGA 450

Qy 421 GGCCCTCAGTGCGGGGCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC 480
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Qy 481 CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA 540
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 Db 511 CTTCTCTCTGGACTCGGTGGCCAGGGACAAAAGAGAGCTTTGGCGTTTCCTGATGCAGAA 570

Qy 541 CTTGTGCTGCCCCAATAGCACGGCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCCGA 600
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Qy 601 GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA 660
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 Db 631 GGTCTATCGCTTGCTTTTGGTCCTTTACCTGACCTGGATGGAAAGTTGGGGTTCTCAG 690

Qy 661 GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT 720
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Qy 721 GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG 780
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 Db 751 GCTGGCTCCTGCCCTTTTGGAGCAACTCACATGTGCTCCAGGCTCTGGGGAGCTGGGCCG 810

Qy 781 GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG 840
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 Db 811 GATTCTTACCATGCCTGAGGGTCATCAGGTAGACCTTCAGGGCTACCGGGATGCTGTCTG 870

Qy 841 CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA 900

Db	871		CAGCGGGCAGGCTACAGCTCGTGCCAGCATTTCACTGATCTAGCCACTGAGCTCCGGAA	930
Qy	901		CCAGCTGGACGTGGCCAAGGTCTCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	960
Db	931		CCAGCTGGACATAGCCAAGATTGCCAGCAGCTGGGCTTCAATGTCCCCAACGGCTCAGA	990
Qy	961		CTCCTCGCCACAGGCGCCACCCACGGAGGCTGCAGGCGCTTCTGGGGACCTGCTGGA	1020
Db	991		TCCACAGCCGCAGGCACCGTCCCCACAGAGTCTGCAGGCACTCTTAGGGGACCTGCTGGA	1050
Qy	1021		TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTCGGCCCTGGCCCTGCTACTGCCCCA	1080
Db	1051		TGTCCAGAAGGTTCTACAGGATGTGGATGTCCTATCAGCCCTTGCCCTGCTGCTGCCTCA	1110
Qy	1081		GGGTGCCTGCACTGGCCGGACCCCGGACCCCGAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Db	1111		AGGTGCCTGTGCTGGCCGGGCCCCGCACCTCAAGCTGGCAGCCCGAGTGGCCCGGCCAA	1170
Qy	1141		TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCTC	1200
Db	1171		CAGCACCGGGGTAGGGGCAAATACAGGTCCCAACACCACCGTTGAGGAGGGCACCCAGTC	1230
Qy	1201		TGCTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
Db	1231		ACCTGTCACCCAGCCTCTCCGGACACTCTGCAAGGCCAGTGCTCAGCCTTTGTGCAGCT	1290
Qy	1261		CTGGGCGGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCT	1320
Db	1291		CTGGGCTGGCTTGCAAGCCCATCTTGTGTGGCAACAACCGTACCATTGAGCCTGAAGCACT	1350
Qy	1321		GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380
Db	1351		CCGAGGGGCAACATGAGCTCACTGGGCTTTACGAGCAAAGAACAACGAACCTGGGCCT	1410
Qy	1381		CCTCGTGACCTCATGACCAGCAACCCCAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
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Qy	1441		CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1500
Db	1471		TGACCATGTTATCCTCAAGGCAAATGAGACCTTTGCCTTTGTGGGCAACGTGACGCACTA	1530
Qy	1501		TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1531		CGCCCAGGTCTGGCTCAACATCTCCGCAGAGATCCGGAGCTTCCTGGAGCAGGGCAGGCT	1590
Qy	1561		GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620
Db	1591		GCAGCAGCATCTGCACTGGCTGCAGCAGTACGTGGCTGACCTCCGGCTACACCCTGAAGC	1650
Qy	1621		ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1680
Db	1651		AATGAACCTGTCACTGGACGAGCTGCCCCCTGCTCTGCGCCTGGACTACTTTTCTCTGCC	1710
Qy	1681		CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGAT	1740

Db	1711	CAATGGCACAGCCCTTCTGCAGCAGCTAGACACAATAGACAATGCAGCCTGTGGCTGGAT	1770
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCGACGAGGAGAGCAT	1800
Db	1771	CCAGTTCATGTCCAAGGTGAGTGTGGACATCTTCAAGGGGTTTCCTGATGAGGAGAGCAT	1830
Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1860
Db	1831	CGTGAACTACACTCTCAATCAGGCCTACCAGGACAATGTTACAGTATTTGCCAGCGTGAT	1890
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1920
Db	1891	TTTCCAGACACGGAAGGATGGTTCCTCCCCCACATGTCCATTACAAGATTCGCCAGAA	1950
Qy	1921	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1980
Db	1951	CTCAAGCTTCACCGAGAAAACCAACGAGATCCGTCTGTCTTACTGGCGTCCAGGGCCAA	2010
Qy	1981	TACTGGCGGCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Db	2011	CACTGGTGGCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATAGAACG	2070
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Db	2071	TGCCATCATCAACACGTTTGTGGGGCACGACGTGGTTCGAACCCGGCAACTACGTGCAGAT	2130
Qy	2101	GTTCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2160
Db	2131	GTTCCCGTACCCCTGCTACACCCGTGACGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2190
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Db	2191	ACTGTGCATGGTGATCTCCTGGGTTTACTCTGTGGCCATGACCATACAGCACATCGTGGC	2250
Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280
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Qy	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2340
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Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2400
Db	2371	CGCCATCCTCAAGTATGGCCAGGTCCTCATGCACAGCCACGTGCTCATCATATGGCTCTT	2430
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2460
Db	2431	CCTTGCTGTCTATGCTGTGGCCACTATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2490
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Db	2491	TAAGGCCAAGTTGGCCTCGGCCTGCGGCGGCATCATCTACTTCCTGAGCTACGTTCCCTA	2550
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
Db	2551	CATGTATGTAGCAATCCGTGAGGAAGTAGCCACGATAAGATCACTGCCTTCGAGAAGTG	2610

Qy 2581 CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA 2640
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 Db 2611 CATTGCGTCCCTGATGTCCACAACAGCCTTCGGCCTGGGTCCAAGTACTTTGCTCTGTA 2670

Qy 2641 TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGA 2700
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Qy 2701 CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT 2760
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 Db 2731 TGACTTCAACCTGCTCCTTGCTGTCACCATGCTGATGGTGGACACAGTGGTCTATGGCGT 2790

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Qy 2821 CTTCCCACTGCAGAAGTCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG 2880
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Qy 2881 CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCTATGGAGGAGGACCAGGCCTGTGCCAT 2940
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Qy 2941 GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT 3000
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Qy 3061 CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC 3120
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Qy 3181 CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT 3240
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Qy 3301 CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA 3360
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Qy 3361 GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTGCGGTGGCATGAA 3420
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Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCTGGACGA	3480
Db	3451		
		GCGCAAGCTTTCAGTAGCCATTGCCTTCGTGGGTGGCTCTAGAGCCATTATCTTAGATGA	3510
Qy	3481	GCCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCTGAAGTA	3540
Db	3511		
		GCCCCACAGCTGGCGTGGACCCCTATGCTCGACGTGCCATCTGGGACCTCATTCTGAAGTA	3570
Qy	3541	CAAGCCAGGCCGACCATCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3571		
		CAAGCCGGGTGCGACTATCTCCTGTCCACCACATCACATGGATGAGGCCGACCTGCTGGG	3630
Qy	3601	GGACCGCATTTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3631		
		GGACCGCATTTGCCATCATCTCCCATGGGAAGCTCAAATGCTGCGGCTCTCCCCTCTTCCT	3690
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3720
Db	3691		
		CAAGGGTGCTACGGCGATGGCTACCGCCTCACACTGGTCAAGCGGCCTGCGGAGCCTGG	3750
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGGCCCCGCTGAGCAGCTG	3780
Db	3751		
		CACCTCCCAAGAGCCAGGGATGGCTTCCAGCCCCCTCAGGTGCTCCTCAGCTGAGCAACTG	3810
Qy	3781	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3811		
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Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCACGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3871		
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Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3931		
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Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCTGGAGGAGGATCAGTCGCT	4020
Db	3991		
		GCTGATGGACACAACCCTGGAGGAGGTGTTCCTCAAGGTGTCTGAAGAAGACCAGTCACT	4050
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4051		
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Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4111		
		CCTGACGGCTGTGGAGAGTCAAGCAGGCAACCTGGCTCGGTGCTCAGAGCTGGCACAGTC	4170
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCGTGGCGACGAGGGAGCTGG	4200
Db	4171		
		CCAGGCTTCACTGCAGTCTGCATCTTCTGTGGGCTCCGCCGTGGGGATGAGGGTGCTGG	4230
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4231		
		CTACACCGACGGCTACGGTGACTACCGTCCCCTCTTTGACAACCTTGCAGGACCCAGACAG	4290
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCTGAGGGTCTGCCAGGGCAGCCGCAA	4320

Db	4291	TGTCAGCTTACAAGAGGCTGAAATGGAGGCCCTGGCTCGGGTAGGCCAGGGCAGCCGCAA	4350
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4351	GCTAGAGGGCTGGTGGCTGAAGATGCGGCAGTTCCATGGGCTCCTGGTGAAGCGCTTCCA	4410
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Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4471	CTGTGTGGCCATGACTGTGGCATTGTCTGTCCCTGAGATCGGTGACCTGCCTCCACTGGT	4530
Qy	4501	CCTGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4531	CCTGTGCGCTTCTCAGTACCACAACCTATACCCAGCCCCGTGGCAACTTTATCCCCTATGC	4590
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCAGCAGCT	4620
Db	4591	CAATGAGGAACGCCGCGAGTACCGATTACGGCTGTACCTGATGCCAGCCCCAGCAGTT	4650
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4651	GGTGAGCACATTCCGGCTGCCCTCTGGTGTGGGTGCCACTTGTGTGCTCAAGTCTCCAGC	4710
Qy	4681	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4711	CAACGGCTCCCTGGGGCCCATGCTGAACCTGAGCAGTGGAGAGTCCCGCCTGCTGGCCGC	4770
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4771	ACGGTTCTTCGACAGTATGTGCCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATT	4830
Qy	4801	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGA---	4857
Db	4831	CGTGCCACCCCCACCCTCGCCCGCCCCCTTCCGACTCACCCCTGTCCCCGGATGAGGATTC	4890
Qy	4858	CCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCGGC	4917
Db	4891	ACTGCTAGCCTGGAATACGTCCCTGCCCCCTACTGCTGGACCAGAGACGTGGACGTGGGC	4950
Qy	4918	ACCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCAC	4977
Db	4951	GCCTTCTCTGCCACGCCTGGTTCACGAGCCGGTCCGCTGTACCTGCTCTGCACAGGGCAC	5010
Qy	4978	CGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGG	5037
Db	5011	GGGCTTCTCGTGCCCCAGCAGTGTGGGTGGGCACCCACCCAGATGAGAGTGGTCACGGG	5070
Qy	5038	CGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGA	5097
Db	5071	GGACATCCTGACTGACATCACCGGCCACAATGTTTCCGAGTACCTGCTCTTCACCTCTGA	5130
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Db	5131	CCGTTTCCGACTGCACCGCTATGGAGCCATCACCTTTGGTAATATCCAGAAGTCCATCCC	5190
Qy	5158	AGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGC	5217
Db	5191	AGCACCCATTGGTACCCGGACCCCTCTCATGGTCCGGAAGATTGCAGTGGGAGGGTGGC	5250
Qy	5218	CCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAA	5277
Db	5251	CCAGGTGCTCTACAACAACAAGGGCTACCACAGCATGCCCACCTACCTCAACAGCCTCAA	5310
Qy	5278	CAACGCCATCCTGCGTGCCAACTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCAT	5337
Db	5311	CAATGCCATTCTGCGTGCAAACCTACCCAAAAGCAAGGGCAATCCAGCAGCCTACGGTAT	5370
Qy	5338	CACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCT	5397
Db	5371	CACCGTCACCAACCACCCCATGAACAAGACCAGTGCTAGCCTCTCCCTGGATTACCTACT	5430
Qy	5398	GCAGGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGC	5457
Db	5431	GCAGGGCACAGACGTGGTCATCGCCATCTTCATCATTTGTGGCCATGTCCTTCGTGCCGGC	5490
Qy	5458	CAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGT	5517
Db	5491	CAGCTTCGTGGTCTTCCTTGTGGCCGAGAAATCCACCAAGGCCAAACACCTGCAGTTCGT	5550
Qy	5518	CAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTA	5577
Db	5551	CAGCGGCTGCAACCCCTGTCATCTACTGGCTAGCCAACTACGTGTGGGACATGCTCAATTA	5610
Qy	5578	CCTGGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACAC	5637
Db	5611	CCTGGTCCCCGCCACCTGCTGCATCATCATCCTCTTCGTGTTTGACTTGCCGGCCTACAC	5670
Qy	5638	GTCGCCACCAACTTCCCTGCCGTCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCAC	5697
Db	5671	GTCACCCACCAACTTCCCCGCGGTGCTCTCCTTGTTCCTGCTCTATGGATGGTCCATCAC	5730
Qy	5698	GCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTTCCT	5757
Db	5731	ACCCATCATGTACCCGGCCTCCTTCTGGTTTGAGGTCCCTAGCTCAGCCTACGTGTTTCCT	5790
Qy	5758	CATTGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCTGCTACAGCT	5817
Db	5791	CATCGTCATCAACCTCTTCATTGGCATCACGGCCACAGTGGCCACCTTCTTCTGCAGCT	5850
Qy	5818	CTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCAT	5877
Db	5851	CTTTGAGCATGACAAGGATCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCAT	5910
Qy	5878	TTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAA	5937
Db	5911	CTTCCCCAACTACAACCTGGGCCACGGACTCATGGAGATAGCCTACAACGAATACATCAA	5970
Qy	5938	CGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACAT	5997
Db	5971	CGAATACTATGCCAAGATCGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACAT	6030

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Qy	6058	CATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGT	6117
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Qy	6118	GGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAA	6177
Db	6151	GGAAGACGATGTAGACGTGGCCAGTGAGCGGCAAAGAGTGCTCCGTGGCGATGCTGACAA	6210
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Db	6211	TGACATGGTCAAGATCGAGAACCTGACTAAGGTGTACAAGTCTCGGAAGATCGGCCGCAT	6270
Qy	6238	CCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGG	6297
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Qy	6298	CGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGAC	6357
Db	6331	GGTCAATGGTGCCGGGAAGACCAGCACCTTCAAGATGTTGACTGGAGATGAGAGCACAA	6390
Qy	6358	GGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCA	6417
Db	6391	AGGGGGCGAGGCCTTTGTCAATGGACACAGTGCTGCTCAAGGACCTGCTCCAGGTTGAGCA	6450
Qy	6418	GAGCCTCGGCTACTGCCCCAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCA	6477
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Qy	6478	CCTGCAGCTGTACACGGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAA	6537
Db	6511	CCTGCAGCTGTATACTCGGCTTCGAGGCATCCCCTGGAAGGATGAGGCGCAGGTGGTGAG	6570
Qy	6538	GTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAG	6597
Db	6571	GTGGGCCCTGGAGAAGCTGGAGCTGACGAAGTGTGCAGACAAGCCAGCCGGTAGCTACAG	6630
Qy	6598	CGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCAT	6657
Db	6631	TGGGGGCAACAAACGGAACTTTCCACAGCCATCGCTCTCATTGGGTACCCTGCCTTCAT	6690
Qy	6658	CTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCT	6717
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Qy	6718	CATCCTCGACCTCATCAAGACAGGGCGTTCAAGTGGTGCTGACATCACACAGCATGGAGGA	6777
Db	6751	CATTCTGGACCTCATCAAGACAGGACGTTCAAGTGGTGCTGACCTCACACAGCATGGAGGA	6810
Qy	6778	GTGCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGG	6837
Db	6811	ATGCGAGGCTGTGTGCACACGGCTGGCCATCATGGTGAATGGACGGCTGCGCTGCCTGGG	6870

Qy	6838	CAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGC	6897
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Qy	6898	GAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCAT	6957
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Qy	6958	GCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCT	7017
Db	6991	GCTCAAGGAACGCCACCATACGAAGGTGCAGTATCAGCTCAAGTCGGAGCACATCTCGCT	7050
Qy	7018	GGCCCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTC	7077
Db	7051	GGCTCAGGTGTTTCAGCAAGATGGAGCACGTGGTTCGGTGTA	7110
Qy	7078	GGTCAGCCAGACCACACTGGACAATGTGTTTCGTGA	7137
Db	7111	AGTCAGCCAGACCACACTCTGGATAACGTGTTTGTGA	7170
Qy	7138	CCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCT	7197
Db	7171	TGTGGAGCAGCAAGAGGCTGA---GCCATCCACCTTGCCGTCCCCCTTG---GACTACT	7224
Qy	7198	CAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCC	7257
Db	7225	TAGCCTGCTGCGGCCCGCCCTGCACCCACAGAGCTCCGGGCACTGGTGGCCGATGAGCC	7284
Qy	7258	CGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCT	7317
Db	7285	TGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAAGAGCGGGCCCAGCT	7344
Qy	7318	GTCCTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTC	7377
Db	7345	CTCCTTCAACACCGATACGCTCTGCTGACGTTCAAGAGTCACATCAGGGATG-----	7396
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Db	7397	-----CAGCTGTTTGGGGCAGAAGTCAGGCGGTGGCCGTAGCCCCAGTCACACA	7445
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Db	7446	TGCCAGGGCCTGGAAAGGCAGGTTTCAGGACCAAGGGCTCCCGCCCTCC-----	7494
Qy	7497	CTCGGCCATGCCCTGCGGTCAGTGCAGTTCGCGCCCTAATTGTGCCAAAGGCTGACCCG	7556
Db	7495	-----TCCCAACTACCATCCTCCCGATCGTGCCAAAGGCTGGGCTG	7536
Qy	7557	GCCC-GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCC	7615
Db	7537	GCCCTGGGCTGCACACACCCTCACCTGCTTTGCCTTAAAGCCTTGGGTCTGGCCAGC	7596
Qy	7616	CCTCGCCCCCTGCCTGGCACTGCTCACC-GCCCAAGGCACGCCGGCTGGACCAGGCA-CT	7673
Db	7597	CCCTTACCCTGCCAGCACCATCCACCTTCCAGGGTGACATGGGCTGCCCCAAGTATCC	7656
Qy	7674	GCTGGCCTTTCTCCTGCCCCGCCCTCGGAACCAGCTTTTCTCTTACGATGAAGGCTGAT	7733

Db 7657 TGTGACCCTTCTCTGCAGCGGCCACCAGTCTACCCAGGCCAGCATCTTGCACAGATGTCT 7716
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RESULT 13

BD140903

LOCUS BD140903 8040 bp DNA linear PAT 18-SEP-2002

DEFINITION Human and rat ABCA2 gene.

ACCESSION BD140903

VERSION BD140903.1 GI:23235848

KEYWORDS WO 0208424-A/4.

SOURCE Rattus sp.

ORGANISM Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 8040)

AUTHORS Inagaki,N.

TITLE Human and rat ABCA2 gene

JOURNAL Patent: WO 0208424-A 4 31-JAN-2002;
BANYU PHARMACEUTICAL CO LTD,NOBUYA INAGAKI

COMMENT OS Rattus sp. (rat)

PN WO 0208424-A/4

PD 31-JAN-2002

PF 26-JUL-2001 WO 2001JP006457

PR 26-JUL-2000 JP 00P 225462

PI NOBUYA INAGAKI

PC

C12N15/12,C07K14/47,C12N1/15,C12N1/19,C12N1/21,C12N5/00,G01N33/ 68, PC

G01N33/15,G01N33/50

CC Human and rat ABCA2 gene

FH Key Location/Qualifiers

FT source 1. .8040
FT /organism='Rattus sp. (rat)'.
FEATURES Location/Qualifiers

source 1. .8040
/organism="Rattus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10118"

ORIGIN

Query Match 72.3%; Score 5810; DB 6; Length 8040;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 6768; Conservative 0; Mismatches 1205; Indels 85; Gaps 15;

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      |||
Db      34 CCGCGGCGCTGAGGCGGCGGAGCGCGGCCCGGCCATGGGCTTCCTGCACCAGCTGCAGCT 93

Qy      61 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGAGCCCGTGGGTCTTGGCCTTCGAGAT 120
      |||
Db      94 GCTGCTCTGGAAGAACGTGACGCTGAAGCGCCGAGCCCGTGGGTCTTGGCCTTTCGAGAT 153

Qy     121 CTTTCATCCCCCTGGTGTCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 180
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Db     154 CTTTCATCCCCCTTGTCTCTTCTTCATCCTGTTGGGACTGCGGCAGAAGAAGCCCACCAT 213

Qy     181 CTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCCTGACGTCTGCCGGCATCCTGCC 240
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Qy	721	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	780
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Qy	781	GATCCTCACTGTGCCTGAGAGTCAGAAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	840
Db	811	GATTCTTACCATGCCTGAGGGTCATCAGGTAGACCTTCAGGGCTACCGGGATGCTGTCTG	870
Qy	841	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	900
Db	871	CAGCGGGCAGGCTACAGCTCGTGCCACAGCATTTCAGTGATCTAGCCACTGAGCTCCGGAA	930
Qy	901	CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	960
Db	931	CCAGCTGGACATAGCCAAGATTGCCACAGCAGCTGGGCTTCAATGTCCCCAACGGCTCAGA	990
Qy	961	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGACCTGCTGGA	1020
Db	991	TCCACAGCCGCAGGCACCGTCCCCACAGAGTCTGCAGGCACTCTTAGGGGACCTGCTGGA	1050
Qy	1021	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGCCCTGGCCCTGCTACTGCCCCA	1080
Db	1051	TGTCCAGAAGGTTCTACAGGATGTGGATGTCCTATCAGCCCTTGCCCTGCTGCTGCCTCA	1110
Qy	1081	GGGTGCCTGCACTGGCCGGACCCCGGACCCCGAGCCAGTGGTGGGGTGGGGCGGCCAA	1140
Db	1111	AGGTGCCTGTGCTGGCCGGGCCCCCGCACCTCAAGCTGGCAGCCCGAGTGGCCCGGCCAA	1170
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Db	1171	CAGCACCGGGGTAGGGGCAAATACAGGTCCCAACACCACCGTTGAGGAGGGCACCCAGTC	1230
Qy	1201	TGCTGCAGCACTGGCCACCCCGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
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Qy	1261	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCT	1320
Db	1291	CTGGGCTGGCTTGCAGCCCATCTTGTGTGGCAACAACCGTACCATTGAGCCTGAAGCACT	1350
Qy	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380
Db	1351	CCGGAGGGGCAACATGAGCTCACTGGGCTTTACGAGCAAAGAACAACGGAACCTGGGCCT	1410
Qy	1381	CCTCGTGACCTCATGACCAGCAACCCCAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
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Qy	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1500
Db	1471	TGACCATGTTATCCTCAAGGCCAAATGAGACCTTTGCCTTTGTGGGCAACGTGACGCACTA	1530
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Db	1531	CGCCCAGGTCTGGCTCAACATCTCCGCAGAGATCCGGAGCTTCCTGGAGCAGGGCAGGCT	1590
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Db	1591	GCAGCAGCATCTGCACTGGCTGCAGCAGTACGTGGCTGACCTCCGGCTACACCCTGAAGC	1650
Qy	1621	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACTTCTCGCTGCC	1680
Db	1651	AATGAACCTGTCACTGGACGAGCTGCCCCCTGCTCTGCGCCTGGACTACTTTTCTCTGCC	1710
Qy	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGAT	1740
Db	1711	CAATGGCACAGCCCTTCTGCAGCAGCTAGACACAATAGACAATGCAGCCTGTGGCTGGAT	1770
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1800
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Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCAGTGTGAT	1860
Db	1831	CGTGAACTACACTCTCAATCAGGCCTACCAGGACAATGTTACAGTATTTGCCAGCGTGAT	1890
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1920
Db	1891	TTTCCAGACACGGAAGGATGGTTCCTCCCCCACATGTCCATTACAAGATTCGCCAGAA	1950
Qy	1921	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1980
Db	1951	CTCAAGCTTCACCGAGAAAACCAACGAGATCCGTGCTTACTGGCGTCCAGGGCCCAA	2010
Qy	1981	TACTGGCGGCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Db	2011	CACTGGTGGCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATAGAACG	2070
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Db	2071	TGCCATCATCAACACGTTTGTGGGGCACGACGTGGTGAACCCGGCAACTACGTGCAGAT	2130
Qy	2101	GTTCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2160
Db	2131	GTTCCCGTACCCCTGCTACACCCGTGACGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2190
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Db	2191	ACTGTGCATGGTGATCTCCTGGGTTTACTCTGTGGCCATGACCATACAGCACATCGTGGC	2250
Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280
Db	2251	GGAGAAAGAGCATCGGCTAAAGGAGGTGATGAAGACGATGGGCCTGAACAACGCCGTGCA	2310
Qy	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2340
Db	2311	CTGGGTGGCCTGGTTCATCACGGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCCCTGAC	2370
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Db	2371	CGCCATCCTCAAGTATGGCCAGGTCTCATGCACAGCCACGTGCTCATCATATGGCTCTT	2430
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2460
Db	2431	CCTTGCTGTCTATGCTGTGGCCACTATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2490
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
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Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
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Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640
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Db	2671	TGAAGTGGCAGGTGTGGGCATCCAGTGGCACACGTTTCAGCCAGTCCCCAGTGGGAAGGGGA	2730
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Db	2731	TGACTTCAACCTGCTCCTTGCTGTCAACCATGCTGATGGTGGACACAGTGGTCTATGGCGT	2790
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Db	2791	ACTCACTTGGTACATTGAGGCTGTGCACCCAGGTATGTATGGGCTGCCCCGGCCCTGGTA	2850
Qy	2821	CTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2851	CTTCCCACTACAGAAGTCCTATTGGCTGGGCAGTGGGCGGACAGAGACCTGGGAGTGGAG	2910
Qy	2881	CTGGCCGTGGGCACGCACCCCCGCCCTCAGTGTTCATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2911	CTGGCCATGGGCACACGCACCACGCCCTCAGCGTTATGGAGGAGGACCAGGCCTGTGCCAT	2970
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACCCACCTGCCTCT	3000
Db	2971	GGAGAGCCGGCACTTCGAGGAGACTCGCGGTATGGAGGAGGAGCCCACCCACCTGCCTTT	3030
Qy	3001	GGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3031	GGTCGTCTGCGTGGACAAAGCTCACCAAGGTCTATAAAAATGACAAGAAGCTGGCCTTAAA	3090
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3091	CAAACCTGAGCCTCAATCTCTACGAGAACCAGGTGGTCTCTTTCTTAGGCCATAACGGGGC	3150
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCG	3180
Db	3151	TGGCAAGACCACCTACCATGTCTATCCTGACTGGACTGTTCCACCCACGTCGGGCTCAGC	3210
Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3211	CACTATCTATGGCCACGACATCCGCACAGAGATGGATGAGATCCGTAAGAACCTGGGCAT	3270

Qy	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3271	GTGCCCCACAGCACAACGTGCTCTTTGACCAGCTCACTGTGGAGGAACACCTCTGGTTCTA	3330
Qy	3301	CTCACGGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3331	CTCACGCCTCAAAAAGCATGGCACAAGAGGAGATCCGCAAAGAGATGGACAAGATGATCGA	3390
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTGCGGTGGCATGAA	3420
Db	3391	GGACCTGGAGCTCTCCAACAAGCGCCACTCGCTGGTACAGACGCTGTCTGGAGGCATGAA	3450
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Db	3451	GCGCAAGCTTTTCAGTAGCCATTGCCTTCGTGGGTGGCTCTAGAGCCATTATCTTAGATGA	3510
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Db	3511	GCCCACAGCTGGCGTGGACCCCTATGCTCGACGTGCCATCTGGGACCTCATTCTGAAGTA	3570
Qy	3541	CAAGCCAGGCCGCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3571	CAAGCCGGGTGCGCACTATCCTCCTGTCCACCCATCACATGGATGAGGCCGACCTGCTGGG	3630
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3631	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAATGCTGCGGCTCTCCCCTCTTCCT	3690
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3720
Db	3691	CAAGGGTGCCTACGGCGATGGCTACCGCCTCACACTGGTCAAGCGGCCCTGCGGAGCCTGG	3750
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTG	3780
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Db	3931	CGAGCGCCTCTTTTCAGCAATTGGAGCACAGCCTGGAGCGCACTGCATCTGAGCAGTTTGG	3990
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTTCCTCAAGGTGTCTGAGGAGGATCAGTCGCT	4020
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Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
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Qy	5398	GCAGGGCACGGATGTCGTATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGC	5457
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Qy	5638	GTCGCCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCAC	5697
Db	5671	GTCACCCACCAACTTCCCCGCGGTGCTCTCCTTGTTCTGCTCTATGGATGGTCCATCAC	5730
Qy	5698	GCCCATCATGTACCCGGCCTCCTTCTGGTTTCGAGGTCCCCAGCTCCGCCTACGTGTTCTT	5757
Db	5731	ACCCATCATGTACCCGGCCTCCTTCTGGTTTGAGGTCCCTAGCTCAGCCTACGTGTTCTT	5790
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Db	5791	CATCGTCATCAACCTCTTCATTGGCATCACGGCCACAGTGGCCACCTTCCTTCTGCAGCT	5850
Qy	5818	CTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCAT	5877
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RESULT 14

AB037937

LOCUS AB037937 8040 bp mRNA linear ROD 12-OCT-2000

DEFINITION Rattus norvegicus mRNA for ABC2, complete cds.

ACCESSION AB037937

VERSION AB037937.1 GI:10799948

KEYWORDS ABC2.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (sites)

AUTHORS Zhao,L.X., Zhou,C.J., Tanaka,A., Nakata,M., Hirabayashi,T.,
 Amachi,T., Shioda,S., Ueda,K. and Inagaki,N.

TITLE Cloning, characterization and tissue distribution of the rat

ATP-binding cassette (ABC) transporter ABC2/ABCA2

JOURNAL Biochem. J. 350 Pt 3, 865-872 (2000)

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AUTHORS Inagaki, N.

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FEATURES

Location/Qualifiers

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CDS 68. .7372

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AVHPGMYGLPRPWYFPLQKSYWLGSGRTETWEWSWPWAHAPRLSVMEEDQACAMESRH
FEETRGMEEEPHTLPLVVCVDKLTKVYKNDKKLALNKLNLNLYENQVVSFLGHNGAGK
TTTMSILTGLFPPTSGSATIYGHDIRTEMDEIRKNLGMCPQHNVLFQDLTVEEHLWIFY
SRLKSMAQEEIRKEMDKMIEDLELSNKRHSLVQTLSGGMKRKLSVAIAFVGGSRAILL
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PLFLKGAYGDGYRLTLVKRPAEPGTSQEPGMASPSGRPQLSNCSEMQVSQFIRKHVA
SSLVSDTSTELSYILPSEAVKKGAFAERLFFQQLHSLDALHLSFSLMDTTLLEEVLK
VSEEDQSLENSEADVKE SRKDALPGAEGLTAVESQAGNLARCSELAQSQASLQSASSV
GSARGDEGAGYTDGYGDYRPLFDNLQDPDSVSLQEAEMEALARVQGSRKLEGWLLKM
RQFHGLLVKRFRHCARRNSKALCSQILLPAFFVCVAMTVALSVPEIGDLPLVLSPSQY
HNYTQPRGNFI PYANEERREYRLRLSPDASPQQLVSTFRLPSGVGATCVLKSPANGSL
GPMLNLSSGESRLLAARFFDSMCLESFTQGLPLSNFVPPPPSPAPSDSPLSPDEDSLL
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DILTDTIGHNVSEYLLFTSDRFRHLHRYGAITFGNIQKSIPAPIGTRTPLMVRKIAVRR
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WMLNLYLPATCCIIILFVFDLPAYTSPTNFPAVLSLFLLYGWSITPIMYPASFWFEV
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QPQRLPVSTKPVEDDQVVDASERQVLRGDADNDMVKIENLTKVYKSRKIGRILAVDRL
CLGVRPGECFGLLGUNGAGKTSTFKMLTGDESTTGGEAFVNGHSVLKDLLQVQQSLGY
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CEAVCTRLAIMVNGRLRCLGSIQHLKNRFGDGYMITVTRKSSQNVKDVVRFFNRNFPE
AMLKERHHTKVQYQLKSEHISLAQVFSKMEHVGVGLGIEDYSVSQTTLDNVFVNFPAK
QSDNVEQQEAPSTLPSPLGLLSLLRPRPAPTELRLVADEPEDLDTEDGLISFEE
RAQLSFNTDTLC"

ORIGIN

Query Match 72.3%; Score 5810; DB 10; Length 8040;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 6768; Conservative 0; Mismatches 1205; Indels 85; Gaps 15;

Qy	1	CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT	60
Db	34	CCGCGGCGCTGAGGCGGCGGAGCGCGGCCCGGCCATGGGCTTCCTGCACCAGCTGCAGCT	93
Qy	61	GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGCTCCTGGCCTTCGAGAT	120
Db	94	GCTGCTCTGGAAGAACGTGACGCTGAAGCGCCGGAGCCCGTGGGCTCCTGGCCTTCGAGAT	153
Qy	121	CTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT	180
Db	154	CTTCATCCCCCTTGTCCTCTTCTTCATCCTGTTGGGACTGCGGCAGAAGAAGCCCACCAT	213
Qy	181	CTCCGTGAAGGAAGTCCCCTTCTACACAGCGCGCCCCTGACGTCTGCCGGCATCCTGCC	240
Db	214	CTCTGTGAAGGAAG---CTTTCTACACGGCAGCACCGCTGACATCGGCCGGCATCCTGCC	270
Qy	241	TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTGGGCTTCCTGCAGTACGC	300
Db	271	TGTCATGCAGTCGCTTTGCCCTGATGGCCAGCGTGATGAGTTTGGCTTCCTGCAGTATGC	330
Qy	301	CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT	360
Db	331	CAACTCCACGGTCACCCAGCTTCTGGAACGCCTCAACCGTGTAGTGGAAGAGAGCAACTT	390
Qy	361	GTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA	420
Db	391	GTTTGACCCAGAGCGACCTAGCCTGGGCTCAGAGCTTGAGGCACTGCACCAACGTCTGGA	450
Qy	421	GGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC	480
Db	451	GGCCCTCAGCTCGGGCCCTGGCACCTGGGAGAGCCACTCAGCTAGACCTGCAGTTTCATC	510
Qy	481	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGAGGAGCTCTGGCGTTTCCTGACGCAAAA	540
Db	511	CTTCTCTCTGGACTCGGTGGCCAGGGACAAAAGAGAGCTTTGGCGTTTCCTGATGCAGAA	570
Qy	541	CTTGTCGCTGCCCCAATAGCACGGCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCGA	600
Db	571	CCTGTCACTGCCCCAACAGCACGGCCCAAGCCCTCCTGGCTGCCCCTGTAGACCTTCTGA	630

Qy 601 GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA 660
 ||||| | | |||| | ||||| | | |||| | | |||| | | |||| |
 Db 631 GGTCTATCGCTTGCTTTTTGGTCCCTTACCTGACCTGGATGGAAAGTTGGGGTTCCCTCAG 690

Qy 661 GGGTCAGGAGCCCTGGAGCCGCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT 720
 | ||||| ||||| | |||| | ||||| ||||| ||||| ||||| |||||
 Db 691 GAAGCAGGAGCCCTGGAGTCACCTGGGTAGCAATCCTCTGTTCCAAATGGAGGAGCTGCT 750

Qy 721 GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG 780
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 751 GCTGGCTCCTGCCCTTTTGGAGCAACTCACATGTGCTCCAGGCTCTGGGGAGCTGGGCCG 810

Qy 781 GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG 840
 ||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 811 GATTCTTACCATGCCTGAGGGTCATCAGGTAGACCTTCAGGGCTACCGGGATGCTGTCTG 870

Qy 841 CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA 900
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 Db 871 CAGCGGGCAGGCTACAGCTCGTGCCAGCATTTCAAGTATCTAGCCACTGAGCTCCGGAA 930

Qy 901 CCAGCTGGACGTGGCCAAGGTCTCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA 960
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 Db 931 CCAGCTGGACATAGCCAAGATTGCCAGCAGCTGGGCTTCAATGTCCCCAACGGCTCAGA 990

Qy 961 CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGACCTGCTGGA 1020
 | |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 991 TCCACAGCCGCAGGACCCGTCCCCACAGAGTCTGCAGGCACTCTTAGGGGACCTGCTGGA 1050

Qy 1021 TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGCCCTGGCCCTGCTACTGCCCCA 1080
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1051 TGTCCAGAAGGTTCTACAGGATGTGGATGTCCTATCAGCCCTTGCCCTGCTGCTGCCTCA 1110

Qy 1081 GGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGGGGTGGGGCGGCCAA 1140
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 Db 1111 AGGTGCCTGTGCTGGCCGGGCCCCCGCACCTCAAGCTGGCAGCCCGAGTGGCCCGGCCAA 1170

Qy 1141 TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC 1200
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 Db 1171 CAGCACCGGGGTAGGGGCAAATACAGGTCCCAACACCACCGTTGAGGAGGGCACCCAGTC 1230

Qy 1201 TGCTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT 1260
 ||| | | ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1231 ACCTGTACCCCAGCCTCTCCGGACACTCTGCAAGGCCAGTGCTCAGCCTTTGTGCAGCT 1290

Qy 1261 CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCT 1320
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1291 CTGGGCTGGCTTGACAGCCCATCTTGTGTGGCAACAACCGTACCATTGAGCCTGAAGCACT 1350

Qy 1321 GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT 1380
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1351 CCGGAGGGGCAACATGAGCTCACTGGGCTTTACGAGCAAAGAACAACGAACCTGGGCCT 1410

Qy 1381 CCTCGTGACCTCATGACCAGCAACCCCAAATCCTGTACGCGCCTGCGGGCTCTGAGGT 1440
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1411 TCTTGTGACCTCATGACCAGCAACCCCAAATCCTGTATGCACCCGAGGCTCTGAAGC 1470

Qy 1441 CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA 1500

Db	1471	TGACCATGTTATCCTCAAGGCAAATGAGACCTTTGCCTTTGTGGGCAACGTGACGCACTA	1530
Qy	1501	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1531	CGCCCAGGTCTGGCTCAACATCTCCGCAGAGATCCGGAGCTTCCTGGAGCAGGGCAGGCT	1590
Qy	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620
Db	1591	GCAGCAGCATCTGCACTGGCTGCAGCAGTACGTGGCTGACCTCCGGCTACACCCTGAAGC	1650
Qy	1621	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1680
Db	1651	AATGAACCTGTCACTGGACGAGCTGCCCCCTGCTCTGCGCCTGGACTACTTTTCTCTGCC	1710
Qy	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATAACCATTGACAACGCGGCCTGCGGCTGGAT	1740
Db	1711	CAATGGCACAGCCCTTCTGCAGCAGCTAGACACAATAGACAATGCAGCCTGTGGCTGGAT	1770
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCGACGAGGAGAGCAT	1800
Db	1771	CCAGTTCATGTCCAAGGTGAGTGTGGACATCTTCAAGGGGTTTCTGATGAGGAGAGCAT	1830
Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCAGTGTGAT	1860
Db	1831	CGTGAACTACACTCTCAATCAGGCCTACCAGGACAATGTTACAGTATTTGCCAGCGTGAT	1890
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1920
Db	1891	TTTCCAGACACGGAAGGATGGTTCCCTCCCCCACATGTCCATTACAAGATTGCCAGAA	1950
Qy	1921	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1980
Db	1951	CTCAAGCTTCACCGAGAAAACCAACGAGATCCGTCTGTCTTACTGGCGTCCAGGGCCCAA	2010
Qy	1981	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Db	2011	CACCTGGTGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATAGAACG	2070
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Db	2071	TGCCATCATCAACACGTTTGTGGGGCACGACGTGGTGAACCCGGCAACTACGTGCAGAT	2130
Qy	2101	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2160
Db	2131	GTTCCCGTACCCCTGCTACACCCGTGACGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2190
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Db	2191	ACTGTGCATGGTGATCTCCTGGGTTTACTCTGTGGCCATGACCATAACGACATCGTGGC	2250
Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280
Db	2251	GGAGAAAGAGCATCGGCTAAAGGAGGTGATGAAGACGATGGGCCTGAACAACGCCGTGCA	2310
Qy	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCGAGCTGTCCATCTCCGTGACAGCACTCAC	2340

Db	2311	CTGGGTGGCCTGGTTCATCACGGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCCCTGAC	2370
Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTTCATCATCTGGCTCTT	2400
Db	2371	CGCCATCCTCAAGTATGGCCAGGTCCTCATGCACAGCCACGTGCTCATCATATGGCTCTT	2430
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2460
Db	2431	CCTTGCTGTCTATGCTGTGGCCACTATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2490
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Db	2491	TAAGGCCAAGTTGGCCTCGGCCTGCGGCGGCATCATCTACTTCCTGAGCTACGTTCCCTA	2550
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
Db	2551	CATGTATGTAGCAATCCGTGAGGAAGTAGCCACGATAAGATCACTGCCTTCGAGAAGTG	2610
Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640
Db	2611	CATTGCGTCCCTGATGTCCACAACAGCCTTCGGCCTGGGTTCCAAGTACTTTGCTCTGTA	2670
Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGA	2700
Db	2671	TGAAGTGGCAGGTGTGGGCATCCAGTGGCACACGTTTCAGCCAGTCCCCAGTGAAGGGGA	2730
Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760
Db	2731	TGACTTCAACCTGCTCCTTGCTGTCACCATGCTGATGGTGGACACAGTGGTCTATGGCGT	2790
Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2791	ACTCACTTGGTACATTGAGGCTGTGCACCCAGGTATGTATGGGCTGCCCCGGCCCTGGTA	2850
Qy	2821	CTTCCCCTGACAGAAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2851	CTTCCCCTACAGAAAGTCCTATTGGCTGGGCAGTGGGCGGACAGAGACCTGGGAGTGGAG	2910
Qy	2881	CTGGCCGTGGGCACGCACCCCCGCCTCAGTGTCTATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2911	CTGGCCATGGGCACACGCACCCAGCCTCAGCGTTATGGAGGAGGACCAGGCCTGTGCCAT	2970
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3000
Db	2971	GGAGAGCCGGCACCTTCGAGGAGACTCGCGGTATGGAGGAGGAGCCACCCACCTGCCTTT	3030
Qy	3001	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3031	GGTCGTCTGCGTGGACAAGCTCACCAAGGTCTATAAAAATGACAAGAAGCTGGCCTTAA	3090
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3091	CAAACCTGAGCCTCAATCTCTACGAGAACCAGGTGGTCTCTTTCTAGGCCATAACGGGGC	3150
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTCCGC	3180
Db	3151	TGGCAAGACCACTACCATGTCTATCCTGACTGGACTGTTCCACCCACGTCGGGCTCAGC	3210

Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3211	CACTATCTATGGCCACGACATCCGCACAGAGATGGATGAGATCCGTAAGAACCTGGGCAT	3270
Qy	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3271	GTGCCCCAGCACAACGTGCTCTTTGACCAGCTCACTGTGGAGGAACACCTCTGGTTCTA	3330
Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3331	CTCACGCCTCAAAAGCATGGCACAAGAGGAGATCCGCAAAGAGATGGACAAGATGATCGA	3390
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3420
Db	3391	GGACCTGGAGCTCTCCAACAAGCGCCACTCGCTGGTACAGACGCTGTCTGGAGGCATGAA	3450
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3480
Db	3451	GCGCAAGCTTTTCAGTAGCCATTGCCTTCGTGGGTGGCTCTAGAGCCATTATCTTAGATGA	3510
Qy	3481	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3540
Db	3511	GCCCACAGCTGGCGTGGACCCCTATGCTCGACGTGCCATCTGGGACCTCATCTGAAGTA	3570
Qy	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3571	CAAGCCGGGTGCGACTATCCTCCTGTCCACCCATCACATGGATGAGGCCGACCTGCTGGG	3630
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3631	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAATGCTGCGGCTCTCCCCTCTTCCT	3690
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3720
Db	3691	CAAGGGTGCCTACGGCGATGGCTACCGCCTCACACTGGTCAAGCGGCCTGCGGAGCCTGG	3750
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGCCCCGCTGAGCAGCTG	3780
Db	3751	CACCTCCCAAGAGCCAGGGATGGCTTCAGCCCCCTCAGGTCGTCTCAGCTGAGCAACTG	3810
Qy	3781	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3811	CTCAGAGATGCAAGTGTCCAGTTCATCCGCAAGCATGTGGCTTCCTCCCTGCTGGTGTC	3870
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3871	AGACACGAGCACCGAGCTCTCCTACATCCTGCCCAGCGAGGCTGTCAAGAAAGGGGCCTT	3930
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3931	CGAGCGCCTCTTTCAGCAATTGGAGCACAGCCTGGACGCACTGCATCTGAGCAGTTTTGG	3990
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4020
Db	3991	GCTGATGGACACAACCCTGGAGGAGGTGTTCCTCAAGGTGTCTGAAGAAGACCAGTCACT	4050

Qy	4021	GGAGAACAGTGTAGGCCCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4051	GGAGAATAGTGTAGGCCGATGTGAAGGAGTCCCGGAAGGATGCACTGCCTGGGGCAGAGGG	4110
Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCCGTGCTCGGAGCTGACCCAGTC	4140
Db	4111	CCTGACGGCTGTGGAGAGTCAAGCAGGCAACCTGGCTCGGTGCTCAGAGCTGGCACAGTC	4170
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCGTGGCGACGAGGGAGCTGG	4200
Db	4171	CCAGGCTTCACTGCAGTCTGCATCTTCTGTGGGCTCCGCCCCGTGGGGATGAGGGTGCTGG	4230
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4231	CTACACCGACGGCTACGGTGACTACCGTCCCCCTCTTTGACAACTTGAGGACCCAGACAG	4290
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAA	4320
Db	4291	TGTCAGCTTACAAGAGGCTGAAATGGAGGCCCTGGCTCGGGTAGGCCAGGGCAGCCGCAA	4350
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4351	GCTAGAGGGCTGGTGGCTGAAGATGCGGCAGTTCCATGGGCTCCTGGTGAAGCGCTTCCA	4410
Qy	4381	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4411	CTGTGCTCGCCGGAACCTCAAAGCGCTCTGCTCCCAGATTCTGCTGCCTGCCTTCTTCGT	4470
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCCGCTGGT	4500
Db	4471	CTGTGTGGCCATGACTGTGGCATTGTCTGTCCCTGAGATCGGTGACCTGCCTCCACTGGT	4530
Qy	4501	CCTGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4531	CCTGTGCTTCTCAGTACCACAACCTATACCCAGCCCCGTGGCAACTTTATCCCCTATGC	4590
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCCAGCAGCT	4620
Db	4591	CAATGAGGAACGCCGCGAGTACCGATTACGGCTGTACCTGATGCCAGCCCCCAGCAGTT	4650
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4651	GGTGAGCACATTCCGGCTGCCCTCTGGTGTGGGTGCCACTTGTGTGCTCAAGTCTCCAGC	4710
Qy	4681	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4711	CAACGGCTCCCTGGGGCCCATGCTGAACCTGAGCAGTGGAGAGTCCGCGCTGCTGGCCGC	4770
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4771	ACGGTTCTTCGACAGTATGTGCCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATT	4830
Qy	4801	CGTGCCACCCCCACCCTCGCCCCGCCCATCTGACTCGCCAGCGTCCCCGGATGAGGA---	4857
Db	4831	CGTGCCACCCCCACCCTCGCCCCGCCCTTCCGACTCACCCCTGTCCCCGGATGAGGATTC	4890
Qy	4858	CCTGCAGGCCTGGAACGTCTCCCTGCCGCCACCCTGGGGCCAGAAATGTGGACGTGGGC	4917

Db	4891	ACTGCTAGCCTGGAATACGTCCCTGCCCCCTACTGCTGGACCAGAGACGTGGACGTGGGC	4950
Qy	4918	ACCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCAC	4977
Db	4951	GCCTTCTCTGCCACGCCTGGTTCACGAGCCGGTCCGCTGTACCTGCTCTGCACAGGGCAC	5010
Qy	4978	CGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGG	5037
Db	5011	GGGCTTCTCGTGCCCCAGCAGTGTGGGTGGGCACCCACCCAGATGAGAGTGGTCACGGG	5070
Qy	5038	CGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGA	5097
Db	5071	GGACATCCTGACTGACATCACCGGCCACAATGTTTCCGAGTACCTGCTCTTCACCTCTGA	5130
Qy	5098	CCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAGTCCATCCC	5157
Db	5131	CCGTTTCCGACTGCACCGCTATGGAGCCATCACCTTTGGTAATATCCAGAAGTCCATCCC	5190
Qy	5158	AGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGC	5217
Db	5191	AGCACCCATTGGTACCCGGACCCCTCTCATGGTCCGGAAGATTGCAGTGCAGGGGTGGC	5250
Qy	5218	CCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAA	5277
Db	5251	CCAGGTGCTCTACAACAACAAGGGCTACCACAGCATGCCCACCTACCTCAACAGCCTCAA	5310
Qy	5278	CAACGCCATCCTGCGTGCCAACCTGCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCAT	5337
Db	5311	CAATGCCATTCTGCGTGCAAACCTACCCAAAAGCAAGGGCAATCCAGCAGCCTACGGTAT	5370
Qy	5338	CACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCT	5397
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AUTHORS Luciani,M.F., Denizot,F., Savary,S., Mattei,M.G. and Chimini,G.
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 JOURNAL Genomics 21 (1), 150-159 (1994)
 MEDLINE 94375008
 PUBMED 8088782
 REFERENCE 2 (bases 1 to 4744)
 AUTHORS Chimini,G.
 TITLE Direct Submission
 JOURNAL Submitted (05-NOV-1993) G. Chimini, Centre d'Immunologie de
 Marseille Luminy, Parc Scientifique de Luminy, 13288 Marseille,
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 REMARK revised by [3]
 REFERENCE 3 (bases 1 to 7629)
 AUTHORS Chimini,G.
 TITLE Direct Submission
 JOURNAL Submitted (21-DEC-2000) G. Chimini, Centre d'Immunologie de
 Marseille Luminy, Parc Scientifique de Luminy, 13288 Marseille,
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 COMMENT On Dec 22, 2000 this sequence version replaced gi:495258.
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Db	2275	CTGTCTATCTCCGTGACAGCTCTGACCGCCATCCTCAAGTACTGCCAGGTGCTCATGCAC	2334
Qy	2375	AGCCACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTT	2434
Db	2335	AGCCACGTGCTCATTATCTGGCTCTTCCTTGCCGTCTACGCTGTGGCCACTATCATGTTT	2394
Qy	2435	TGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATC	2494
Db	2395	TGCTTCCTGGTGTCTGTGCTGTACTCTAAGGCTAAGTTGGCCTCAGCCTGTGGCGGTATC	2454
Qy	2495	ATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCAT	2554
Db	2455	ATCTACTTCCTGAGCTACGTTCCCTACATGTATGTAGCGATCCGCGAGGAGGTAGCCCAT	2514
Qy	2555	GATAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGT	2614
Db	2515	GACAAGATCACTGCCTTCGAGAAGTGCATTGCGTCCC-GATGTCCACAACAGCCTTTGGC	2573
Qy	2615	CTGGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGG-----CATCCAGTGGCA	2670
Db	2574	CTGGGTTCCAAGTACTTTGCACTGTATGAAGTGGCAGGAGTGGGCATCCATCCAGTGGCA	2633
Qy	2671	CACCTTCAGCCAGTCCCCGGTGGAGGGGACGACTTCAACTTGCTCCTGGCTGTCACCAT	2730
Db	2634	CACGTTTCAGCCAGTCCCCAGTGAAGGAGATGACTTCAATCTGCTCCTTGCTGTCACCAT	2693
Qy	2731	GCTGATGGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCC	2790
Db	2694	GCTTATGGTGGACACGGTGGTCTACGGCGTGCTCACTTGGTACATTGAGGCTGTGCACCC	2753
Qy	2791	AGGCATGTACGGGCTGCCCCGGCCCTGGTACTTCCCACTGCAGAAGTCCTACTGGCTGGG	2850
Db	2754	AGGTATGTATGGGCTGCCCCGGCCCTGGTAC-TCCCGCTACAGAAGTCCTATTGGCTGGG	2812
Qy	2851	CAGTGGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCGCCTCAG	2910
Db	2813	CAGTGGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCATGGGCACACACACCGCGCCTCAG	2872
Qy	2911	TGTCATGGAGGAGGA-CCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTG	2969
Db	2873	CGTTATGGAGGAGGATCCAGGCCTGTGCCATGGAGAGCCGGCACTTCGAGGAGACCCGCG	2932
Qy	2970	GCATGGAGGAGGAGGCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAACTCACCAAGG	3029
Db	2933	GCATGGAGGAGGAGGCCACCCACCTGCCCTTGGTCGTCTGTGTGGACAAGCTCACCAAGG	2992
Qy	3030	TCTACAAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACC	3089
Db	2993	TCTATAAGAATGACAAGAAGCTGGCCTTAAACAACTGAGCCTCAATCTGTATGAGAATC	3052

Qy	3090	AGGTGGTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGA	3149	
Db	3053			
		3053 AGGTGGTCTCTTCTAGGCCACAACGGGGCGGGCAAGACCACGACCATGTTCGATCCTGA	3112	
Qy	3150	CCGGCCTGTTCCCTCCAACGTCGGGTTCCGCCACCATCTACGGGCACGACATCCGCACGG	3209	
Db	3113			
		3113 CTGGACTGTTCCACCCACGTCGGGCTCAGCCACTATCTATGGGCACGACATCCGCACCG	3172	
Qy	3210	AGATGGATGAGATCCGCAAGAACCTGGGCATGTGCCCAGCACAATGTGCTCTTTGACC	3269	
Db	3173			
		3173 AGATGGATGAGATCCGCAAGAACCTGGGCATGTGCCCACAGCACAACGTGCTCTTTGACC	3232	
Qy	3270	GGCTCACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGG	3329	
Db	3233			
		3233 GGCTCACGGTGGAGGAGCACCTCTGGTTCTACTCACGCCTCAAAAGCATGGCACAGGAGG	3292	
Qy	3330	AGATCCGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACT	3389	
Db	3293			
		3293 AGATCCGCAAAGAGACGGACAAGATGATTGAGGACCTGGAACCTCTTAACAAGCGGCACT	3352	
Qy	3390	CACTGGTGCAGACATTGTCTGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCG	3449	
Db	3353			
		3353 CACTGGTGCAGACGTTGTCTGGAGGCATGAAGCGCAAGCTTTCGGTAGCCATTGCCTTTG	3412	
Qy	3450	TGGGCGGCTCTCGCGCCATCATCCTGGACGAGCCCACGGCGGGCGTGGACCCCTACGCGC	3509	
Db	3413			
		3413 TGGGTGGCTCTAGAGCCATTATCTTAGACGAGCCCACGGCTGGCGTGGACCCCTATGCTC	3472	
Qy	3510	GCCGCGCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCA	3569	
Db	3473			
		3473 GCCGTGCCATCTGGGACCTCATCTGAAGTACAAGCCGGGCCGCACTATCCTCCTGTCTA	3532	
Qy	3570	CCCACCACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGA	3629	
Db	3533			
		3533 CCCATCACATGGATGAGGCTGACCTGCTGGGGGATCGCATTGCCATCATCTCCCATGGGA	3592	
Qy	3630	AGCTCAAGTGCTGCGGCTCCCCGCTCTTCTCAAGGGCACCTATGGCGACGGGTACCGCC	3689	
Db	3593	:		
		3593 AGCTCAAATGCTGTGGCTCTCCCTCTTCTCAAGGGAGCCTATGSSGATGGGTACCGCC	3652	
Qy	3690	TCACGCTGGTCAAGCGGCCCCGCCGAGCCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCA	3749	
Db	3653			
		3653 TCACATTGGTCAAGCAGCCTGCAGAACCTGGCACCTCCAAGAGCCAGGGCTGGCTTCCA	3712	
Qy	3750	GGCCCCCAGGTCGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCAGTTTCATCC	3809	
Db	3713			
		3713 GGGCTCAGGTTGTCTCGGCTGAGCAGCTGCTCGGAGCCGCAAGTGTCCAGTTTCATCC	3772	
Qy	3810	GCAAGCATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCC	3869	
Db	3773			
		3773 GCAAGCATGTGGCTTCCTCCCTGCTGGTCTCAGACACGAGCACCGAGCTCTCCTACATCC	3832	
Qy	3870	TGCCCAGCGAGGCCGCCAAGAAGGGGGCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCA	3929	
Db	3833			
		3833 TGCCCAGCGAGGCCGTCAAGAAGGGGGCTTTCGAGCGCCTCTTTCAGCAACTGGAACACA	3892	
Qy	3930	GCCTGGATGCACTGCACCTCAGCAGCTTCGGGCTGATGGACACGACCTGGAGGAAGTGT	3989	

Db	3893	GCCTGGATGCGCTCCATCTGAGCAGTTTTGGGCTGATGGACACAACCTCTGGAGGAGGTGT	3952
Qy	3990	TCCTCAAGGTGTCGGAGGAGGATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGT	4049
Db	3953	TCCTCAAGGTGTCCTGAAGAAGATCAGTCACTGGAGAACACGCAGGCTGATGTGAAGGAGT	4012
Qy	4050	CCAGGAAGGATGTGCTCCCTGGGGCGGAGGGCCCCGGCTCTGGGGAGGGTCACGCTGGCA	4109
Db	4013	CCCGGAAGGATGTNCTGCCTGGGGCAGAGGGCCTGACAGCTGTGGGGGGTCAAGCTGGCA	4072
Qy	4110	ATCTGGCCCGGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTG	4169
Db	4073	ACCTGGCTCGGTGCTCAGAGCTGGCACAGTCACAGGCATCGCTGCAGTCTGCATCCTCTG	4132
Qy	4170	TGGGCTCTGCCCCTGGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCC	4229
Db	4133	TGGGCTCTGCCCCTGGGGAGGAGGGCACCGGCTACTCTGATGGCTACGGTGACTACCGTC	4192
Qy	4230	CCCTCTTTGATAACCCACAGGACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGG	4289
Db	4193	CCCTCTTTGACAACCTTGACAGGACCCAGACAATGTCAGCTTACAAGAGGCAGAGATGGAGG	4252
Qy	4290	CCCTGTCGAGGGTCGGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCC	4349
Db	4253	CCCTGGCTCAGGTGGGCCAGGGCAGCCGAACTCGAGGGCTGGTGGCTGAAGATGCGGC	4312
Qy	4350	AGTTCCACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCT	4409
Db	4313	AGTTCCATGGGCTCCTGGTGAAGCGCTTCCACTGTGCTCGTGGAACTCCAAGCTCTCT	4372
Qy	4410	TCTCCCAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCG	4469
Db	4373	GCTCTCAGATTCTGCTGCCTGCCTTCTTTGTCTGTGTGGCCATGACTGTGGCGTTGTCTG	4432
Qy	4470	TCCCGGAGATTGGTGATCTGCCCCGCTGGTCCTGTACCTTCCCAGTACCACAACCTACA	4529
Db	4433	TCCCTGAGATTGGTGACCTACCTCCACTGGTCCTGTACCCCTCTCAGTACCACAACCTACA	4492
Qy	4530	CCCAGCCCCGTGGCAATTTTCATCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGC	4589
Db	4493	CCCAGCCCCGTGGCAACTTTATCCCTTATGCCAATGAGGAACGCCAGGAGTACCGATTAC	4552
Qy	4590	GGCTATCGCCCGACGCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTCGGGGG	4649
Db	4553	GGCTGTACCTGATGCCAGCCCCCAGCAGCTGGTGAGCACATTCCGGCTGCCCTCTGGTG	4612
Qy	4650	TGGGTGCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCACGTTGAACC	4709
Db	4613	TGGGTGCCACTTGTGTGCTCAAGTCTCCTGCCAACGGCTCCCTGGGACCCATGCTGAACT	4672
Qy	4710	TGAGCAGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGT	4769
Db	4673	TAAGCAGTGAGAGTCCCGCCTGCTGGCGGCACGGTTCTTCGACAGTATGTGCCTGGAGT	4732
Qy	4770	CCTTCACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCCCCCCAT	4829

Db 4733 CCTTCACACAGGGGCTGCCACTGTCCAACCTTCGTGCCACCTCCGCCCTCACCCGCCCCCTT 4792

Qy 4830 CTGACTCGCCAGCGTCCCCGGATGAGGA---CCTGCAGGCCTGGAACGTCTCCCTGCCGC 4886
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Db 4793 CTGACTCACCCGTGTSCCAGATGAGGATTCAGTGAAGCCTGGAACATGTCCCTGCCAC 4852

Qy 4887 CCACCGCTGGGCCAGAAATGTGGACGTCCGGACCCCTCCCTGCCGCGCCTGGTACGGGAGC 4946
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Db 4853 CTACTGCTGGGCCAGAGACGTGGACGTCCGGCGCCTTCTCTGCCACGCCTAGTGCATGAGC 4912

Qy 4947 CCGTCCGCTGCACCTGCTCTGCGCAGGGCACCGGCTTCTCCTGCCCCAGCAGTGTGGGCG 5006
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Db 4913 CAGTCCGCTGTACCTGCTCTGCACAGGGCACGGGGTCTCATGCCCCAGCAGTGTGGGTG 4972

Qy 5007 GGCACCCGCCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACATCACCGGCCACA 5066
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Db 4973 GACACCCACCCAGATGAGAGTGGTCACAGGTGACATCCTGACTGACATCACTGGCCACA 5032

Qy 5067 ATGTCTCTGAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCA 5126
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Db 5033 ATGTTTCTGAGTACCTGCTCTTCACCTCTGACCGTTTCCGACTACACCGATATGGAGCCA 5092

Qy 5127 TCACCTTTGGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCA 5186
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Db 5093 TCACCTTTGGTAATGTTTCAAGTCTATCCCAGCATCCTTTGGTGCCCGGTCCCTCCTA 5152

Qy 5187 TGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCAGGTTTTCTACAACAACAAGGGCTATC 5246
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Db 5153 TGGTGCGGAAGATTGCAGTGCGGAGGGTGGCTCAGGTGCTCTACAATAACAAGGGCTACC 5212

Qy 5247 ACAGCATGCCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACCTGCCCCA 5306
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Db 5213 ACAGCATGCCCACCTACCTCAACAGCCTCAACAATGCCATTCTGCGTGCAAACCTACCCA 5272

Qy 5307 AGAGCAAGGGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGA 5366
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Db 5273 AAAGCAAGGGCAATCCAGCAGCCTATGGCATCACCGTCACCAACCACCCCATGAACAAGA 5332

Qy 5367 CCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGGGCACGGATGTCGTCATCGCCATCT 5426
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Db 5333 CCAGTGCTAGCCTCTCCCTGGATTACCTACTGCAGGNACAGATGTGGTCATCGCCATCT 5392

Qy 5427 TCATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGA 5486
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Db 5393 TCATCATTTGTGGCCATGTCCTTCGTGCCAGCCAGCTTTGTGGTCTTCCTTGTGGCAGAGA 5452

Qy 5487 AGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAGCGGCTGCAACCCCATCATCTACTGGC 5546
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Db 5453 AATCCACCAAGGCCAAACACCTGCAGTTTCGTGAGCGGGTGAACCCCTGTCATCTACTGGC 5512

Qy 5547 TGGCGAACTACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCTGCTGTGTCATCA 5606
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Qy 5607 TCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTCGCCACCAACTTCCCTGCCGTCTCT 5666
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Db 5573 TCCTCTTTGTCTTTGACTTACCTGCCTACACATCACCCACCAACTTCCCCGCGGTGCTCT 5632

Qy	5667	CCCTCTTCCTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGGCCTCCTTCTGGT	5726
Db	5633	CCTTGTTTCCTGCTCTATGGGTGGTCCATCACACCCATCATGTACCCAGCCTCCTTCTGGT	5692
Qy	5727	TCGAGGTCCCCAGCTCCGCCTACGTGTTCTCATTTGTCATCAATCTCTTCATCGGCATCA	5786
Db	5693	TTGAGGTCCCTAGCTCAGCCTACGTGTTCTCATTTGTCATCAACCTCTTCATCGGCATCA	5752
Qy	5787	CCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCAGGACAAGGACCTGAAGGTTG	5846
Db	5753	CAGCCACGGTGGCCACTTTTCCTTCTGCAGCTTTTGTGAGCATGACAAGGATCTGAAGGTTG	5812
Qy	5847	TCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTGGGCCACGGGC	5906
Db	5813	TCAACAGTTACCTGAAAAGCTGCTTCCTCATCTTCCCCAACTACAACCTGGGCCACGGGC	5872
Qy	5907	TCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATTGGCCAGTTTG	5966
Db	5873	TCATGGAGATGGCCTACAATGAGTACATCAACGAATACTACGCCAAGATTGGCCAGTTTG	5932
Qy	5967	ACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTACCCGCGGACTGGTGGCCATGGCGG	6026
Db	5933	ACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTACACGTTGGACTGGTGGCCATGACAG	5992
Qy	6027	TTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTTCCTGCGGCGGC	6086
Db	5993	TCGAGGGCTTCGTGGGATTCTTCCTCACCATCATGTGCCAGTATAACTTCCTACGGCAGC	6052
Qy	6087	CACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTGGCCAGTGAGC	6146
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Qy	6147	GGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAGAACCTGACCA	6206
Db	6113	GACAGAGAGTGCTCCGTGGCGATGCTGACAATGACATGGTCAAGATTGAGAACCTGACCA	6172
Qy	6207	AGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTG	6266
Db	6173	AGGTGTACAAGTCTCGGAAGATTGGCCGGATCCTGGCAGTGGACCGCCTTTGCCTGGGTG	6232
Qy	6267	TGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCT	6326
Db	6233	TGCGCCCTGGAGAGTGCTTTGGGCTCCTTGGTGTCAATGGTGCAGGGAAGACCAGCACCT	6292
Qy	6327	TCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTCGTCAATGGACACA	6386
Db	6293	TCAAGATGCTGACTGGAGATGAGAGCACAACTGGGGGAGAGGCCTTTGTCAATGGACACA	6352
Qy	6387	GCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCGAGTGTGACG	6446
Db	6353	GCGTGCTCAAGGACCTGCTCCAGGTACAGCAGAGCCTTGGCTACTGCCCCGAGTTTGATG	6412
Qy	6447	CGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCTGCAGCTGTACACGCGGCTGCGTGGGA	6506
Db	6413	CCCTGTTTGTATGAGCTCACGGCTCGTGAACACCTGCAGCTGTACACGCGGCTGCGTGGCA	6472

Qy	6507	TCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGACCA	6566
Db	6473	TCCCCTGGAAGGATGAGGCACAGGTAGTGAAGTGGGCCCTAGAGAAGCTGGAAGTACAA	6532
Qy	6567	AGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCACGG	6626
Db	6533	AGTATGCAGACAAGCCAGCTGGCACCTACAGTGGAGGCAACAAACGGAAGCTTTCCACAG	6592
Qy	6627	CCATCGCCCTCATTTGGGTACCCAGCCTTCATCTTCTGGACGAGCCACCACAGGCATGG	6686
Db	6593	CCATTGCCCTCATTTGGGTACCCTGCCTTCATCTTTCTAGATGAGCCCACTGGCATGG	6652
Qy	6687	ACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCCTCGACCTCATCAAGACAGGGCGTT	6746
Db	6653	ACCCCTAAGGCCCGGCGCTTCCTGTGGAACCTCATCTGGACCTCATCAAGACGGGACGTT	6712
Qy	6747	CAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCACGCGGCTGGCCA	6806
Db	6713	CGGTGGTGCTGACGTACACAGCATGGAGGAGTGTGAGGCTCTGTGCACACGCTTGGCCA	6772
Qy	6807	TCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACCGGTTTG	6866
Db	6773	TCATGGTGAACGGGCGGCTGCGCTGCCTGGGCAGCATCCAGCACCTTAAGAACAGGTTTG	6832
Qy	6867	GAGATGGCTACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTGAAGGACGTGGTGC	6926
Db	6833	GGGATGGCTACATGATTACTGTAAGGACCAAAGCAGCCAGAACGTGAAGGACGTGGTGC	6892
Qy	6927	GGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACCACACAAAGGTGC	6986
Db	6893	GGTTCTTCAACAGGAACTTCCAGAGGCCATGCTCAAGGAAAGACACCATACGAAGGTGC	6952
Qy	6987	AGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAGCAAGATGGAGCAGG	7046
Db	6953	AGTATCAGCTCAAGTCAGAGCACATCTCGCTGGCTCAGGTGTTTCAGCAAGATGGAGCAGG	7012
Qy	7047	TGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACACTGGACAATGTGT	7106
Db	7013	TGGTGGGTGTGCTGGGCATCGAGGATTACTCAGTCAGCCAGACCACCTGGATAACGTGT	7072
Qy	7107	TCGTGAACTTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGCCGCCAT	7166
Db	7073	TTGTGAACTTTGCCAAGAAGCAGAGTGATAATGTGGAGCAGCAAGAGGCTGAGCCCTCGT	7132
Qy	7167	CCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTGCCCCCA	7226
Db	7133	CCTTGCCGTCCCCCTT-----GGACTGCTCAGCCTGCTGAGGCCCGCCCCGCACCCA	7186
Qy	7227	CGGAGCTCCGGGCACTTGTGGCAGACGAGCCGAGGACCTGGACACGGAGGACGAGGGCC	7286
Db	7187	CAGAGCTCCGGGCATTGGTGGCTGATGAGCCAGAGGACCTGGACACAGAGGATGAAGGCC	7246
Qy	7287	TCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCTTCAACACGGACACGCTCTGCTGAC	7346
Db	7247	TCATCAGCTTCGAGGAAGAGCGGGCCCAGCTCTCTTCAACACTGATACGCTCTGCTGAC	7306
Qy	7347	CACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTGACCACCCAGAGCTGGGCCAGGGAC	7406

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Db      7307 CATCAAGAGCCACATCAGGGATGCAGCTGTGTGGGGCAGATGTCAGGCGGTGGCCGTGGC 7366
Qy      7407 TCAACAATGGGGACAGAAGTCCCCCAGTGCCTGCCAGGGCCTGGAGTGG-AGGTTCAGGA 7465
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Db      7367 CC-----CTAGTCACACATGCCAGGCCCTGGAAAGGCAGGTTCAGGA 7408
Qy      7466 CCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCGGCCATGCCCTGCGGTCACTGCGGTT 7525
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Qy      7526 GCCGCCCCTAATTGTGCCAAAGGCTGACCCGGCCCC-GGGCTGCGTACACCCTTGCCCTGC 7584
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Db      7442 -CCTCCCCGAATTGTGCCAAAGGCTGGCCTGGCCCTGGGCTGCACATACCCTCACCCTGC 7500
Qy      7585 TTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCTCGCCCCTGCCTGGCACTGCTCACC-G 7643
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Db      7501 TTTGCCTTAAAGCCTTGGGTCTGGCCAGCCCCTTACCCTGCCAGCACCATCCACCTT 7560
Qy      7644 CCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCCTTTCTCCTGC 7690
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Db      7561 CCCAGGGTGACATGGGCTGCCCCAAGTATCCTGTGACTCTTCTCTGC 7607

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Search completed: September 8, 2004, 13:23:32
Job time : 29622 secs

OM nucleic - nucleic search, using sw model

Run on: September 7, 2004, 23:46:06 ; Search time 2624 Seconds
 (without alignments)
 13016.583 Million cell updates/sec

Title: US-10-088-467-1
 Perfect score: 8040
 Sequence: 1 ccgcggcgctgaggcgggcg.....aaataaataaacaataatgtc 8040

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
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 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002s:*
 7: geneseqn2003as:*
 8: geneseqn2003bs:*
 9: geneseqn2003cs:*
 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	8040	100.0	8040	4	AAF57452	Aaf57452 Human ABC
2	8040	100.0	8056	6	ABV74350	Abv74350 Human ABC
3	8036.4	100.0	8269	6	ABL53009	Abl53009 Human ATP
4	8032	99.9	8195	4	AAH75187	Aah75187 Nucleotid
5	7973.2	99.2	8037	7	ABX70982	Abx70982 Novel hum
6	7529.2	93.6	7610	6	AAD36299	Aad36299 Human tra
7	6686.8	83.2	6792	5	AAD02722	Aad02722 Human ATP

8	5810	72.3	8040	6	ABL53011	Ab153011	Rat ATP b
9	5810	72.3	8040	7	ABT42135	Abt42135	Toxicity
10	5536.8	68.9	5540	6	AAD27271	Aad27271	Human tra
11	2736.8	34.0	2740	6	AAS62249	Aas62249	cDNA sequ
12	991.4	12.3	7323	3	AAZ94746	Aaz94746	Human ATP
13	988	12.3	9870	6	ABN99317	Abn99317	Polymorph
14	988	12.3	9870	6	ABN99311	Abn99311	Polymorph
15	988	12.3	9870	6	ABN99318	Abn99318	Polymorph
16	988	12.3	9870	6	ABN99326	Abn99326	Polymorph
17	986.6	12.3	6786	8	ACC84923	Acc84923	Human ABC
18	986.6	12.3	7784	2	AAV33392	Aav33392	ATP bindi
19	986.6	12.3	7860	4	AAF92835	Aaf92835	Human ABC
20	986.6	12.3	7860	5	AAF83826	Aaf83826	Human ABC
21	986.4	12.3	6880	3	AAZ94734	Aaz94734	Human ATP
22	986.4	12.3	6880	4	AAI70314	Aai70314	Human ATP
23	986.4	12.3	7260	4	AAI70315	Aai70315	Human ATP
24	986.4	12.3	7260	4	AAD21326	Aad21326	Human ATP
25	986.4	12.3	9497	6	ABV78020	Abv78020	Hypoxia-r
26	986.4	12.3	9741	4	AAS06120	Aas06120	Human ABC
27	986.4	12.3	9741	6	AAD37273	Aad37273	Human ABC
28	986.4	12.3	9854	4	AAS06121	Aas06121	Human ABC
29	986.4	12.3	9870	6	ABN99307	Abn99307	Polymorph
30	986.4	12.3	9870	6	ABN99302	Abn99302	Polymorph
31	986.4	12.3	9870	6	ABN99305	Abn99305	Polymorph
32	986.4	12.3	9870	6	ABN99321	Abn99321	Polymorph
33	986.4	12.3	9870	6	ABN99323	Abn99323	Polymorph
34	986.4	12.3	9870	6	ABN99329	Abn99329	Polymorph
35	986.4	12.3	9870	6	ABN99319	Abn99319	Polymorph
36	986.4	12.3	9870	6	ABN99324	Abn99324	Polymorph
37	986.4	12.3	9870	6	ABN99331	Abn99331	Polymorph
38	986.4	12.3	9870	6	ABN99303	Abn99303	Polymorph
39	986.4	12.3	9870	6	ABN99301	Abn99301	Polymorph
40	986.4	12.3	9870	6	ABN99306	Abn99306	Polymorph
41	986.4	12.3	9870	6	ABN99332	Abn99332	Polymorph
42	986.4	12.3	9870	6	ABN99334	Abn99334	Polymorph
43	986.4	12.3	9870	6	ABN99304	Abn99304	Polymorph
44	986.4	12.3	9870	6	ABN99330	Abn99330	Polymorph
45	986.4	12.3	9870	6	ABN99308	Abn99308	Polymorph

ALIGNMENTS

RESULT 1

AAF57452

ID AAF57452 standard; cDNA; 8040 BP.

XX

AC AAF57452;

XX

DT 11-JUN-2001 (first entry)

XX

DE Human ABCA2 transporter protein encoding cDNA.

XX

KW ABCA2; transporter protein; gene therapy; cell transport; human; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers
 FT CDS 35..7345
 FT /*tag= a
 FT /product= "ABCA2 transporter protein"
 XX
 PN WO200121798-A2.
 XX
 PD 29-MAR-2001.
 XX
 PF 31-AUG-2000; 2000WO-US040789.
 XX
 PR 20-SEP-1999; 99US-0154839P.
 XX
 PA (FOXC-) FOX CHASE CANCER CENT.
 XX
 PI Tew KD, Vulevic B, Chen Z;
 XX
 DR WPI; 2001-257989/26.
 DR P-PSDB; AAB62210.
 XX
 PT New nucleic acid molecule for screening inhibitors of human ABCA2
 PT mediated transport, encoding a human ABCA2 transporter protein with a
 PT multi-domain structure including glycosylation and phosphorylation sites.
 XX
 PS Claim 1; Fig 6A-B; 68pp; English.
 XX
 CC This cDNA encodes a human ABCA2 transporter protein having a multi-
 CC domain structure including a number of glycosylation and phosphorylation
 CC sites, a lipocalin signature motif, nucleotide binding folds having
 CC walker A and B ATP binding sites, and a number of membrane spanning
 CC helices. Human ABCA2 transporter polypeptides and nucleic acid encoding
 CC them are useful for identification, detection and/or molecular
 CC characterization of components involved in the transport of molecules
 CC across cell membranes. The nucleic acid is useful as a probe to detect
 CC the presence of and/or expression of genes encoding ABCA2 proteins, and
 CC in gene therapy. A host cell comprising the nucleic acid is useful for
 CC screening compounds that inhibit human ABCA2 mediated transport
 XX
 SQ Sequence 8040 BP; 1458 A; 2690 C; 2407 G; 1485 T; 0 U; 0 Other;

Query Match 100.0%; Score 8040; DB 4; Length 8040;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 8040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 60

 Qy 61 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCCTGGCCTTCGAGAT 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCCTGGCCTTCGAGAT 120

 Qy 121 CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 180

 Qy 181 CTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCTGACGTCTGCCGGCATCCTGCC 240

Db	181	 CTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCCTGACGTCTGCCGGCATCCTGCC	240
Qy	241	TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGC	300
Db	241	 TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGC	300
Qy	301	CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT	360
Db	301	 CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT	360
Qy	361	GTTTGACCCAGCGCGGCCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA	420
Db	361	 GTTTGACCCAGCGCGGCCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA	420
Qy	421	GGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC	480
Db	421	 GGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC	480
Qy	481	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA	540
Db	481	 CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA	540
Qy	541	CTTGTCGCTGCCCCAATAGCACGGCCCAAGCACTCTTGGCCGCCCCTGTGGACCCGCCCCGA	600
Db	541	 CTTGTCGCTGCCCCAATAGCACGGCCCAAGCACTCTTGGCCGCCCCTGTGGACCCGCCCCGA	600
Qy	601	GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	660
Db	601	 GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	660
Qy	661	GGGTGAGGAGCCCTGGAGCCGCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	720
Db	661	 GGGTGAGGAGCCCTGGAGCCGCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	720
Qy	721	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	780
Db	721	 GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	780
Qy	781	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	840
Db	781	 GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	840
Qy	841	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	900
Db	841	 CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	900
Qy	901	CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	960
Db	901	 CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	960
Qy	961	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1020
Db	961	 CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1020
Qy	1021	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCTGTGCGCCCTGGCCCTGCTACTGCCCCA	1080

Db	1021	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGGCCCTGGCCCTGCTACTGCCCCA	1080
Qy	1081	GGGTGCCTGCACTGGCCGGACCCCGGACCCCGAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Db	1081	GGGTGCCTGCACTGGCCGGACCCCGGACCCCGAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Qy	1141	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCTC	1200
Db	1141	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCTC	1200
Qy	1201	TGCTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
Db	1201	TGCTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
Qy	1261	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTTGAACCCGAGGCGCT	1320
Db	1261	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTTGAACCCGAGGCGCT	1320
Qy	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380
Db	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380
Qy	1381	CCTCGTGACCTCATGACCAGCAACCCCAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
Db	1381	CCTCGTGACCTCATGACCAGCAACCCCAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
Qy	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1500
Db	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1500
Qy	1501	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1501	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Qy	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620
Db	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620
Qy	1621	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTCTCGCTGCC	1680
Db	1621	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTCTCGCTGCC	1680
Qy	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGAT	1740
Db	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGAT	1740
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1800
Db	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1800
Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1860
Db	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1860
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1920
Db	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1920

Qy	1921	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1980
Db	1921	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1980
Qy	1981	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Db	1981	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Db	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Qy	2101	GTTCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTGATTGAGCACATGATGCC	2160
Db	2101	GTTCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTGATTGAGCACATGATGCC	2160
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Db	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280
Db	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280
Qy	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2340
Db	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2340
Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2400
Db	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2400
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTA	2460
Db	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTA	2460
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Db	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAAGTG	2580
Db	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAAGTG	2580
Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640
Db	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640
Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2700
Db	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2700
Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760
Db	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760

Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Qy	2821	CTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2821	CTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Qy	2881	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2881	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGTGCCAT	2940
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3000
Db	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3000
Qy	3001	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3001	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCCGC	3180
Db	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCCGC	3180
Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Qy	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3420
Db	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3420
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3480
Db	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3480
Qy	3481	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3540
Db	3481	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3540
Qy	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660

Db	3601	 GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3720
Db	3661	 CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3720
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTG	3780
Db	3721	 GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTG	3780
Qy	3781	CTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3781	 CTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3841	 AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3901	 CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4020
Db	3961	 GCTGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4020
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4021	 GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Qy	4081	CCCGGCGTCTGGGGAGGGTTCAGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4081	 CCCGGCGTCTGGGGAGGGTTCAGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4200
Db	4141	 GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4200
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4201	 CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTCGGCCAGGGCAGCCGCAA	4320
Db	4261	 TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTCGGCCAGGGCAGCCGCAA	4320
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4321	 GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Qy	4381	CTGCGCCCCGCCGCAACTCCAAGGCACTCTTCTCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4381	 CTGCGCCCCGCCGCAACTCCAAGGCACTCTTCTCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500

Db	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Qy	4501	CCTGTACCTTCCCAGTACCACAACTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4501	CCTGTACCTTCCCAGTACCACAACTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCT	4620
Db	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCT	4620
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Qy	4681	CAACGGCTCGCTGGGGCCCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4681	CAACGGCTCGCTGGGGCCCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Qy	4801	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4860
Db	4801	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4860
Qy	4861	GCAGGCCTGGAACGTCTCCCTGCCGCCCCACCGCTGGGCCAGAAATGTGGACGTCCGCACC	4920
Db	4861	GCAGGCCTGGAACGTCTCCCTGCCGCCCCACCGCTGGGCCAGAAATGTGGACGTCCGCACC	4920
Qy	4921	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	4980
Db	4921	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	4980
Qy	4981	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACC CGCCCCAGATGCGGGTGGTCACAGGCGA	5040
Db	4981	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACC CGCCCCAGATGCGGGTGGTCACAGGCGA	5040
Qy	5041	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5100
Db	5041	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5100
Qy	5101	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5160
Db	5101	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5160
Qy	5161	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5220
Db	5161	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5220
Qy	5221	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTCAACAA	5280
Db	5221	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTCAACAA	5280
Qy	5281	CGCCATCCTGCGTGCCAACTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5340
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Qy	5341	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5400
Db	5341	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5400
Qy	5401	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5460
Db	5401	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5460
Qy	5461	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGCA	5520
Db	5461	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGCA	5520
Qy	5521	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5580
Db	5521	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5580
Qy	5581	GGTCCCCGCTACCTGCTGTGTATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTC	5640
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Qy	5641	GCCCAACCAACTTCCCTGCCGTCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCC	5700
Db	5641	GCCCAACCAACTTCCCTGCCGTCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCC	5700
Qy	5701	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCAT	5760
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Qy	5761	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5820
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Qy	5821	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5880
Db	5821	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5880
Qy	5881	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5940
Db	5881	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5940
Qy	5941	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGGGACATTGT	6000
Db	5941	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGGGACATTGT	6000
Qy	6001	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6060
Db	6001	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6060
Qy	6061	GTGCCAGTACAACCTTCCTGCGGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6120
Db	6061	GTGCCAGTACAACCTTCCTGCGGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6120
Qy	6121	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6180
Db	6121	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6180

Qy	6181	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6240
Db	6181	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6240
Qy	6241	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6300
Db	6241	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6300
Qy	6301	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6360
Db	6301	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6360
Qy	6361	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6420
Db	6361	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6420
Qy	6421	CCTCGGCTACTGCCCCGAGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCT	6480
Db	6421	CCTCGGCTACTGCCCCGAGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCT	6480
Qy	6481	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6540
Db	6481	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6540
Qy	6541	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6600
Db	6541	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6600
Qy	6601	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTTGGGTACCCAGCCTTCATCTT	6660
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Qy	6661	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCGGCGCTTCCTCTGGAACCTCAT	6720
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Qy	6721	CCTCGACCTCATCAAGACAGGGCGTTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTG	6780
Db	6721	CCTCGACCTCATCAAGACAGGGCGTTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTG	6780
Qy	6781	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6840
Db	6781	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6840
Qy	6841	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6900
Db	6841	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6900
Qy	6901	CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6960
Db	6901	CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6960
Qy	6961	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7020
Db	6961	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7020
Qy	7021	CCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7080

Db	7021	 CCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7080
Qy	7081	CAGCCAGACCACACTGGACAATGTGTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT	7140
Db	7081	 CAGCCAGACCACACTGGACAATGTGTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT	7140
Qy	7141	GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7200
Db	7141	 GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7200
Qy	7201	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA	7260
Db	7201	 CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA	7260
Qy	7261	GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7320
Db	7261	 GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7320
Qy	7321	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7380
Db	7321	 CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7380
Qy	7381	TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGC	7440
Db	7381	 TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGC	7440
Qy	7441	CAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCG	7500
Db	7441	 CAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCG	7500
Qy	7501	GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAAAGGCTGACCCGGCCC	7560
Db	7501	 GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAAAGGCTGACCCGGCCC	7560
Qy	7561	GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCCGGCCCCTCG	7620
Db	7561	 GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCCGGCCCCTCG	7620
Qy	7621	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7680
Db	7621	 CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7680
Qy	7681	TTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA	7740
Db	7681	 TTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA	7740
Qy	7741	GCGGGCTGTGGGCGGAGCTGGGTCACTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCT	7800
Db	7741	 GCGGGCTGTGGGCGGAGCTGGGTCACTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCT	7800
Qy	7801	CTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGAAGCCATCAGCTTGGGCCAG	7860
Db	7801	 CTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGAAGCCATCAGCTTGGGCCAG	7860
Qy	7861	CTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCC	7920

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Db      7861 CTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCC 7920
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        |||
Db      7921 CCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCCCTGCCCCGCCACCTCCC 7980
Qy      7981 TGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAAATAAACAAAATGTC 8040
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Db      7981 TGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAAATAAACAAAATGTC 8040

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RESULT 2

ABV74350

ID ABV74350 standard; DNA; 8056 BP.

XX

AC ABV74350;

XX

DT 29-JAN-2003 (first entry)

XX

DE Human ABC transporter ABCA2 encoding polynucleotide SEQ ID NO 3.

XX

KW Human; ABC transporter; ABCB9; ABCB1; ABCA2; ABCG4; ABCG1;

KW amyloid precursor protein; adenosine tri-phosphate; nootropic;

KW ATP-binding cassette transporter; beta-amyloid plaque formation;

KW Alzheimer's disease; Parkinson's disease; Huntington's disease;

KW gene therapy; transgenic; neuroprotective; anticonvulsant;

KW antiparkinsonian; gene; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1350..7364

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FT /transl_except= (pos:1437..1439,aa:X)

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FT /transl_except= (pos:1623..1625,aa:P)

FT /transl_except= (pos:1743..1745,aa:P)

FT /transl_except= (pos:1869..1871,aa:G)

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Db	137	CTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT	196
Qy	181	CTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCCTGACGTCTGCCGGCATCCTGCC	240
Db	197	CTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCCTGACGTCTGCCGGCATCCTGCC	256
Qy	241	TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTTCGGCTTCCTGCAGTACGC	300
Db	257	TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTTCGGCTTCCTGCAGTACGC	316
Qy	301	CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT	360
Db	317	CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT	376
Qy	361	GTTTGACCCAGCGCGGCCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA	420
Db	377	GTTTGACCCAGCGCGGCCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA	436
Qy	421	GGCCCTCAGTGCGGGCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC	480
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Qy	481	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA	540
Db	497	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA	556
Qy	541	CTTGTCGCTGCCCCAATAGCACGGCCCAAGCACTCTTGCCGCCCCGTGTGGACCCGCCCCGA	600
Db	557	CTTGTCGCTGCCCCAATAGCACGGCCCAAGCACTCTTGCCGCCCCGTGTGGACCCGCCCCGA	616
Qy	601	GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	660
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Qy	661	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	720
Db	677	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	736
Qy	721	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGGCCG	780
Db	737	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGGCCG	796
Qy	781	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	840
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Qy	841	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	900
Db	857	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	916
Qy	901	CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	960

Db	917	CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	976
Qy	961	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1020
Db	977	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1036
Qy	1021	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTCGGCCCTGGCCCTGCTACTGCCCCA	1080
Db	1037	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTCGGCCCTGGCCCTGCTACTGCCCCA	1096
Qy	1081	GGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Db	1097	GGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1156
Qy	1141	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCTC	1200
Db	1157	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCTC	1216
Qy	1201	TGCTGCAGCACTGGCCACCCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
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Qy	1261	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCT	1320
Db	1277	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCT	1336
Qy	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380
Db	1337	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1396
Qy	1381	CCTCGTGCACCTCATGACCAGCAACCCCAAAATCCTGTACGCGCTGCGGGCTCTGAGGT	1440
Db	1397	CCTCGTGCACCTCATGACCAGCAACCCCAAAATCCTGTACGCGCTGCGGGCTCTGAGGT	1456
Qy	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1500
Db	1457	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1516
Qy	1501	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1517	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1576
Qy	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620
Db	1577	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1636
Qy	1621	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1680
Db	1637	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1696
Qy	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGAT	1740
Db	1697	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGAT	1756
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1800
Db	1757	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1816

Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCAC	1860
Db	1817	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCAC	1876
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTG	1920
Db	1877	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTG	1936
Qy	1921	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGC	1980
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Qy	1981	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTG	2040
Db	1997	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTG	2056
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGG	2100
Db	2057	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGG	2116
Qy	2101	GTTCCCTTACCCCTGCTACACACGCGATGACTTCCTGT	2160
Db	2117	GTTCCCTTACCCCTGCTACACACGCGATGACTTCCTGT	2176
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCC	2220
Db	2177	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCC	2236
Qy	2221	GGAGAAGGAGCACC GGCTCAAGGAGGTGATGAAGACC	2280
Db	2237	GGAGAAGGAGCACC GGCTCAAGGAGGTGATGAAGACC	2296
Qy	2281	CTGGGTGGCCTGGTTCATCACC GGCTTTGTGCAGCTG	2340
Db	2297	CTGGGTGGCCTGGTTCATCACC GGCTTTGTGCAGCTG	2356
Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCC	2400
Db	2357	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCC	2416
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCT	2460
Db	2417	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCT	2476
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCT	2520
Db	2477	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCT	2536
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATA	2580
Db	2537	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATA	2596
Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGG	2640
Db	2597	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGG	2656

Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2700
Db	2657	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2716
Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760
Db	2717	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2776
Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2777	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2836
Qy	2821	CTTCCCCTGCAGAAGTCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2837	CTTCCCCTGCAGAAGTCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2896
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Db	2897	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCATGGAGGAGGACCAGGCCTGTGCCAT	2956
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3000
Db	2957	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3016
Qy	3001	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3017	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3076
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3077	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3136
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGGC	3180
Db	3137	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGGC	3196
Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
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Db	3257	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3316
Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
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Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3420
Db	3377	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3436
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3480
Db	3437	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3496
Qy	3481	GCCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3540

Db	3497	 GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3556
Qy	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3557	 CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3616
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3617	 GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3676
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3720
Db	3677	 CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3736
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGCCCCGCTGAGCAGCTG	3780
Db	3737	 GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGCCCCGCTGAGCAGCTG	3796
Qy	3781	CTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3797	 CTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3856
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3857	 AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3916
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3917	 CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3976
Qy	3961	GCTGATGGACACGACCCCTGGAGGAAGTGTTCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4020
Db	3977	 GCTGATGGACACGACCCCTGGAGGAAGTGTTCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4036
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4037	 GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4096
Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4097	 CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4156
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4200
Db	4157	 GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4216
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4217	 CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4276
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTCGGCCAGGGCAGCCGCAA	4320
Db	4277	 TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTCGGCCAGGGCAGCCGCAA	4336
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCACGGGCTGCTGGTCAAACGCTTCCA	4380

Db	4337	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4396
Qy	4381	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4397	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4456
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4457	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4516
Qy	4501	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4517	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4576
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCAGCAGCT	4620
Db	4577	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCAGCAGCT	4636
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4637	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4696
Qy	4681	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4697	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4756
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4757	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4816
Qy	4801	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4860
Db	4817	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4876
Qy	4861	GCAGGCCTGGAACGTCTCCCTGCCGCCACCGCTGGGCCAGAAATGTGGACGTCCGGCACC	4920
Db	4877	GCAGGCCTGGAACGTCTCCCTGCCGCCACCGCTGGGCCAGAAATGTGGACGTCCGGCACC	4936
Qy	4921	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACCGG	4980
Db	4937	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACCGG	4996
Qy	4981	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5040
Db	4997	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5056
Qy	5041	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5100
Db	5057	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5116
Qy	5101	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5160
Db	5117	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5176
Qy	5161	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCCA	5220
Db	5177	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCCA	5236

Qy	5221	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTCAACAA	5280
Db	5237	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTCAACAA	5296
Qy	5281	CGCCATCCTGCGTGCCAACCTGCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5340
Db	5297	CGCCATCCTGCGTGCCAACCTGCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5356
Qy	5341	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5400
Db	5357	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5416
Qy	5401	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5460
Db	5417	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5476
Qy	5461	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAG	5520
Db	5477	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAG	5536
Qy	5521	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5580
Db	5537	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5596
Qy	5581	GGTCCCCGCTACCTGCTGTGTATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTC	5640
Db	5597	GGTCCCCGCTACCTGCTGTGTATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTC	5656
Qy	5641	GCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCC	5700
Db	5657	GCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCC	5716
Qy	5701	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCAT	5760
Db	5717	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCAT	5776
Qy	5761	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCTGCTACAGCTCTT	5820
Db	5777	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCTGCTACAGCTCTT	5836
Qy	5821	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5880
Db	5837	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5896
Qy	5881	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5940
Db	5897	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5956
Qy	5941	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGT	6000
Db	5957	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGT	6016
Qy	6001	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6060
Db	6017	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6076

Qy	6061	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6120
Db	6077	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6136
Qy	6121	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6180
Db	6137	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6196
Qy	6181	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6240
Db	6197	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6256
Qy	6241	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGGCTCCTGGGCGT	6300
Db	6257	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGGCTCCTGGGCGT	6316
Qy	6301	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6360
Db	6317	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6376
Qy	6361	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6420
Db	6377	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6436
Qy	6421	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCT	6480
Db	6437	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCT	6496
Qy	6481	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6540
Db	6497	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6556
Qy	6541	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6600
Db	6557	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6616
Qy	6601	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTT	6660
Db	6617	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTT	6676
Qy	6661	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6720
Db	6677	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6736
Qy	6721	CCTCGACCTCATCAAGACAGGGCGTTCAGTGGTGTGACATCACACAGCATGGAGGAGTG	6780
Db	6737	CCTCGACCTCATCAAGACAGGGCGTTCAGTGGTGTGACATCACACAGCATGGAGGAGTG	6796
Qy	6781	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6840
Db	6797	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6856
Qy	6841	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6900
Db	6857	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6916
Qy	6901	CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6960

Db	6917	 CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6976
Qy	6961	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7020
Db	6977	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7036
Qy	7021	CCAGGTGTTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7080
Db	7037	CCAGGTGTTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7096
Qy	7081	CAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT	7140
Db	7097	CAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT	7156
Qy	7141	GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7200
Db	7157	GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7216
Qy	7201	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCCGA	7260
Db	7217	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCCGA	7276
Qy	7261	GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7320
Db	7277	GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7336
Qy	7321	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7380
Db	7337	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7396
Qy	7381	TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGC	7440
Db	7397	TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGC	7456
Qy	7441	CAGGGCCTGGAGTGGAGGTTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCCTGTACTCG	7500
Db	7457	CAGGGCCTGGAGTGGAGGTTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCCTGTACTCG	7516
Qy	7501	GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCC	7560
Db	7517	GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCC	7576
Qy	7561	GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCTCG	7620
Db	7577	GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCTCG	7636
Qy	7621	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7680
Db	7637	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7696
Qy	7681	TTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA	7740
Db	7697	TTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA	7756
Qy	7741	GCGGGCTGTGGGCGGAGCTGGGTGAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCT	7800

Db 7757 GCGGGCTGTGGGCGGAGCTGGGTCAGTCCCGTATTTATTTTGTCTTGAGAAGAGGCTCCT 7816

Qy 7801 CTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAG 7860
 |||

Db 7817 CTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAG 7876

Qy 7861 CTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCC 7920
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Db 7877 CTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCC 7936

Qy 7921 CCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCCACCTCCC 7980
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Db 7937 CCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCCACCTCCC 7996

Qy 7981 TGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAAAATGTC 8040
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Db 7997 TGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAAAATGTC 8056

RESULT 3

ABL53009

ID ABL53009 standard; DNA; 8269 BP.

XX

AC ABL53009;

XX

DT 06-JUN-2002 (first entry)

XX

DE Human ATP binding cassette transporter protein, ABCA2, coding sequence.

XX

KW Human; ABCA2; gene; neuroprotective; nootropic; antiparkinsonian;

KW adenosine triphosphate binding cassette transporter protein;

KW ATP binding cassette transporter protein; Alzheimer's disease;

KW prion disease; Huntington's disease; Parkinson's disease; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 250..7560

FT /*tag= a

FT /product= "Human ABCA2"

XX

PN WO200208424-A1.

XX

PD 31-JAN-2002.

XX

PF 26-JUL-2001; 2001WO-JP006457.

XX

PR 26-JUL-2000; 2000JP-00225462.

XX

PA (BANY) BANYU PHARM CO LTD.

PA (INAG/) INAGAKI N.

XX

PI Inagaki N;

XX

DR WPI; 2002-179907/23.

DR P-PSDB; ABB76715.

XX

PT Adenosine triphosphate (ATP) binding cassette transporter gene ABCA2 of
PT human or rat origin and encoded protein, useful for screening inhibitors,
PT promoters and regulators of ABCA2 activity as drugs and diagnosis of
PT ABCA2-related diseases.

XX

PS Claim 2; Page 47-52; 118pp; Japanese.

XX

CC The present sequence is the coding sequence for human adenosine
CC triphosphate (ATP) binding cassette transporter protein (ABCA2). ABCA2
CC can be used in the diagnosis, treatment and prevention of diseases such
CC as Alzheimer's disease, prion diseases, Huntington's disease, and
CC Parkinson's disease

XX

SQ Sequence 8269 BP; 1525 A; 2724 C; 2469 G; 1551 T; 0 U; 0 Other;

Query Match 100.0%; Score 8036.4; DB 6; Length 8269;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8037; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      3 GCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCTGC 62
          |||
Db     218 GCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCTGC 277

Qy      63 TGCTCTGGAAGAACGTGACGCTCAAACGCCGAGCCCGTGGGTCTTGGCCTTCGAGATCT 122
          |||
Db     278 TGCTCTGGAAGAACGTGACGCTCAAACGCCGAGCCCGTGGGTCTTGGCCTTCGAGATCT 337

Qy     123 TCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCATCT 182
          |||
Db     338 TCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCATCT 397

Qy     183 CCGTGAAGGAAGTCCCCCTTCTACACAGCGGCGCCCTGACGTCTGCCGGCATCCTGCCTG 242
          |||
Db     398 CCGTGAAGGAAGTCTCCTTCTACACAGCGGCGCCCTGACGTCTGCCGGCATCCTGCCTG 457

Qy     243 TCATGCAATCGCTGTGCGCGGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGCCA 302
          |||
Db     458 TCATGCAATCGCTGTGCGCGGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGCCA 517

Qy     303 ACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCTGT 362
          |||
Db     518 ACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCTGT 577

Qy     363 TTGACCCAGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGAGG 422
          |||
Db     578 TTGACCCAGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGAGG 637

Qy     423 CCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTCCT 482
          |||
Db     638 CCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTCCT 697

Qy     483 TCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAACT 542
          |||
Db     698 TCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAACT 757

Qy     543 TGTCGCTGCCCAATAGCACGGCCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCGAGG 602
          |||
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Db	758	TGTCGCTGCCCCAATAGCACGGCCCAAGCACTCTTGGCCGCCCGTGTGGACCCGCCCGAGG	817
Qy	603	TCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAAGG	662
Db	818	TCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAAGG	877
Qy	663	GTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCTGC	722
Db	878	GTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCTGC	937
Qy	723	TGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCGGA	782
Db	938	TGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCGGA	997
Qy	783	TCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTGCA	842
Db	998	TCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTGCA	1057
Qy	843	GTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAACC	902
Db	1058	GTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAACC	1117
Qy	903	AGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGACT	962
Db	1118	AGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGACT	1177
Qy	963	CCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGACCTGCTGGATG	1022
Db	1178	CCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGACCTGCTGGATG	1237
Qy	1023	CCCAGAAGGTTCTGCAGGATGTGGATGTCTGTGCGCCCTGGCCCTGCTACTGCCCCAGG	1082
Db	1238	CCCAGAAGGTTCTGCAGGATGTGGATGTCTGTGCGCCCTGGCCCTGCTACTGCCCCAGG	1297
Qy	1083	GTGCCTGCACTGGCCGGACCCCCGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAATG	1142
Db	1298	GTGCCTGCACTGGCCGGACCCCCGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAATG	1357
Qy	1143	GCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCTCTG	1202
Db	1358	GCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCTCTG	1417
Qy	1203	CTGCAGCACTGGCCACCCCGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCTCT	1262
Db	1418	CTGCAGCACTGGCCACCCCGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCTCT	1477
Qy	1263	GGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCTGC	1322
Db	1478	GGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCTGC	1537
Qy	1323	GGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCTCC	1382
Db	1538	GGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCTCC	1597
Qy	1383	TCGTGCACCTCATGACCAGCAACCCCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGTCG	1442
Db	1598	TCGTGCACCTCATGACCAGCAACCCCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGTCG	1657

Qy	1443	ACCGCGTCATCCTCAAGGCCAACGAGACTTTTGGCTTTTGTGGGCAACGTGACTCACTATG	1502
Db	1658	ACCGCGTCATCCTCAAGGCCAACGAGACTTTTGGCTTTTGTGGGCAACGTGACTCACTATG	1717
Qy	1503	CCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCTGC	1562
Db	1718	CCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCTGC	1777
Qy	1563	AGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGCAC	1622
Db	1778	AGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGCAC	1837
Qy	1623	TGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCCCCA	1682
Db	1838	TGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCCCCA	1897
Qy	1683	GTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGATCC	1742
Db	1898	GTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGATCC	1957
Qy	1743	AGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCATTG	1802
Db	1958	AGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCATTG	2017
Qy	1803	TCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGATCT	1862
Db	2018	TCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGATCT	2077
Qy	1863	TCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAACT	1922
Db	2078	TCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAACT	2137
Qy	1923	CCAGCTTCACCGAGAAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCCAATA	1982
Db	2138	CCAGCTTCACCGAGAAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCCAATA	2197
Qy	1983	CTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCGCG	2042
Db	2198	CTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCGCG	2257
Qy	2043	CCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGATGT	2102
Db	2258	CCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGATGT	2317
Qy	2103	TCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCCGC	2162
Db	2318	TCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCCGC	2377
Qy	2163	TGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGCGG	2222
Db	2378	TGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGCGG	2437
Qy	2223	AGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCACT	2282
Db	2438	AGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCACT	2497

Qy	2283	GGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCACCG	2342
Db	2498	GGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCACCG	2557
Qy	2343	CCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTTCC	2402
Db	2558	CCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTTCC	2617
Qy	2403	TGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTCCA	2462
Db	2618	TGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTCCA	2677
Qy	2463	AGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTACA	2522
Db	2678	AGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTACA	2737
Qy	2523	TGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTGCA	2582
Db	2738	TGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTGCA	2797
Qy	2583	TCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTATG	2642
Db	2798	TCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTATG	2857
Qy	2643	AGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGACG	2702
Db	2858	AGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGACG	2917
Qy	2703	ACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCATCC	2762
Db	2918	ACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCATCC	2977
Qy	2763	TCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTACT	2822
Db	2978	TCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTACT	3037
Qy	2823	TCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAGCT	2882
Db	3038	TCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAGCT	3097
Qy	2883	GGCCGTGGGCACGCACCCCCGCCTCAGTGTATGGAGGAGGACCAGGCCTGTGCCATGG	2942
Db	3098	GGCCGTGGGCACGCACCCCCGCCTCAGTGTATGGAGGAGGACCAGGCCTGTGCCATGG	3157
Qy	2943	AGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCTGG	3002
Db	3158	AGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCTGG	3217
Qy	3003	TTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAACA	3062
Db	3218	TTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAACA	3277
Qy	3063	AGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGCGG	3122
Db	3278	AGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGCGG	3337
Qy	3123	GCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGGCCA	3182

Db	3338	 GCAAGACCACCACCATGTCCATCCTGACCGGCCCTGTTCCCTCCAACGTCGGGTTCGCCCA	3397
Qy	3183	CCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCATGT	3242
Db	3398	 CCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCATGT	3457
Qy	3243	GCCCGCAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTACT	3302
Db	3458	 GCCCGCAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTACT	3517
Qy	3303	CACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGAGG	3362
Db	3518	 CACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGAGG	3577
Qy	3363	ACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCTGGGTGGCATGAAGC	3422
Db	3578	 ACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCTGGGTGGCATGAAGC	3637
Qy	3423	GCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGAGC	3482
Db	3638	 GCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGAGC	3697
Qy	3483	CCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTACA	3542
Db	3698	 CCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTACA	3757
Qy	3543	AGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGGGG	3602
Db	3758	 AGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGGGG	3817
Qy	3603	ACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCTCTCA	3662
Db	3818	 ACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCTCTCA	3877
Qy	3663	AGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCCGAGCCGGGGG	3722
Db	3878	 AGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCCGAGCCGGGGG	3937
Qy	3723	GCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTGCT	3782
Db	3938	 GCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTGCT	3997
Qy	3783	CCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTCAG	3842
Db	3998	 CCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTCAG	4057
Qy	3843	ACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCAAGAAGGGGGCTTTCG	3902
Db	4058	 ACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCAAGAAGGGGGCTTTCG	4117
Qy	3903	AGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGGGC	3962
Db	4118	 AGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGGGC	4177
Qy	3963	TGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCTGGAGGAGGATCAGTCGCTGG	4022

Db 4178 TGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCGGAGGAGGATCAGTCGCTGG 4237
 Qy 4023 AGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGGCC 4082
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4238 AGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGGCC 4297
 Qy 4083 CGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTCGC 4142
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4298 CGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTCGC 4357
 Qy 4143 AGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGGCT 4202
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4358 AGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGGCT 4417
 Qy 4203 ACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAATG 4262
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4418 ACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAATG 4477
 Qy 4263 TCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAAGC 4322
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4478 TCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAAGC 4537
 Qy 4323 TGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCACT 4382
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4538 TGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCACT 4597
 Qy 4383 GCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGTCT 4442
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4598 GCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGTCT 4657
 Qy 4443 GCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGTCC 4502
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4658 GCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGTCC 4717
 Qy 4503 TGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCCTACGCCA 4562
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4718 TGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCCTACGCCA 4777
 Qy 4563 ACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCCAGCAGCTCG 4622
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4778 ACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCCAGCAGCTCG 4837
 Qy 4623 TGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGCCA 4682
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4838 TGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGCCA 4897
 Qy 4683 ACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGCTC 4742
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4898 ACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGCTC 4957
 Qy 4743 GGTTCCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTTTCG 4802
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4958 GGTTCCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTTTCG 5017
 Qy 4803 TGCCACCCCCACCCTCGCCCCCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCTGC 4862
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 5018 TGCCACCCCCACCCTCGCCCCCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCTGC 5077

Qy	4863	AGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTGGGCACCCT	4922
Db	5078	AGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTGGGCACCCT	5137
Qy	4923	CCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GGCT	4982
Db	5138	CCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GGCT	5197
Qy	4983	TCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGACA	5042
Db	5198	TCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGACA	5257
Qy	5043	TCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCGCT	5102
Db	5258	TCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCGCT	5317
Qy	5103	TCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGCCT	5162
Db	5318	TCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGCCT	5377
Qy	5163	CATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCAGG	5222
Db	5378	CATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCAGG	5437
Qy	5223	TTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAACG	5282
Db	5438	TTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAACG	5497
Qy	5283	CCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCACCG	5342
Db	5498	CCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCACCG	5557
Qy	5343	TCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGG	5402
Db	5558	TCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGG	5617
Qy	5403	GCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCT	5462
Db	5618	GCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCT	5677
Qy	5463	TCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAGCG	5522
Db	5678	TCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAGCG	5737
Qy	5523	GCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCTGG	5582
Db	5738	GCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCTGG	5797
Qy	5583	TCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTCGC	5642
Db	5798	TCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTCGC	5857
Qy	5643	CCACCAACTTCCCTGCCGTCCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCCCA	5702
Db	5858	CCACCAACTTCCCTGCCGTCCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCCCA	5917

Qy	5703	TCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTTCCTCATTG	5762
Db	5918	TCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTTCCTCATTG	5977
Qy	5763	TCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCG	5822
Db	5978	TCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCG	6037
Qy	5823	AGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCC	5882
Db	6038	AGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCC	6097
Qy	5883	CCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGT	5942
Db	6098	CCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGT	6157
Qy	5943	ACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCA	6002
Db	6158	ACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCA	6217
Qy	6003	CCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGT	6062
Db	6218	CCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGT	6277
Qy	6063	GCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGG	6122
Db	6278	GCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGG	6337
Qy	6123	ATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACA	6182
Db	6338	ATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACA	6397
Qy	6183	TGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGG	6242
Db	6398	TGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGG	6457
Qy	6243	CCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCA	6302
Db	6458	CCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCA	6517
Qy	6303	ACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGG	6362
Db	6518	ACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGG	6577
Qy	6363	GCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCC	6422
Db	6578	GCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCC	6637
Qy	6423	TCGGCTACTGCCCAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCTGC	6482
Db	6638	TCGGCTACTGCCCAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCTGC	6697
Qy	6483	AGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGG	6542
Db	6698	AGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGG	6757
Qy	6543	CTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCG	6602

Db	6758	CTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCG	6817
Qy	6603	GCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTTGGGTACCCAGCCTTCATCTTCC	6662
Db	6818	GCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTTGGGTACCCAGCCTTCATCTTCC	6877
Qy	6663	TGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCTCTGGAACCTCATCC	6722
Db	6878	TGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCTCTGGAACCTCATCC	6937
Qy	6723	TCGACCTCATCAAGACAGGGCGTTCACTGGTGCTGACATCACACAGCATGGAGGAGTGCG	6782
Db	6938	TCGACCTCATCAAGACAGGGCGTTCACTGGTGCTGACATCACACAGCATGGAGGAGTGCG	6997
Qy	6783	AGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCA	6842
Db	6998	AGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCA	7057
Qy	6843	TCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCA	6902
Db	7058	TCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCA	7117
Qy	6903	GCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCA	6962
Db	7118	GCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCA	7177
Qy	6963	AGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCC	7022
Db	7178	AGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCC	7237
Qy	7023	AGGTGTTTACGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTCA	7082
Db	7238	AGGTGTTTACGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTCA	7297
Qy	7083	GCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGACAACCTGG	7142
Db	7298	GCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGACAACCTGG	7357
Qy	7143	AGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCC	7202
Db	7358	AGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCC	7417
Qy	7203	TGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCCGAGG	7262
Db	7418	TGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCCGAGG	7477
Qy	7263	ACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCCT	7322
Db	7478	ACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCCT	7537
Qy	7323	TCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTG	7382
Db	7538	TCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTG	7597
Qy	7383	ACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCAGTGCCTGCCA	7442

Db	7598	ACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGCCA	7657
Qy	7443	GGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCGGC	7502
Db	7658	GGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCGGC	7717
Qy	7503	CATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCCGG	7562
Db	7718	CATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCCGG	7777
Qy	7563	GCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCTCGCC	7622
Db	7778	GCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCTCGCC	7837
Qy	7623	CCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCCTT	7682
Db	7838	CCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCCTT	7897
Qy	7683	TCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGAGC	7742
Db	7898	TCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGAGC	7957
Qy	7743	GGGCTGTGGGCGGAGCTGGGTCACTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCTCT	7802
Db	7958	GGGCTGTGGGCGGAGCTGGGTCACTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCTCT	8017
Qy	7803	GGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAGCT	7862
Db	8018	GGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAGCT	8077
Qy	7863	GGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCCC	7922
Db	8078	GGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCCC	8137
Qy	7923	CAACCCCCAGCTGCCATCGCTCTCCCACCCAGCTTGGCCCCCTGCCCCGCCACCTCCCTG	7982
Db	8138	CAACCCCCAGCTGCCATCGCTCTCCCACCCAGCTTGGCCCCCTGCCCCGCCACCTCCCTG	8197
Qy	7983	GGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAAAATGTC	8040
Db	8198	GGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAAAATGTC	8255

RESULT 4

AAH75187

ID AAH75187 standard; cDNA; 8195 BP.

XX

AC AAH75187;

XX

DT 13-NOV-2001 (first entry)

XX

DE Nucleotide sequence of a human 17114 transporter polypeptide.

XX

KW Human; transporter; 20685; 579; 17114; 23821; 33894; 32613;

KW vesicular monoamine transporter; neurotransmitter-symporter;

KW ABC transporter; sulfate transporter; neurological disorder;

KW central nervous system disorder; Parkinson's disease; depression; pain;

KW infectious disease; cell proliferative disorder; cancer; blood disorder;
 KW immune disorder; inflammatory disorder; spleen disorder; lung disorder;
 KW Hodgkin's disease; Niemann-Pick disease; chronic bronchitis; ischemia;
 KW colon disorder; cirrhosis; uterus disorder; endometrium disorder;
 KW endometrial stromal tumour; brain disorder; T-cell disorder; anemia;
 KW Sjogren syndrome; skin disorder; lupus erythematosus; heart disorder;
 KW haematopoietic stem cell; Alzheimer's disease; myocardial infarction;
 KW blood vessel; Kawasaki syndrome; red cell disorder; thymus disorder;
 KW B-cell disorder; kidney disorder; glomerulonephritis; breast disorder;
 KW testis disorder; thyroid disorder; Graves disease; pancreatitis;
 KW skeletal muscle disorder; tumour; pancreas disorder;
 KW small intestine disorder; celiac sprue; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 132. .7442
 FT /*tag= a
 FT /product= "transporter"
 XX
 PN WO200164875-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US006374.
 XX
 PR 29-FEB-2000; 2000US-0185906P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Glucksmann MA;
 XX
 DR WPI; 2001-550178/61.
 DR P-PSDB; AAG67160.
 XX
 PT Novel human transporter polypeptides useful for treating and diagnosing
 PT Parkinson's disease, Hodgkin disease, glomerulonephritis, myocardial
 PT infarction, Grave's disease, Alzheimer's disease, anemia, asthma and
 PT tumors.
 XX
 PS Claim 2; Fig 14A-G; 259pp; English.
 XX
 CC The present sequence encodes a human transporter polypeptide. The
 CC specification describes 20685, 579, 17114, 23821, 33894 or 32613 human
 CC transporter polypeptides. The 20685 transporter is similar to vesicular
 CC monoamine transporters. The 579 transporter is similar to
 CC neurotransmitter-symporters. The 17114 transporter is similar to ABC
 CC transporters. The 32613 transporter is similar to sulfate transporters.
 CC The transporter polypeptides and polynucleotides are useful for treating
 CC and diagnosing neurological and central nervous system disorders (e.g.
 CC Parkinson's disease, depression, pain), infectious disease, cell
 CC proliferative disorders (e.g., cancer), blood disorders, and immune and
 CC inflammatory disorders. They are also useful for treating and diagnosing
 CC disorders involving the spleen (e.g., Hodgkin disease, Niemann-Pick
 CC disease), lung (e.g., chronic bronchitis), colon (cirrhosis), uterus and
 CC endometrium (e.g., endometrial stromal tumours), brain (e.g., ischemia),
 CC T-cells (e.g., Sjogren syndrome), skin (lupus erythematosus),

CC haematopoietic stem cells (e.g., Alzheimer's disease), heart (e.g.,
CC myocardial infarction), blood vessels (e.g., Kawasaki syndrome), red
CC cells (e.g., anemias), disorders involving thymus, B-cells, kidney (e.g.,
CC glomerulonephritis), disorders involving breast, testis, epididymis,
CC prostate, thyroid (e.g., Graves disease), disorders involving skeletal
CC muscle (e.g., tumour), pancreas (e.g., pancreatitis), small intestine
CC (e.g., celiac sprue), disorders related to reduced platelet number and
CC ovary

XX

SQ Sequence 8195 BP; 1522 A; 2723 C; 2455 G; 1494 T; 0 U; 1 Other;

Query Match 99.9%; Score 8032; DB 4; Length 8195;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 8035; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy      1 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 60
          |||
Db      98 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 157

Qy      61 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCCTGGCCTTCGAGAT 120
          |||
Db     158 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCCTGGCCTTCGAGAT 217

Qy     121 CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 180
          |||
Db     218 CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 277

Qy     181 CTCCGTGAAGGAAGTCCCCCTTCTACACAGCGGCGCCCCCTGACGTCTGCCGGCATCCTGCC 240
          |||
Db     278 CTCCGTGAAGGAAGTCTCCTTCTACACAGCGGCGCCCCCTGACGTCTGCCGGCATCCTGCC 337

Qy     241 TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGC 300
          |||
Db     338 TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGC 397

Qy     301 CAACTCCACGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT 360
          |||
Db     398 CAACTCCACGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT 457

Qy     361 GTTTGACCCAGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA 420
          |||
Db     458 GTTTGACCCAGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA 517

Qy     421 GGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC 480
          |||
Db     518 GGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC 577

Qy     481 CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA 540
          |||
Db     578 CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA 637

Qy     541 CTTGTCGCTGCCCCAATAGCACGGCCCAAGCACTCTTGGCCGCCCGTGTGGACCCGCCCGA 600
          |||
Db     638 CTTGTCGCTGCCCCAATAGCACGGCCCAAGCACTCTTGGCCGCCCGTGTGGACCCGCCCGA 697

Qy     601 GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA 660
          |||
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Db	698	GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	757
Qy	661	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	720
Db	758	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	817
Qy	721	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	780
Db	818	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	877
Qy	781	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	840
Db	878	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	937
Qy	841	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	900
Db	938	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	997
Qy	901	CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	960
Db	998	CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	1057
Qy	961	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1020
Db	1058	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1117
Qy	1021	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTTCGGCCCTGGCCCTGCTACTGCCCCA	1080
Db	1118	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTTCGGCCCTGGCCCTGCTACTGCCCCA	1177
Qy	1081	GGGTGCCTGCACTGGCCGGACCCCCGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Db	1178	GGGTGCCTGCACTGGCCGGACCCCCGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1237
Qy	1141	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1200
Db	1238	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1297
Qy	1201	TGCTGCAGCACTGGCCACCCCGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
Db	1298	TGCTGCAGCACTGGCCACCCCGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1357
Qy	1261	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCT	1320
Db	1358	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCT	1417
Qy	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGAACCTGGGCCT	1380
Db	1418	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGAACCTGGGCCT	1477
Qy	1381	CCTCGTGCACCTCATGACCAGCAACCCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
Db	1478	CCTCGTGCACCTCATGACCAGCAACCCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1537
Qy	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTACTA	1500
Db	1538	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTACTA	1597

Qy	1501	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1598	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1657
Qy	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620
Db	1658	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1717
Qy	1621	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1680
Db	1718	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1777
Qy	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATAACATTGACAACGCGGCCTGCGGCTGGAT	1740
Db	1778	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATAACATTGACAACGCGGCCTGCGGCTGGAT	1837
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1800
Db	1838	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1897
Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1860
Db	1898	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1957
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1920
Db	1958	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	2017
Qy	1921	CTCCAGCTTCACCGAGAAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1980
Db	2018	CTCCAGCTTCACCGAGAAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	2077
Qy	1981	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Db	2078	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2137
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Db	2138	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2197
Qy	2101	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2160
Db	2198	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2257
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Db	2258	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2317
Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280
Db	2318	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2377
Qy	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2340
Db	2378	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2437

Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2400
Db	2438	CGCCATCCTGAAGTACGGCCAGGTGCTTATACACAGCCACGTGGTCATCATCTGGCTCTT	2497
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2460
Db	2498	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2557
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Db	2558	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2617
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
Db	2618	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2677
Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640
Db	2678	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2737
Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2700
Db	2738	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2797
Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760
Db	2798	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2857
Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2858	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2917
Qy	2821	CTTCCCCTGCAGAAAGTCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2918	CTTCCCCTGCAGAAAGTCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2977
Qy	2881	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2978	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGTGCCAT	3037
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACCCACCTGCCTCT	3000
Db	3038	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACCCACCTGCCTCT	3097
Qy	3001	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3098	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3157
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3158	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3217
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCG	3180
Db	3218	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCG	3277
Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240

Db	3278	 CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3337
Qy	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3338	 GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3397
Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3398	 CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3457
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTGCGGTGGCATGAA	3420
Db	3458	 GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTGCGGTGGCATGAA	3517
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3480
Db	3518	 GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3577
Qy	3481	GCCCCAGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3540
Db	3578	 GCCCCAGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3637
Qy	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3638	 CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3697
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3698	 GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3757
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCCGAGCCGGG	3720
Db	3758	 CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCCGAGCCGGG	3817
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGGCCCCGCTGAGCAGCTG	3780
Db	3818	 GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGGCCCCGCTGAGCAGCTG	3877
Qy	3781	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3878	 CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3937
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3938	 AGACACAAGCACGGAGCTCTCCTACATCCTGCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3997
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3998	 CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	4057
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTGCGGAGGAGGATCAGTCGCT	4020
Db	4058	 GCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTGCGGAGGAGGATCAGTCGCT	4117
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080

Db	4118	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4177
Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4178	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4237
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4200
Db	4238	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4297
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4298	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4357
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAA	4320
Db	4358	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAA	4417
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4418	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4477
Qy	4381	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4478	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCAGATCTTGCTGCCAGCCTTCTTCGT	4537
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4538	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4597
Qy	4501	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCCTACGC	4560
Db	4598	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCCTACGC	4657
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCCAGCAGCT	4620
Db	4658	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCCAGCAGCT	4717
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4718	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4777
Qy	4681	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4778	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4837
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4838	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4897
Qy	4801	CGTGCCACCCCCACCCTCGCCCCGCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4860
Db	4898	CGTGCCACCCCCACCCTCGCCCCGCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4957
Qy	4861	GCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCGGCACC	4920
Db	4958	GCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCGGCACC	5017

Qy	4921	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACCGG	4980
Db	5018	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACCGG	5077
Qy	4981	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5040
Db	5078	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5137
Qy	5041	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5100
Db	5138	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5197
Qy	5101	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5160
Db	5198	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5257
Qy	5161	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5220
Db	5258	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5317
Qy	5221	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5280
Db	5318	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5377
Qy	5281	CGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5340
Db	5378	CGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5437
Qy	5341	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5400
Db	5438	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5497
Qy	5401	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5460
Db	5498	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5557
Qy	5461	CTTCGTTGTCTTCCTCGTGGCCGAGAAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAG	5520
Db	5558	CTTCGTTGTCTTCCTCGTGGCCGAGAAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAG	5617
Qy	5521	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5580
Db	5618	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5677
Qy	5581	GGTCCCCGCTACCTGCTGTGTGTCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTC	5640
Db	5678	GGTCCCCGCTACCTGCTGTGTGTCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTC	5737
Qy	5641	GCCCACCAACTTCCCTGCCGTCCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCC	5700
Db	5738	GCCCACCAACTTCCCTGCCGTCCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCC	5797
Qy	5701	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCAT	5760
Db	5798	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCAT	5857

Qy	5761	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5820
Db	5858	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5917
Qy	5821	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5880
Db	5918	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5977
Qy	5881	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5940
Db	5978	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	6037
Qy	5941	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGT	6000
Db	6038	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGT	6097
Qy	6001	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6060
Db	6098	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6157
Qy	6061	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6120
Db	6158	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6217
Qy	6121	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6180
Db	6218	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6277
Qy	6181	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6240
Db	6278	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6337
Qy	6241	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6300
Db	6338	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6397
Qy	6301	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6360
Db	6398	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6457
Qy	6361	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6420
Db	6458	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6517
Qy	6421	CCTCGGCTACTGCCCAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCT	6480
Db	6518	CCTCGGCTACTGCCCAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCT	6577
Qy	6481	GCAGCTGTACACGGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6540
Db	6578	GCAGCTGTACACGGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6637
Qy	6541	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6600
Db	6638	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6697
Qy	6601	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTT	6660

Db	6698		CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTT	6757
Qy	6661		CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6720
Db	6758		CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6817
Qy	6721		CCTCGACCTCATCAAGACAGGGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTG	6780
Db	6818		CCTCGACCTCATCAAGACAGGGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTG	6877
Qy	6781		CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCGCTGGGCAG	6840
Db	6878		CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCGCTGGGCAG	6937
Qy	6841		CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6900
Db	6938		CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6997
Qy	6901		CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6960
Db	6998		CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	7057
Qy	6961		CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7020
Db	7058		CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7117
Qy	7021		CCAGGTGTTCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7080
Db	7118		CCAGGTGTTCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7177
Qy	7081		CAGCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGACAACCT	7140
Db	7178		CAGCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGACAACCT	7237
Qy	7141		GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7200
Db	7238		GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7297
Qy	7201		CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA	7260
Db	7298		CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA	7357
Qy	7261		GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7320
Db	7358		GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7417
Qy	7321		CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7380
Db	7418		CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7477
Qy	7381		TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCAGTGCCTGC	7440
Db	7478		TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCAGTGCCTGC	7537
Qy	7441		CAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCG	7500

Db 7538 CAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCG 7597

Qy 7501 GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCC 7560
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Db 7598 GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCC 7657

Qy 7561 GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGGCCCTCG 7620
 |||

Db 7658 GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGGCCCTCG 7717

Qy 7621 CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC 7680
 |||

Db 7718 CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC 7777

Qy 7681 TTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA 7740
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Db 7778 TTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA 7837

Qy 7741 GCGGGCTGTGGGCGGAGCTGGGTCACTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCT 7800
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Db 7838 GCGGGCTGTGGGCGGAGCTGGGTCACTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCT 7897

Qy 7801 CTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAG 7860
 |||

Db 7898 CTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAG 7957

Qy 7861 CTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCC 7920
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Db 7958 CTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCC 8017

Qy 7921 CCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCCACCTCCC 7980
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Db 8018 CCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCCCCTCCC 8077

Qy 7981 TGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAATAATGTC 8040
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Db 8078 TGGGAGCCGGGCCTGTACATAGGGCACAGATGTTTGTTTTAAATAAATAAACAATAATGTC 8137

RESULT 5

ABX70982

ID ABX70982 standard; cDNA; 8037 BP.

XX

AC ABX70982;

XX

DT 05-MAR-2003 (first entry)

XX

DE Novel human cDNA sequence #207.

XX

KW Human; gene; ss; nervous system disorder; peripheral neuropathy;
 KW Huntington's disease; amyotrophic lateral sclerosis; haemophilia;
 KW neurodegenerative disease; Parkinson's disease; Alzheimer's disease;
 KW autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis;
 KW insulin-dependent diabetes mellitus; anaemia; thrombocytopaenia; wound;
 KW ulcer; burn; bone disorder; osteoporosis; osteoarthritis; stroke;
 KW fibrosis; reperfusion injury; infection; allergic rhinitis; asthma;
 KW coagulation disorder; cancer; tumour; inflammatory disease; septic shock;

KW Crohn's disease; anaphylaxis; proliferation; chemotactic;
 KW differentiation; stem cell growth factor; haematopoiesis; chemokinetic;
 KW haemostatic; antiinflammatory; expressed sequence tag; EST.
 XX
 OS Homo sapiens.
 XX
 PN WO200281731-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 29-JAN-2002; 2002WO-US001222.
 XX
 PR 30-JAN-2001; 2001US-00774528.
 XX
 PA (HYSE-) HYSEQ INC.
 PA (GOOD/) GOODRICH R W.
 XX
 PI Tang TY, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Wang J, Wang D, Drmanac RT;
 XX
 DR WPI; 2003-058563/05.
 XX
 PT Novel polypeptide useful for treating neurodegenerative diseases, myeloid
 PT or lymphoid cell disorders, bone disorders, mechanical and traumatic
 PT disorders, coagulation disorders, and inflammatory diseases.
 XX
 PS Claim 1; Page; 612pp; English.
 XX
 CC This invention relates to the cDNA sequences encoding an isolated novel
 CC human polypeptide. The protein encoded by the nucleic acid of the
 CC invention is useful for treating central and peripheral nervous system
 CC diseases (e.g. peripheral neuropathy, Huntington's disease, amyotrophic
 CC lateral sclerosis); neurodegenerative diseases (e.g. Parkinson's disease,
 CC Alzheimer's disease); autoimmune disease (e.g. systemic lupus
 CC erythematosus, rheumatoid arthritis, insulin-dependent diabetes mellitus)
 CC ; myeloid or lymphoid cell disorders (e.g. anaemia and thrombocytopaenia)
 CC ; wounds, ulcers, burns; bone disorders (e.g. osteoporosis,
 CC osteoarthritis); mechanical and traumatic disorders (e.g. stroke, head
 CC trauma); lung or liver fibrosis; reperfusion injury in various tissues;
 CC bacterial, viral or fungal infections; allergic conditions such as
 CC allergic rhinitis, asthma; coagulation disorders (e.g. haemophilia);
 CC cancer and tumours; and inflammatory diseases (e.g. septic shock, Crohn's
 CC disease, anaphylaxis). The protein may be used to inhibit the growth,
 CC infection or function of infectious agents such as bacteria, fungi,
 CC viruses, or to effect bodily characteristics, biorhythms or circadian
 CC cycles of rhythms. The protein may also have
 CC proliferation/differentiation, stem cell growth factor, haematopoiesis
 CC regulation, immune stimulating or suppressing, chemotactic/chemokinetic,
 CC haemostatic and thrombolytic, receptor/ligand, and antiinflammatory
 CC activities. The cDNA sequences of the invention are useful for expressing
 CC recombinant protein for analysis. The present sequence represents a novel
 CC human cDNA sequence of the invention, this sequence is an expressed
 CC sequence tag (EST) and was identified using subtractive hybridisation
 XX
 SQ Sequence 8037 BP; 1472 A; 2686 C; 2393 G; 1486 T; 0 U; 0 Other;

Query Match

99.2%; Score 7973.2; DB 7; Length 8037;

Best Local Similarity 99.7%; Pred. No. 0;
Matches 8003; Conservative 0; Mismatches 3; Indels 18; Gaps 1;

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Qy      35 ATGGGCTTCCTGCACCAGCTGCAGCTGCTGCTCTGGAAGAACGTGACGCTCAAACGCCGG 94
      |||
Db      1 ATGGGCTTCCTGCACCAGCTGCAGCTGCTGCTCTGGAAGAACGTGACGCTCAAACGCCGG 60

Qy     95 AGCCCGTGGGTCTTGGCCTTCGAGATCTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTG 154
      |||
Db     61 AGCCCGTGGGTCTTGGCCTTCGAGATCTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTG 120

Qy    155 GGGCTGCGACAGAAGAAGCCCACCATCTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCG 214
      |||
Db    121 GGGCTGCGACAGAAGAAGCCCACCATCTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCG 180

Qy    215 CCCCTGACGTCTGCCGGCATCCTGCCTGTCATGCAATCGCTGTGCCCCGACGGCCAGCGA 274
      |||
Db    181 CCCCTGACGTCTGCCGGCATCCTGCCTGTCATGCAATCGCTGTGCCCCGACGGCCAGCGA 240

Qy    275 GACGAGTTCGGCTTCCTGCAGTACGCCAACTCCACGGTCACGCAGCTGCTTGAGCGCCTG 334
      |||
Db    241 GACGAGTTCGGCTTCCTGCAGTACGCCAACTCCACGGTCACGCAGCTGCTTGAGCGCCTG 300

Qy    335 GACCGCGTGGTGGAGGAAGGCAACCTGTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAG 394
      |||
Db    301 GACCGCGTGGTGGAGGAAGGCAACCTGTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAG 360

Qy    395 CTCGAGGCCCTACGCCAGCATCTGGAGGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGC 454
      |||
Db    361 CTCGAGGCCCTACGCCAGCATCTGGAGGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGC 420

Qy    455 CACCTGGACAGATCCACAGTGTCTTCCTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAG 514
      |||
Db    421 CACCTGGACAGATCCACAGTGTCTTCCTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAG 480

Qy    515 GAGCTCTGGCGTTTCCTGACGCAAAACTTGTGCTGCCCCAATAGCACGGCCCCAAGCACTC 574
      |||
Db    481 GAGCTCTGGCGTTTCCTGACGCAAAACTTGTGCTGCCCCAATAGCACGGCCCCAAGCACTC 540

Qy    575 TTGGCCGCCCGTGTGGACCCGCCCGAGGTCTACCACCTGCTCTTTGGTCCCTCATCTGCC 634
      |||
Db    541 TTGGCCGCCCGTGTGGACCCGCCCGAGGTCTACCACCTGCTCTTTGGTCCCTCATCTGCC 600

Qy    635 CTGGATTACAGTCTGGCCTCCACAAGGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAAT 694
      |||
Db    601 CTGGATTACAGTCTGGCCTCCACAAGGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAAT 660

Qy    695 CCCCTGTTCCGGATGGAGGAGCTGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGC 754
      |||
Db    661 CCCCTGTTCCGGATGGAGGAGCTGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGC 720

Qy    755 ACGCCGGGCTCGGGGGAGCTGGGCCGGATCCTCACTGTGCCTGAGAGTCAGAAAGGGAGCC 814
      |||
Db    721 ACGCCGGGCTCGGGGGAGCTGGGCCGGATCCTCACTGTGCCTGAGAGTCAGAAAGGGAGCC 780

Qy    815 CTGCAGGGCTACCGGGATGCTGTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTC 874
      |||
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Db	781	CTGCAGGGCTACCGGGATGCTGTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTC	840
Qy	875	TCTGGGCTGTCTGCTGAGCTCCGGAACCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTG	934
Db	841	TCTGGGCTGTCTGCTGAGCTCCGGAACCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTG	900
Qy	935	GGCCTGGATGCCCCAACGGCTCGGACTCCTCGCCACAGGCGCCACCCCCACGGAGGCTG	994
Db	901	GGCCTGGATGCCCCAACGGCTCGGACTCCTCGCCACAGGCGCCACCCCCACGGAGGCTG	960
Qy	995	CAGGCGCTTCTGGGGGACCTGCTGGATGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTG	1054
Db	961	CAGGCGCTTCTGGGGGACCTGCTGGATGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTG	1020
Qy	1055	TCGGCCCTGGCCCTGCTACTGCCCCAGGGTGCTGCACTGGCCGGACCCCCGGACCCCCA	1114
Db	1021	TCGGCCCTGGCCCTGCTACTGCCCCAGGGTGCTGCACTGGCCGGACCCCCGGACCCCCA	1080
Qy	1115	GCCAGTGGTGCGGGTGGGGCGGCCAATGGCACTGGGGCAGGGGCAGTCATGGGCCCCAAC	1174
Db	1081	GCCAGTGGTGCGGGTGGGGCGGCCAATGGCACTGGGGCAGGGGCAGTCATGGGCCCCAAC	1140
Qy	1175	GCCACCGCTGAGGAGGGCGCACCCCTCTGCTGCAGCACTGGCCACCCCGGACACGCTGCAG	1234
Db	1141	GCCACCGCTGAGGAGGGCGCACCCCTCTGCTGCAGCACTGGCCACCCCGGACACGCTGCAG	1200
Qy	1235	GGCCAGTGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAAC	1294
Db	1201	GGCCAGTGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAAC	1260
Qy	1295	AACCGCACCATTTGAACCCGAGGCGCTGCGGCGGGGCAACATGAGCTCCCTGGGCTTCACG	1354
Db	1261	AACCGCACCATTTGAACCCGAGGCGCTGCGGCGGGGCAACATGAGCTCCTTGGGCTTCACG	1320
Qy	1355	AGCAAGGAGCAGCGGAACCTGGGCCTCCTCGTGACCTCATGACCAGCAACCCCAAAATC	1414
Db	1321	AGCAAGAAGCAGCGGAACCTGGGCCTCCTCGTGACCTCATGACCAGCAACCCCAAAATC	1380
Qy	1415	CTGTACGCGCCTGCGGGCTCTGAGGTGCGACCGCGTCATCCTCAAGGCCAACGAGACTTTT	1474
Db	1381	CTGTACGCGCCTGCGGGCTCTGAGGTGCGACCGCGTCATCCTCAAGGCCAACGAGACTTTT	1440
Qy	1475	GCTTTTGTGGGCAACGTGACTCACTATGCCCAGGTCTGGCTCAACATCTCGGCGGAGATC	1534
Db	1441	GCTTTTGTGGGCAACGTGACTCACTATGCCCAGGTCTGGCTCAACATCTCGGCGGAGATC	1500
Qy	1535	CGCAGCTTCCTGGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTATGTA	1594
Db	1501	CGCAGCTTCCTGGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTATGTA	1560
Qy	1595	GCAGAGCTGCGGCTGCACCCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCGGCC	1654
Db	1561	GCAGAGCTGCGGCTGCACCCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCGGCC	1620
Qy	1655	CTGAGACAGGACAACCTTCTCGCTGCCCAGTGGCATGGCCCTCCTGCAGCAGCTGGATACC	1714
Db	1621	CTGAGACAGGACAACCTTCTCGCTGCCCAGTGGCATGGCCCTCCTGCAGCAGCTGGATACC	1680

Qy	1715	ATTGACAACGCGGCCTGCGGCTGGATCCAGTTCATGTCCAAGGTGAGCGTGGACATCTTC	1774
Db	1681	ATTGACAACGCGGCCTGCGGCTGGATCCAGTTCATGTCCAAGGTGAGCGTGGACATCTTC	1740
Qy	1775	AAGGGCTTCCCCGACGAGGAGAGCATTGTCAACTACACCCTCAACCAGGCCTACCAGGAC	1834
Db	1741	AAGGGCTTCCCCGACGAGGAGAGCATTGTCAACTACACCCTCAACCAGGCCTACCAGGAC	1800
Qy	1835	AACGTCACTGTTTTTGGCAGTGTGATCTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCT	1894
Db	1801	AACGTCACTGTTTTTGGCAGTGTGATCTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCT	1860
Qy	1895	CACGTGCACTACAAGATCCGCCAGAACTCCAGCTTCACCGAGAAAACCAACGAGATCCGC	1954
Db	1861	CACGTGCACTACAAGATCCGCCAGAACTCCAGCTTCACCGAGAAAACCAACGAGATCCGC	1920
Qy	1955	CGCGCCTACTGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCCTCTACGGCTTC	2014
Db	1921	CGCGCCTACTGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCCTCTACGGCTTC	1980
Qy	2015	GTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCACGACGTG	2074
Db	1981	GTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCACGACGTG	2040
Qy	2075	GTGGAGCCAGGCAGCTACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTC	2134
Db	2041	GTGGAGCCAGGCAGCTACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTC	2100
Qy	2135	CTGTTTGTCAATTGAGCACATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTG	2194
Db	2101	CTGTTTGTCAATTGAGCACATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTG	2160
Qy	2195	GCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACC GGCTCAAGGAGGTGATGAAG	2254
Db	2161	GCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACC GGCTCAAGGAGGTGATGAAG	2220
Qy	2255	ACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACC GGCTTTGTGCAG	2314
Db	2221	ACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACC GGCTTTGTGCAG	2280
Qy	2315	CTGTCCATCTCCGTGACAGCACTCACC GCCATCCTGAAGTACGGCCAGGTGCTTATGCAC	2374
Db	2281	CTGTCCATCTCCGTGACAGCACTCACC GCCATCCTGAAGTACGGCCAGGTGCTTATGCAC	2340
Qy	2375	AGCCACGTGGTCATCATCTGGCTCTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTC	2434
Db	2341	AGCCACGTGGTCATCATCTGGCTCTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTC	2400
Qy	2435	TGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATC	2494
Db	2401	TGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATC	2460
Qy	2495	ATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCAT	2554
Db	2461	ATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCAT	2520

Qy	2555	GATAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGT	2614
Db	2521	GATAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGT	2580
Qy	2615	CTGGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACC	2674
Db	2581	CTGGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACC	2640
Qy	2675	TTCAGCCAGTCCCCGGTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTG	2734
Db	2641	TTCAGCCAGTCCCCGGTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTG	2700
Qy	2735	ATGGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGC	2794
Db	2701	ATGGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGC	2760
Qy	2795	ATGTACGGGCTGCCCCGGCCCTGGTACTTCCCACTGCAGAAGTCTACTGGCTGGGCAGT	2854
Db	2761	ATGTACGGGCTGCCCCGGCCCTGGTACTTCCCACTGCAGAAGTCTACTGGCTGGGCAGT	2820
Qy	2855	GGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTC	2914
Db	2821	GGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTC	2880
Qy	2915	ATGGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATG	2974
Db	2881	ATGGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATG	2940
Qy	2975	GAGGAGGAGCCCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAAACTCACCAAGGTCTAC	3034
Db	2941	GAGGAGGAGCCCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAAACTCACCAAGGTCTAC	3000
Qy	3035	AAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTG	3094
Db	3001	AAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTG	3060
Qy	3095	GTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGC	3154
Db	3061	GTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGC	3120
Qy	3155	CTGTTCCCTCCAACGTCGGGTTCGCCACCATCTACGGGCACGACATCCGCACGGAGATG	3214
Db	3121	CTGTTCCCTCCAACGTCGGGTTCGCCACCATCTACGGGCACGACATCCGCACGGAGATG	3180
Qy	3215	GATGAGATCCGCAAGAACCTGGGCATGTGCCCGCAGCACAATGTGCTCTTTGACCGGCTC	3274
Db	3181	GATGAGATCCGCAAGAACCTGGGCATGTGCCCGCAGCACAATGTGCTCTTTGACCGGCTC	3240
Qy	3275	ACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATC	3334
Db	3241	ACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATC	3300
Qy	3335	CGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTG	3394
Db	3301	CGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTG	3360
Qy	3395	GTGCAGACATTGTGCGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGC	3454

Db	3361	 GTGCAGACATTGTCGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGC	3420
Qy	3455	GGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGC	3514
Db	3421	 GGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGC	3480
Qy	3515	GCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGCACCATCCTTCTGTCCACCCAC	3574
Db	3481	 GCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGCACCATCCTTCTGTCCACCCAC	3540
Qy	3575	CACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTC	3634
Db	3541	 CACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTC	3600
Qy	3635	AAGTGCTGCGGCTCCCCGCTCTTCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACG	3694
Db	3601	 AAGTGCTGCGGCTCCCCGCTCTTCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACG	3660
Qy	3695	CTGGTCAAGCGGCCCCGCCGAGCCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCC	3754
Db	3661	 CTGGTCAAGCGGCCCCGCCGAGCCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCC	3720
Qy	3755	CCAGGTGCGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAG	3814
Db	3721	 CCAGGTGCGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAG	3780
Qy	3815	CATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCC	3874
Db	3781	 CATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCC	3840
Qy	3875	AGCGAGGCCGCCAAGAAGGGGGCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTG	3934
Db	3841	 AGCGAGGCCGCCAAGAAGGGGGCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTG	3900
Qy	3935	GATGCACTGCACCTCAGCAGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTTCCTC	3994
Db	3901	 GATGCACTGCACCTCAGCAGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTTCCTC	3960
Qy	3995	AAGGTGTGCGGAGGAGGATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGG	4054
Db	3961	 AAGGTGTGCGGAGGAGGATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGG	4020
Qy	4055	AAGGATGTGCTCCCTGGGGCGGAGGGCCCGGCTCTGGGGAGGGTCACGCTGGCAATCTG	4114
Db	4021	 AAGGATGTGCTCCCTGGGGCGGAGGGCCCGGCTCTGGGGAGGGTCACGCTGGCAATCTG	4080
Qy	4115	GCCCCGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGC	4174
Db	4081	 GCCCCGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGC	4140
Qy	4175	TCTGCCCGTGGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTC	4234
Db	4141	 TCTGCCCGTGGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTC	4200
Qy	4235	TTTGATAACCCACAGGACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTG	4294

Db	4201	TTTGATAACCCACAGGACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTG	4260
Qy	4295	TCGAGGGTCGGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTC	4354
Db	4261	TCGAGGGTCGGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTC	4320
Qy	4355	CACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCC	4414
Db	4321	CACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCC	4380
Qy	4415	CAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCG	4474
Db	4381	CAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCG	4440
Qy	4475	GAGATTGGTGATCTGCCCCGCTGGTCCTGTACCTTCCCAGTACCACAACCTACACCCAG	4534
Db	4441	GAGATTGGTGATCTGCCCCGCTGGTCCTGTACCTTCCCAGTACCACAACCTACACCCAG	4500
Qy	4535	CCCCGTGGCAATTTTCATCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGGCTA	4594
Db	4501	CCCCGTGGCAATTTTCATCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGGCTA	4560
Qy	4595	TCGCCCCGACGCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGT	4654
Db	4561	TCGCCCCGACGCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGT	4620
Qy	4655	GCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCCCACGTTGAACCTGAGC	4714
Db	4621	GCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCCCACGTTGAACCTGAGC	4680
Qy	4715	AGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCTTTC	4774
Db	4681	AGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCTTTC	4740
Qy	4775	ACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCCGCCCATCTGAC	4834
Db	4741	ACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCCGCCCATCTGAC	4800
Qy	4835	TCGCCAGCGTCCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCT	4894
Db	4801	TCGCCAGCGTCCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCT	4860
Qy	4895	GGGCCAGAAATGTGGACGTCGGCACCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGC	4954
Db	4861	GGGCCAGAAATGTGGACGTCGGCACCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGC	4920
Qy	4955	TGCACCTGCTCTGCGCAGGGCACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCG	5014
Db	4921	TGCACCTGCTCTGCGCAGGGCACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCG	4980
Qy	5015	CCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCT	5074
Db	4981	CCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCT	5040
Qy	5075	GAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTT	5134
Db	5041	GAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTT	5100

Qy	5135	GGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGG	5194
Db	5101	GGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGG	5160
Qy	5195	AAGATCGCGGTGCGCAGGGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATG	5254
Db	5161	AAGATCGCGGTGCGCAGGGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATG	5220
Qy	5255	CCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAG	5314
Db	5221	CCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAG	5280
Qy	5315	GGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCC	5374
Db	5281	GGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCC	5340
Qy	5375	AGCCTCTCCCTGGATTACCTGCTGCAGGGCACGGATGTCGTCATCGCCATCTTCATCATC	5434
Db	5341	AGCCTCTCCCTGGATTACCTGCTGCAGGGCACGGATGTCGTCATCGCCATCTTCATCATC	5400
Qy	5435	GTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACC	5494
Db	5401	GTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACC	5460
Qy	5495	AAGGCCAAGCATCTGCAGTTTGTGTCAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAAC	5554
Db	5461	AAGGCCAAGCATCTGCAGTTTGTGTCAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAAC	5520
Qy	5555	TACGTGTGGGACAT-----GCTCAACTACCTGGTCCCCGCTACCTGC	5596
Db	5521	TACGTGTGGGACATGCCGCCCCACCCCTGCAGCTCAACTACCTGGTCCCCGCTACCTGC	5580
Qy	5597	TGTGTCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTCGCCCACCAACTTCCCT	5656
Db	5581	TGTGTCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTCGCCCACCAACTTCCCT	5640
Qy	5657	GCCGTCCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGGCC	5716
Db	5641	GCCGTCCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGGCC	5700
Qy	5717	TCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCATGTGTCATCAATCTCTTC	5776
Db	5701	TCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCATGTGTCATCAATCTCTTC	5760
Qy	5777	ATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGGAC	5836
Db	5761	ATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGGAC	5820
Qy	5837	CTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTG	5896
Db	5821	CTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTG	5880
Qy	5897	GGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATT	5956
Db	5881	GGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATT	5940

Qy	5957	GGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGGTG	6016
Db	5941	GGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGGTG	6000
Qy	6017	GCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAAC TTC	6076
Db	6001	GCCATGGCGGTTGAGGGCGTCGTGGGTTTCCTCCTGACCATCATGTGCCAGTACAAC TTC	6060
Qy	6077	CTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTG	6136
Db	6061	CTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTG	6120
Qy	6137	GCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAG	6196
Db	6121	GCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAG	6180
Qy	6197	AACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTG	6256
Db	6181	AACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTG	6240
Qy	6257	TGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAG	6316
Db	6241	TGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAG	6300
Qy	6317	ACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTCGTC	6376
Db	6301	ACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTCGTC	6360
Qy	6377	AATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCG	6436
Db	6361	AATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCG	6420
Qy	6437	CAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCGGGAGCACCTGCAGCTGTACACGCGG	6496
Db	6421	CAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCGGGAGCACCTGCAGCTGTACACGCGG	6480
Qy	6497	CTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTG	6556
Db	6481	CTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTG	6540
Qy	6557	GAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAG	6616
Db	6541	GAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAG	6600
Qy	6617	CTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCACC	6676
Db	6601	CTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCACC	6660
Qy	6677	ACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCCTCGACCTCATCAAG	6736
Db	6661	ACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCCTCGACCTCATCAAG	6720
Qy	6737	ACAGGGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCACG	6796
Db	6721	ACAGGGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCACG	6780
Qy	6797	CGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAG	6856

Db	6781	CGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAG	6840
Qy	6857	AACCGGTTTGGAGATGGCTACATGATCACGGTGC GGACCAAGAGCAGCCAGAGTGTGAAG	6916
Db	6841	AACCGGTTTGGAGATGGCTACATGATCACGGTGC GGACCAAGAGCAGCCAGAGTGTGAAG	6900
Qy	6917	GACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACCAC	6976
Db	6901	GACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACCAC	6960
Qy	6977	ACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAAGCAAG	7036
Db	6961	ACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAAGCAAG	7020
Qy	7037	ATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACACTG	7096
Db	7021	ATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACACTG	7080
Qy	7097	GACAAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACG	7156
Db	7081	GACAAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACG	7140
Qy	7157	GAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCCGG	7216
Db	7141	GAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCCGG	7200
Qy	7217	TCTGCCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGAGGACCTGGACACGGAG	7276
Db	7201	TCTGCCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGAGGACCTGGACACGGAG	7260
Qy	7277	GACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCTTCAACACGGACACG	7336
Db	7261	GACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCTTCAACACGGACACG	7320
Qy	7337	CTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTGACCACCCAGAGCTG	7396
Db	7321	CTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTGACCACCCAGAGCTG	7380
Qy	7397	GGCCAGGGACTCAACAATGGGGACAGAAGTCCCCAGTGCCTGCCAGGGCCTGGAGTGGA	7456
Db	7381	GGCCAGGGACTCAACAATGGGGACAGAAGTCCCCAGTGCCTGCCAGGGCCTGGAGTGGA	7440
Qy	7457	GGTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCGGCCATGCCCTGCGGTC	7516
Db	7441	GGTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCGGCCATGCCCTGCGGTC	7500
Qy	7517	ACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCCGGGCTGCGTACACCCT	7576
Db	7501	ACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCCGGGCTGCGTACACCCT	7560
Qy	7577	TGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCTCGCCCCTGCCTGGCACTG	7636
Db	7561	TGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCTCGCCCCTGCCTGGCACTG	7620
Qy	7637	CTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCCTTTCTCCTGCCCGGCC	7696

Db 7621 CTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCCTTTCTCCTGCCCGGCC 7680

Qy 7697 TCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGAGCGGGCTGTGGGCGGA 7756
 |||

Db 7681 TCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGAGCGGGCTGTGGGCGGA 7740

Qy 7757 GCTGGGTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCTCTGGCCCTGCTCTCCT 7816
 |||

Db 7741 GCTGGGTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCTCTGGCCCTGCTCTCCT 7800

Qy 7817 GCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAGCTGGCAGGTGGCAGGA 7876
 |||

Db 7801 GCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAGCTGGCAGGTGGCAGGA 7860

Qy 7877 ATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCCCCCCAACCCCCAGCTGC 7936
 |||

Db 7861 ATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCCCCCCAACCCCCAGCTGC 7920

Qy 7937 CATCGCTCTCCCACCCAGCTTGGCCCCCTGCCCCGCCACCTCCCTGGGAGCCGGGCCTGT 7996
 |||

Db 7921 CATCGCTCTCCCACCCAGCTTGGCCCCCTGCCCCGCCACCTCCCTGGGAGCCGGGCCTGT 7980

Qy 7997 ACATAGCGCACAGATGTTTGTTTTAAATAAAATAACAAAATGTC 8040
 |||

Db 7981 ACATAGCGCACAGATGTTTGTTTTAAATAAAATAACAAAATGTC 8024

RESULT 6

AAD36299

ID AAD36299 standard; cDNA; 7610 BP.

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AC AAD36299;

XX

DT 09-AUG-2002 (first entry)

XX

DE Human transporter and ion channel (TRICH) 2 cDNA.

XX

KW Human; transporter and ion channel; TRICH; transport disorder;
 KW diabetes mellitus; angina; Alzheimer's disease; neurological; epilepsy;
 KW stroke; Huntington's disease; meningitis; muscle; myocarditis; cancer;
 KW infectious myositis; arrhythmia; asthma; immunological; gene therapy;
 KW acquired immunodeficiency syndrome; AIDS; allergy; atherosclerosis;
 KW cell proliferative disorder; cerebroprotective; cirrhosis; hepatitis;
 KW transgenic; neuroprotective; anticonvulsant; nootropic; cytostatic;
 KW antiinflammatory; hepatotropic; psoriasis; gene; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 111..7421

FT /*tag= a

FT /product= "Human TRICH2 protein"

XX

PN WO200222684-A2.

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PD 21-MAR-2002.

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PF 14-SEP-2001; 2001WO-US028938.

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PR 15-SEP-2000; 2000US-0232685P.

PR 22-SEP-2000; 2000US-0234842P.

PR 29-SEP-2000; 2000US-0236882P.

PR 05-OCT-2000; 2000US-0239057P.

PR 13-OCT-2000; 2000US-0240540P.

PR 18-OCT-2000; 2000US-0241700P.

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PA (INCY-) INCYTE GENOMICS INC.

XX

PI Lee EA, Yue H, Lal PG, Walia NK, Baughn MR, Warren BA, Lee S;

PI Sanjanwala MS, Yao MG, Ramkumar J, Thornton M, Gandhi AR;

PI Policky JL, Elliott VS, Arvizu C, Raumann BE, Bruns CM, Naini A;

PI Hafalia AJA, Nguyen DB, Xu Y, Lu DAM, Ison CH, Griffin JA;

PI Reddy RM, Burford N;

XX

DR WPI; 2002-393948/42.

DR P-PSDB; AAE22903.

XX

PT Polypeptides of human transporters and ion channels, useful for
PT diagnosing, treating or preventing transport, neurological, muscle,
PT immunological and cell proliferative disorders.

XX

PS Claim 12; Page 181-183; 204pp; English.

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CC The invention relates to human transporters and ion channels (TRICH) and
CC their corresponding nucleic acid sequences. TRICH is useful for screening
CC an agonist/antagonist that modulates its activity. TRICH is useful as an
CC immunogen for preparing antibodies which are useful for diagnosing a
CC condition of disease associated with its expression in a subject, and for
CC detecting and purifying it from a sample. TRICH DNA is useful as probe or
CC a primer for assessing toxicity of a test compound. Composition
CC comprising TRICH or its agonist is useful for treating a disease or
CC condition associated with decreased expression of functional TRICH and
CC composition comprising TRICH antagonist is useful for treating a disease
CC or condition associated with TRICH overexpression of TRICH. TRICH
CC sequence is used in the diagnosis and treatment of transport disorder
CC e.g. diabetes mellitus, angina, Alzheimer's disease; neurological
CC disorder e.g. epilepsy, stroke, Huntington's disease, bacterial and viral
CC meningitis, muscle disorder e.g. myocarditis, infectious myositis,
CC arrhythmias, asthma, immunological disorder e.g. acquired
CC immunodeficiency syndrome (AIDS), allergies, atherosclerosis; and cell
CC proliferative disorders e.g. cirrhosis, hepatitis, psoriasis and cancers.
CC TRICH DNA is used in gene therapy. TRICH DNA is useful for creating
CC knockin humanised animals (pigs) or transgenic animals (mice or rats) to
CC model human disease. The present sequence is human TRICH cDNA

XX

SQ Sequence 7610 BP; 1379 A; 2541 C; 2302 G; 1388 T; 0 U; 0 Other;

Query Match 93.6%; Score 7529.2; DB 6; Length 7610;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 7531; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 60

|||||

Db 77 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 136

Qy	61	GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTGGCCTTCGAGAT	120
Db	137	GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTGGCCTTCGAGAT	196
Qy	121	CTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT	180
Db	197	CTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT	256
Qy	181	CTCCGTGAAGGAAGTCCCCCTTCTACACAGCGGCGCCCCTGACGTCTGCCGGCATCCTGCC	240
Db	257	CTCCGTGAAGGAAGTCTCCTTCTACACAGCGGCGCCCCTGACGTCTGCCGGCATCCTGCC	316
Qy	241	TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTTCGGCTTCCTGCAGTACGC	300
Db	317	TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTTCGGCTTCCTGCAGTACGC	376
Qy	301	CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT	360
Db	377	CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT	436
Qy	361	GTTTGACCCAGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA	420
Db	437	GTTTGACCCAGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA	496
Qy	421	GGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC	480
Db	497	GGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC	556
Qy	481	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGAGGAGCTCTGGCGTTTCCTGACGCAAAA	540
Db	557	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGAGGAGCTCTGGCGTTTCCTGACGCAAAA	616
Qy	541	CTTGTCGCTGCCCAATAGCACGGCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCGA	600
Db	617	CTTGTCGCTGCCCAATAGCACGGCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCGA	676
Qy	601	GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	660
Db	677	GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	736
Qy	661	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	720
Db	737	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	796
Qy	721	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	780
Db	797	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	856
Qy	781	GATCCTCACTGTGCCTGAGAGTCAGAAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	840
Db	857	GATCCTCACTGTGCCTGAGAGTCAGAAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	916
Qy	841	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	900
Db	917	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	976

Qy	901	CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	960
Db	977	CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	1036
Qy	961	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1020
Db	1037	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1096
Qy	1021	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGGCCCTGGCCCTGCTACTGCCCCA	1080
Db	1097	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGGCCCTGGCCCTGCTACTGCCCCA	1156
Qy	1081	GGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Db	1157	GGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1216
Qy	1141	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1200
Db	1217	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1276
Qy	1201	TGCTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
Db	1277	TGCTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1336
Qy	1261	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTTGAACCCGAGGCGCT	1320
Db	1337	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTTGAACCCGAGGCGCT	1396
Qy	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380
Db	1397	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1456
Qy	1381	CCTCGTGCACCTCATGACCAGCAACCCCAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
Db	1457	CCTCGTGCACCTCATGACCAGCAACCCCAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1516
Qy	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1500
Db	1517	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1576
Qy	1501	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1577	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1636
Qy	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620
Db	1637	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1696
Qy	1621	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1680
Db	1697	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1756
Qy	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGAT	1740
Db	1757	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGAT	1816
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1800

Db	1817	 CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1876
Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1860
Db	1877	 TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1936
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1920
Db	1937	 CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1996
Qy	1921	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1980
Db	1997	 CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	2056
Qy	1981	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Db	2057	 TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2116
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Db	2117	 CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2176
Qy	2101	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2160
Db	2177	 GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2236
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Db	2237	 GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2296
Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280
Db	2297	 GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2356
Qy	2281	CTGGGTGGCCTGTTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2340
Db	2357	 CTGGGTGGCCTGTTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2416
Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2400
Db	2417	 CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2476
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2460
Db	2477	 CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2536
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Db	2537	 CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2596
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
Db	2597	 CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2656
Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640

Db	2657	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2716
Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2700
Db	2717	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2776
Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760
Db	2777	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2836
Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2837	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2896
Qy	2821	CTTCCCCTGCAGAAAGTCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2897	CTTCCCCTGCAGAAAGTCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2956
Qy	2881	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCTATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2957	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCTATGGAGGAGGACCAGGCCTGTGCCAT	3016
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACCCACCTGCCTCT	3000
Db	3017	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACCCACCTGCCTCT	3076
Qy	3001	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3077	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3136
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3137	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3196
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCG	3180
Db	3197	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCG	3256
Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3257	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3316
Qy	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3317	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3376
Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3377	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3436
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTGGGTGGCATGAA	3420
Db	3437	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTGGGTGGCATGAA	3496
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3480
Db	3497	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3556

Qy	3481	GCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3540
Db	3557	GCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3616
Qy	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3617	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3676
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3677	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3736
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCGAGCCGGG	3720
Db	3737	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCGAGCCGGG	3796
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTG	3780
Db	3797	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTG	3856
Qy	3781	CTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3857	CTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3916
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3917	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3976
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3977	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	4036
Qy	3961	GCTGATGGACACGACCCCTGGAGGAAGTGTTCTCAAGGTGTCTGGAGGAGGATCAGTCGCT	4020
Db	4037	GCTGATGGACACGACCCCTGGAGGAAGTGTTCTCAAGGTGTCTGGAGGAGGATCAGTCGCT	4096
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4097	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4156
Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4157	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4216
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4200
Db	4217	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4276
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4277	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4336
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTCGGCCAGGGCAGCCGCAA	4320
Db	4337	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTCGGCCAGGGCAGCCGCAA	4396

Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4397	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCACGGGCTGCTGGTCAAACGCTTCCA	4456
Qy	4381	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4457	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4516
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4517	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4576
Qy	4501	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4577	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4636
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCAGCAGCT	4620
Db	4637	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCAGCAGCT	4696
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4697	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4756
Qy	4681	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4757	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4816
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4817	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4876
Qy	4801	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4860
Db	4877	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4936
Qy	4861	GCAGGCCTGGAACGTCTCCCTGCCGCCCCACCGCTGGGCCAGAAATGTGGACGTGGGCACC	4920
Db	4937	GCAGGCCTGGAACGTCTCCCTGCCGCCCCACCGCTGGGCCAGAAATGTGGACGTGGGCACC	4996
Qy	4921	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACCGG	4980
Db	4997	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACCGG	5056
Qy	4981	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5040
Db	5057	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5116
Qy	5041	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTACCTCCGACCG	5100
Db	5117	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTACCTCCGACCG	5176
Qy	5101	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAGTCCATCCCAGC	5160
Db	5177	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAGTCCATCCCAGC	5236
Qy	5161	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5220

Db	5237	CTCATTGTCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5296
Qy	5221	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5280
Db	5297	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5356
Qy	5281	CGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5340
Db	5357	CGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5416
Qy	5341	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5400
Db	5417	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5476
Qy	5401	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5460
Db	5477	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5536
Qy	5461	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGCA	5520
Db	5537	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGCA	5596
Qy	5521	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5580
Db	5597	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5656
Qy	5581	GGTCCCCGCTACCTGCTGTGTATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTC	5640
Db	5657	GGTCCCCGCTACCTGCTGTGTATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTC	5716
Qy	5641	GCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCC	5700
Db	5717	GCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCC	5776
Qy	5701	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCAT	5760
Db	5777	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCAT	5836
Qy	5761	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCTGCTACAGCTCTT	5820
Db	5837	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCTGCTACAGCTCTT	5896
Qy	5821	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5880
Db	5897	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5956
Qy	5881	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5940
Db	5957	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	6016
Qy	5941	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGT	6000
Db	6017	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGT	6076
Qy	6001	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6060

Db	6077	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6136
Qy	6061	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6120
Db	6137	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6196
Qy	6121	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6180
Db	6197	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6256
Qy	6181	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6240
Db	6257	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6316
Qy	6241	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6300
Db	6317	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6376
Qy	6301	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6360
Db	6377	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6436
Qy	6361	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6420
Db	6437	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6496
Qy	6421	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCCGGGAGCACCT	6480
Db	6497	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCCGGGAGCACCT	6556
Qy	6481	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6540
Db	6557	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6616
Qy	6541	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6600
Db	6617	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6676
Qy	6601	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTT	6660
Db	6677	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTT	6736
Qy	6661	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCGGCGCTTCCTCTGGAACCTCAT	6720
Db	6737	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCGGCGCTTCCTCTGGAACCTCAT	6796
Qy	6721	CCTCGACCTCATCAAGACAGGGCGTTCAAGTGGTGTGACATCACACAGCATGGAGGAGTG	6780
Db	6797	CCTCGACCTCATCAAGACAGGGCGTTCAAGTGGTGTGACATCACACAGCATGGAGGAGTG	6856
Qy	6781	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6840
Db	6857	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6916
Qy	6841	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6900
Db	6917	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6976

Qy	6901	CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6960
Db	6977	CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	7036
Qy	6961	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7020
Db	7037	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7096
Qy	7021	CCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7080
Db	7097	CCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7156
Qy	7081	CAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT	7140
Db	7157	CAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT	7216
Qy	7141	GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7200
Db	7217	GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7276
Qy	7201	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCCGA	7260
Db	7277	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCCGA	7336
Qy	7261	GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7320
Db	7337	GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7396
Qy	7321	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7380
Db	7397	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7456
Qy	7381	TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGC	7440
Db	7457	TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGC	7516
Qy	7441	CAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCCTGTACTCG	7500
Db	7517	CAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCCTGTACTCG	7576
Qy	7501	GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCT	7534
Db	7577	GCCATGTCCTGCGGTCACTGCGGTTGCCGCCCT	7610

RESULT 7

AAD02722

ID AAD02722 standard; cDNA; 6792 BP.

XX

AC AAD02722;

XX

DT 31-MAY-2001 (first entry)

XX

DE Human ATP binding cassette2 (ABC2) transporter protein cDNA.

XX

KW Human; adenosine triphosphate; ATP binding cassette2 transporter;

KW ABC2 transporter; nootropic; neuroprotective; anticonvulsant; neurotoxic;
KW beta-amyloid; multidrug resistance; therapy; Alzheimer's disease;
KW prion disease; Parkinson's disease; Huntington's disease; panic disorder;
KW cholesterol misregulation; inflammatory disease; blood brain barrier;
KW cancer; mood disorder; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT 5'UTR 1. .90

FT /*tag= a

FT misc_signal 88. .94

FT /*tag= b

FT /note= "Translation initiation motif"

FT CDS 91. .6096

FT /*tag= c

FT /product= "Human ABC2 transporter protein"

FT /transl_except= (pos:178. .180, aa:Xaa)

FT /transl_except= (pos:298. .300, aa:Xaa)

FT /transl_except= (pos:928. .930, aa:Xaa)

FT /transl_except= (pos:1519. .1521, aa:Xaa)

FT /transl_except= (pos:1762. .1764, aa:Xaa)

FT /transl_except= (pos:4501. .4503, aa:Xaa)

FT /transl_except= (pos:5041. .5043, aa:Xaa)

FT /transl_except= (pos:5155. .5157, aa:Xaa)

FT /transl_except= (pos:5260. .5262, aa:Xaa)

FT /note= "Xaa is an unknown amino acid; The coding sequence
is specifically claimed as SEQ ID NO 3 in claim 1"

FT 3'UTR 6097. .6792

FT /*tag= d

FT polyA_signal 6772. .6781

FT /*tag= e

XX

PN WO200114414-A2.

XX

PD 01-MAR-2001.

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PF 18-AUG-2000; 2000WO-CA000962.

XX

PR 20-AUG-1999; 99US-0150073P.

PR 30-AUG-1999; 99US-0151457P.

PR 17-AUG-2000; 2000US-00641040.

XX

PA (ACTI-) ACTIVEPASS PHARM INC.

XX

PI Le Bihan S, Wilson C, Charest DL;

XX

DR WPI; 2001-202931/20.

DR P-PSDB; AAY72649.

XX

PT Novel adenosine triphosphate (ATP) binding cassette transporter protein
PT 2, useful as target for developing modulators that modulate activity of
PT transporter protein and thus treat Alzheimer's disease and Parkinson's
PT disease.

XX

PS Claim 1; Fig 1; 92pp; English.

XX

CC The present sequence is human adenosine triphosphate (ATP) binding
CC cassette2 (ABC2) transporter protein cDNA. ABC2 transporter molecules are
CC transmembrane proteins which catalyse ATP-dependent transport of
CC endogenous or exogenous substrates across the biological membranes. ABC2
CC transporters have been associated with the transport of neurotoxic
CC polypeptides (e.g., beta-amyloid) and substrates across the blood-brain-
CC barrier. ABC2 sequence is useful as target for developing modulators that
CC are useful for modulating amyloid deposition and thus for treating
CC Alzheimer's disease, prion diseases, Parkinson's disease and Huntington's
CC disease. It is also useful as targets for developing modulating agents of
CC multidrug resistance exhibited by e.g., cancer cells. ABC transporters
CC are also useful for treating mood and panic disorders, cholesterol
CC misregulation and inflammatory diseases. It can also be used to treat
CC disorders characterised by insufficient or excessive production of an
CC ABC2 transporter protein or its inhibitors. Fragments of ABC transporters
CC are used as immunogens for producing antibodies

XX

SQ Sequence 6792 BP; 1271 A; 2251 C; 1997 G; 1263 T; 0 U; 10 Other;

Query Match 83.2%; Score 6686.8; DB 5; Length 6792;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 6748; Conservative 9; Mismatches 33; Indels 7; Gaps 4;

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Qy      1244 TCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACC 1303
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Db            1 TCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACC 60

Qy      1304 ATTGAACCCGAGGCGCTGCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAG 1363
          |||
Db            61 ATTGAACCCGAGGCGCTGCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAG 120

Qy      1364 CAGCGGAACCTGGGCCTCCTCGTGACCTCATGACCAGCAACCCCAAAATCCTGTACGCG 1423
          |||
Db            121 CAGCGGAACCTGGGCCTCCTCGTGACCTCATGACCAGCAACCCCAAAATCCTGTACGSG 180

Qy      1424 CCTGCGGGCTCTGAGGTCGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTG 1483
          |||
Db            181 CCTGCGGGCTCTGAGGTCGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTG 240

Qy      1484 GGCAACGTGACTCACTATGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTC 1543
          |||
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Qy      1544 CTGGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTG 1603
          |||
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Qy      1604 CGGCTGCACCCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAG 1663
          |||
Db            361 CGGCCGCACCCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAG 420

Qy      1664 GACAACTTCTCGCTGCCAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTTGACAAC 1723
          |||
Db            421 GACAACTTCTCGCTGCCAGTGGCATGGCCCTCCTACAGCAGCTGGATACCATTTGACAAC 480

Qy      1724 GCGGCCTGCGGCTGGATCCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTC 1783
          |||
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Db	481	GCGCCCTGCGGCTGGATCCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTC	540
Qy	1784	CCCGACGAGGAGAGCATTGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACT	1843
Db	541	CCCGACGAGGAGAGCATTGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACT	600
Qy	1844	GTTTTTGCCAGTGTGATCTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCAC	1903
Db	601	GTTTTTGCCGCTGTGATCTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCAC	660
Qy	1904	TACAAGATCCGCCAGAACTCCAGCTTACCGAGAAAACCAACGAGATCCGCCGCGCCTAC	1963
Db	661	TACAAGATCCGCCAGAACTCCAGCTTACCGAGAAAACCAACGAGATCCGCCGCGCCTAC	720
Qy	1964	TGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATC	2023
Db	721	TGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATC	780
Qy	2024	CAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCA	2083
Db	781	CAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCA	840
Qy	2084	GGCAGCTACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTC	2143
Db	841	GGCAGCTACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTC	900
Qy	2144	ATTGAGCACATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACC	2203
Db	901	ATTGAGCACATGATGCCGCTGTGCATGGYGATCTCCTGGGTCTACTCCGTGGCCATGACC	960
Qy	2204	ATCCAGCACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGC	2263
Db	961	ATCCAGCACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGC	1020
Qy	2264	CTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATC	2323
Db	1021	CTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATC	1080
Qy	2324	TCCGTGACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTG	2383
Db	1081	TCCGTGACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTG	1140
Qy	2384	GTCATCATCTGGCTCTTCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTG	2443
Db	1141	GTCATCATCTGGCTCTTCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTG	1200
Qy	2444	GTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTC	2503
Db	1201	GTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGC---TGGTGGCATCATCTACTTC	1257
Qy	2504	CTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATC	2563
Db	1258	CTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATC	1317
Qy	2564	ACGGCCTTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCT	2623
Db	1318	ACGGCCTTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCT	1377

Qy	2624	AAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAG	2683
Db	1378	AAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAG	1437
Qy	2684	TCCCCGGTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGAC	2743
Db	1438	TCCCCGGTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGAC	1497
Qy	2744	GCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGG	2803
Db	1498	GCCGTGGTCTATGGCATCCTCMCGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGG	1557
Qy	2804	CTGCCCCGGCCCTGGTACTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACA	2863
Db	1558	CTGCCCCGGCCCTGGTACTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACA	1617
Qy	2864	GAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAG	2923
Db	1618	GAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAG	1677
Qy	2924	GACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAG	2983
Db	1678	GACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAG	1737
Qy	2984	CCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGAC	3043
Db	1738	CCCACCCACCTGCCTCTGGTTGTCTKCGTGGACAACTCACCAAGGTCTACAAGGACGAC	1797
Qy	3044	AAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTC	3103
Db	1798	AAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGGGGTCTCCTTC	1857
Qy	3104	TTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCT	3163
Db	1858	TTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCT	1917
Qy	3164	CCAACGTCGGGTTCGCGCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATC	3223
Db	1918	CCAACGTCGGGTTCGCGCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATC	1977
Qy	3224	CGCAAGAACCTGGGCATGTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAG	3283
Db	1978	CGCAAGAAC--GGGCATGTGCCC-CAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAG	2034
Qy	3284	GAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAG	3343
Db	2035	GAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCCCAGAGAG	2094
Qy	3344	ATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACA	3403
Db	2095	ATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACA	2154
Qy	3404	TTGTCGGGTGGCATGAAGCGCAAGGTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGC	3463
Db	2155	TTGTCGGGTGGCATGAAGCGCAAGGTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGC	2214

Qy	3464	GCCATCATCCTGGACGAGCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGG	3523
Db	2215	GCCATCATCCTGGACGAGCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGG	2274
Qy	3524	GACCTCATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGAT	3583
Db	2275	GACCTCATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGAT	2334
Qy	3584	GAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGC	3643
Db	2335	GAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGC	2394
Qy	3644	GGCTCCCCGCTCTTCCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAG	3703
Db	2395	GGCTCCCCGCTCTTCCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAG	2454
Qy	3704	CGGCCCCGCCGAGCCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCCG	3763
Db	2455	CGGCCCCGCCGAGCCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCCG	2514
Qy	3764	GCCCCGCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCC	3823
Db	2515	GCCCCCTCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCC	2574
Qy	3824	TCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCAGCGAGGCC	3883
Db	2575	TCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCAGCGAGGCC	2634
Qy	3884	GCCAAGAAGGGGGCTTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTG	3943
Db	2635	GCCAAGAAGGGGGCTTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTG	2694
Qy	3944	CACCTCAGCAGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTCTG	4003
Db	2695	CACCTCAGCAGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTCTG	2754
Qy	4004	GAGGAGGATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTG	4063
Db	2755	GGGGGGGATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTG	2814
Qy	4064	CTCCCTGGGGCGGAGGGCCCGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCCGTGC	4123
Db	2815	CTCCCTGGGGCGGAGGGCCACGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCCGTGC	2874
Qy	4124	TCGGAGCTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCGT	4183
Db	2875	TCGGAGCTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCTG	2934
Qy	4184	GGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTCTTGATAAC	4243
Db	2935	GGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCCCCCTCTTGATAAC	2994
Qy	4244	CCACAGGACCCAGACAATGTCTAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTC	4303
Db	2995	CCACAGGACCCAGACAATGTCTAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTC	3054
Qy	4304	GGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTG	4363

Db	3055	 GGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCACGGGCTG	3114
Qy	4364	CTGGTCAAACGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTG	4423
Db	3115	 CTGGTCAAACGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTG	3174
Qy	4424	CTGCCAGCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGT	4483
Db	3175	 CTGCCAGCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGT	3234
Qy	4484	GATCTGCCCCCGCTGGTCTGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGC	4543
Db	3235	 GATCTTCCCCCGCTGGTCTGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGC	3294
Qy	4544	AATTTTCATCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCCGAC	4603
Db	3295	 AATTTTCATCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCCGAC	3354
Qy	4604	GCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGC	4663
Db	3355	 GCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGC	3414
Qy	4664	GTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCCACGTTGAACCTGAGCAGCGGGGAG	4723
Db	3415	 GTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCCACGTTGAACCTGAGCAGCGGGGAG	3474
Qy	4724	TCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGG	4783
Db	3475	 TCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGG	3534
Qy	4784	CTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCG	4843
Db	3535	 CTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCG	3594
Qy	4844	TCCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAA	4903
Db	3595	 TCCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAA	3654
Qy	4904	ATGTGGACGTCGGCACCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGC	4963
Db	3655	 ATGTGGACGTCGGCACCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGC	3714
Qy	4964	TCTGCGCAGGGCACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATG	5023
Db	3715	 TCTGCGCAGGGCACCGGCTTCTCCTGCCCCAACAGTGTGGGCGGGCACCCGCCCCAGATG	3774
Qy	5024	CGGGTGGTCACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTG	5083
Db	3775	 CGGGTGGTCACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTG	3834
Qy	5084	CTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTC	5143
Db	3835	 CTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTC	3894
Qy	5144	CTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCG	5203

Db	3895	CTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCCGG	3954
Qy	5204	GTGCGCAGGGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTAC	5263
Db	3955	TGCGCCAGGGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTAC	4014
Qy	5264	CTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACTGCCCAAGAGCAAGGGCAACCCG	5323
Db	4015	CTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACTGCCCAAGAGCAAGGGCAACCCG	4074
Qy	5324	GCGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCC	5383
Db	4075	GCGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCC	4134
Qy	5384	CTGGATTACCTGCTGCAGGGCAGGATGTCGTTCATCGCCATCTTCATCATCGTGGCCATG	5443
Db	4135	CTGGATTACCTGCTGCAGGGCAGGATGTCGTTCATCGCCATCTTCATCATCGTGGCCATG	4194
Qy	5444	TCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAG	5503
Db	4195	TCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAG	4254
Qy	5504	CATCTGCAGTTTGTGTCAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGG	5563
Db	4255	CACCTGCAGTTTGTGTCAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGG	4314
Qy	5564	GACATGCTCAACTACCTGGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTTCGAC	5623
Db	4315	GACATGCTCAACTACCTGGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTTCGAC	4374
Qy	5624	CTGCCGGCCTACACGTCGCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCCTGCTCTAT	5683
Db	4375	CTGCCGGCCTACACGTCGCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCCTGCTCTAT	4434
Qy	5684	GGGTGGTCCATCAGGCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCC	5743
Db	4435	GGGTGGTCCATCAGGCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCC	4494
Qy	5744	GCCTACGTGTTTCCTCATTTGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACC	5803
		:	
Db	4495	GCCTACGKGTTCCTCATTTGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACC	4554
Qy	5804	TTCCTGCTACAGCTCTTCGAGCAGGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAA	5863
Db	4555	TTCCTGCTACAGCTCTTCGAGCAGGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAA	4614
Qy	5864	AGCTGCTTCCTCATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTAC	5923
Db	4615	AGCTGCTTCCTCATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTAC	4674
Qy	5924	AACGAGTACATCAACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCG	5983
Db	4675	AACGAGTACATCAACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCG	4734
Qy	5984	TTCGAGTGGGACATTGTACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGC	6043
Db	4735	TTCGAGTGGGACATTGTACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGC	4794

Qy	6044	TTCCTCCTGACCATCATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTG	6103
Db	4795	TTCCTCCTGACCATCATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTG	4854
Qy	6104	TCTACCAAGCCTGTGGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGG	6163
Db	4855	TCTACCAAGCCTGTGGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGGGTGCTCCGG	4914
Qy	6164	GGAGACGCCGACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGG	6223
Db	4915	GGAGACGCCGACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGG	4974
Qy	6224	AAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGC	6283
Db	4975	AAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGC	5034
Qy	6284	TTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGC	6343
		:	
Db	5035	TTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGC	5094
Qy	6344	GACGAGAGCACGACGGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTG	6403
Db	5095	GACGAGAGCACGACGGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTG	5154
Qy	6404	CTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCGAGTGACGCGCTGTTGACGAGCTC	6463
		:	
Db	5155	CHCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCGAGTGACGCGCTGTTGACGAGCTC	5214
Qy	6464	ACGGCCCCGGGAGCACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAG	6523
		:	
Db	5215	ACGGCCCCGGGAGCACCTGCAGCTGTACACGCGGCTNCGTGGGATCYCCTGGAAGGACGAG	5274
Qy	6524	GCCCCGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCG	6583
Db	5275	GCCCCGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCG	5334
Qy	6584	GCTGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGG	6643
Db	5335	GCTGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGG	5394
Qy	6644	TACCCAGCCTTCATCTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGC	6703
Db	5395	TACCCAGCCTTCATCTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGC	5454
Qy	6704	TTCCTCTGGAACCTCATCCTCGACCTCATCAAGACAGGGCGTTTCAGTGGTGCTGACATCA	6763
Db	5455	TTCCTCTGGAACCTCATCCTTGACCTCATCAAGACAGGGCGTTTCAGTGGTGCTGACATCA	5514
Qy	6764	CACAGCATGGAGGAGTGCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGC	6823
Db	5515	CACAGCATGGAGGAGTGCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGC	5574
Qy	6824	CTGCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATC	6883
Db	5575	CTGCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATC	5634

Qy	6884	ACGGTGCGGACCAAGAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAAC	6943
Db	5635	ACGGTGCGGACCAAGAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAAC	5694
Qy	6944	TTCCCGGAAGCCATGCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCG	7003
Db	5695	TTCCCGGAAGCCATGCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCG	5754
Qy	7004	GAGCACATCTCGCTGGCCCAGGTGTTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGC	7063
Db	5755	GAGCACATCTCGCTGGCCCAGGTGTTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGC	5814
Qy	7064	ATCGAGGACTACTCGGTTCAGCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAAG	7123
Db	5815	ATCGAGGACTACTCGGTTCAGCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAAG	5874
Qy	7124	AAGCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCT	7183
Db	5875	AAGCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCT	5934
Qy	7184	CTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTT	7243
Db	5935	CTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTT	5994
Qy	7244	GTGGCAGACGAGCCCCGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAG	7303
Db	5995	GTGGCAGACGAGCCCCGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAG	6054
Qy	7304	GAGCGGGCCCAGCTGTCCTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCA	7363
Db	6055	GAGCGGGCCCAGCTGTCCTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCA	6114
Qy	7364	GGGAGGACACGCTCCACTGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGA	7423
Db	6115	GGGAGGACACGCTCCACTGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGA	6174
Qy	7424	AGTCCCCCAGTGCCTGCCAGGGCCTGGAGTGGAGGTTTTCAGGACCAAGGGGCTTCTGGTCC	7483
Db	6175	AGTCCCCCAGTGCCTGCCAGGGCCTGGAGTGGAGGTTTTCAGGACCAAGGGGCTTCTGGTCC	6234
Qy	7484	TCCAGCCCCTGTACTCGGCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCC	7543
Db	6235	TCCAGCCCCTGTACTCGGCCATG-CCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCC	6293
Qy	7544	AAAGGCTGACCCGGCCCGGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGG	7603
Db	6294	AAAGGCTGACCCGGCCCGGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGG	6353
Qy	7604	GTCTGCCCCGGCCCCCTCGCCCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGG	7663
Db	6354	GTCTGCCCCGGCCCCCTCGCCCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGG	6413
Qy	7664	ACCAGGCACTGCTGGCCTTTTCTCCTGCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGAT	7723
Db	6414	ACCAGGCACTGCTGGCCTTTTCTCCTGCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGAT	6473
Qy	7724	GAAGGCTGATGCCGAGAGCGGGCTGTGGGCGGAGCTGGGTCAGTCCCGTATTTATTTTGC	7783

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      |||
Db      6474 GAAGGCTGATGCCGAGAGCGGGCTGTGGGCGGAGCTGGGTTCAGTCCCGTATTTATTTTGC 6533
      |||
QY      7784 TTTGAGAAGAGGCTCCTCTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAG 7843
      |||
Db      6534 TTTGAGAAGAGGCTCCTCTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAG 6593
      |||
QY      7844 CCATCAGCTTGGGCCAGCTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGG 7903
      |||
Db      6594 CCATCAGCTTGGGCCAGCTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGG 6653
      |||
QY      7904 CAAGGGGCCAGACCCCCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCC 7963
      |||
Db      6654 CAAGGGGCCAGACCCCCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCC 6713
      |||
QY      7964 CTGCCCCGCCACCTCCCTGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAA 8023
      |||
Db      6714 CTGCCCCGCCACCTCCCTGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAA 6773
      |||
QY      8024 TAAATAAAACAAAATGTC 8040
      |||
Db      6774 TAAATAAAACAAAATGTC 6790

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RESULT 8

ABL53011

ID ABL53011 standard; DNA; 8040 BP.

XX

AC ABL53011;

XX

DT 06-JUN-2002 (first entry)

XX

DE Rat ATP binding cassette transporter protein, ABCA2, coding sequence.

XX

KW Rat; ABCA2; gene; neuroprotective; nootropic; antiparkinsonian;

KW adenosine triphosphate binding cassette transporter protein;

KW ATP binding cassette transporter protein; Alzheimer's disease;

KW prion disease; Huntington's disease; Parkinson's disease; ds.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT CDS 67. .7372

FT /*tag= a

FT /product= "Rat ABCA2"

XX

PN WO200208424-A1.

XX

PD 31-JAN-2002.

XX

PF 26-JUL-2001; 2001WO-JP006457.

XX

PR 26-JUL-2000; 2000JP-00225462.

XX

PA (BANY) BANYU PHARM CO LTD.

PA (INAG/) INAGAKI N.

XX

PI Inagaki N;
 XX
 DR WPI; 2002-179907/23.
 DR P-PSDB; ABB76716.
 XX
 PT Adenosine triphosphate (ATP) binding cassette transporter gene ABCA2 of
 PT human or rat origin and encoded protein, useful for screening inhibitors,
 PT promoters and regulators of ABCA2 activity as drugs and diagnosis of
 PT ABCA2-related diseases.
 XX
 PS Claim 7; Page 82-87; 118pp; Japanese.
 XX
 CC The present sequence is the coding sequence for rat adenosine
 CC triphosphate (ATP) binding cassette transporter protein (ABCA2). ABCA2
 CC can be used in the diagnosis, treatment and prevention of diseases such
 CC as Alzheimer's disease, prion diseases, Huntington's disease, and
 CC Parkinson's disease
 XX
 SQ Sequence 8040 BP; 1673 A; 2464 C; 2199 G; 1704 T; 0 U; 0 Other;

Query Match 72.3%; Score 5810; DB 6; Length 8040;
 Best Local Similarity 84.0%; Pred. No. 0;
 Matches 6768; Conservative 0; Mismatches 1205; Indels 85; Gaps 15;

Qy	1	CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT	60
Db	34	CCGCGGCGCTGAGGCGGCGGAGCGCGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT	93
Qy	61	GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTGGCCTTCGAGAT	120
Db	94	GCTGCTCTGGAAGAACGTGACGCTGAAGCGCCGGAGCCCGTGGGTCTGGCGTTTGAGAT	153
Qy	121	CTTCATCCCCCTGGTGTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT	180
Db	154	CTTCATCCCCCTGTCTCTTCTCATCCTGTTGGGACTGCGGCAGAAGAAGCCCACCAT	213
Qy	181	CTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCTGACGTCTGCCGGCATCCTGCC	240
Db	214	CTCTGTGAAGGAAG---CTTTCTACACGGCAGCACCGCTGACATCGGCCGGCATCCTGCC	270
Qy	241	TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGC	300
Db	271	TGTCATGCAGTCGCTTTGCCCTGATGGCCAGCGTGATGAGTTTGGCTTCCTGCAGTATGC	330
Qy	301	CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT	360
Db	331	CAACTCCACGGTCACCCAGCTTCTGGAACGCCTCAACCGTGTAGTGAAGAGAGCAACTT	390
Qy	361	GTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA	420
Db	391	GTTTGACCCAGAGCGACCTAGCCTGGGCTCAGAGCTTGAGGCACTGCACCAACGTCTGGA	450
Qy	421	GGCCCTCAGTGC GG GCGG GCGG CACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC	480
Db	451	GGCCCTCAGCTCGGGCCCTGGCACCTGGGAGAGCCACTCAGCTAGACCTGCAGTTTCATC	510
Qy	481	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCTTGACGCAAAA	540

Db	511	 CTTCTCTCTGGACTCGGTGGCCAGGGACAAAAGAGAGCTTTGGCGTTTCCTGATGCAGAA	570
Qy	541	CTTGTCGCTGCCCAATAGCACGGCCCAAGCACTCTTGGCCGCCCGTGTGGACCCGCCCGA	600
Db	571	CCTGTCACTGCCCAACAGCACGGCCCAAGCCCTCCTGGCTGCCCGTGTAGACCCCTCTGA	630
Qy	601	GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	660
Db	631	GGTCTATCGCTTGCTTTTTGGTCCTTTACCTGACCTGGATGGAAAGTTGGGGTTCCTCAG	690
Qy	661	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	720
Db	691	GAAGCAGGAGCCCTGGAGTCACCTGGGTAGCAATCCTCTGTTCCAAATGGAGGAGCTGCT	750
Qy	721	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	780
Db	751	GCTGGCTCCTGCCCTTTTGGAGCAACTCACATGTGCTCCAGGCTCTGGGGAGCTGGGCCG	810
Qy	781	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	840
Db	811	GATTCTTACCATGCCTGAGGGTCATCAGGTAGACCTTCAGGGCTACCGGGATGCTGTCTG	870
Qy	841	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	900
Db	871	CAGCGGCAGGCTACAGCTCGTGCCAGCATTTCAGTGATCTAGCCACTGAGCTCCGGAA	930
Qy	901	CCAGCTGGACGTGGCCAAGGTCTCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	960
Db	931	CCAGCTGGACATAGCCAAGATTGCCAGCAGCTGGGCTTCAATGTCCCCAACGGCTCAGA	990
Qy	961	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGACCTGCTGGA	1020
Db	991	TCCACAGCCGAGGCACCGTCCCCACAGAGTCTGCAGGCACTCTTAGGGGACCTGCTGGA	1050
Qy	1021	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGCCCTGGCCCTGCTACTGCCCCA	1080
Db	1051	TGTCCAGAAGGTTCTACAGGATGTGGATGTCCTATCAGCCCTTGCCCTGCTGCTGCCTCA	1110
Qy	1081	GGGTGCCTGCACTGGCCGGACCCCCGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Db	1111	AGGTGCCTGTGCTGGCCGGGCCCCGACCTCAAGCTGGCAGCCCAGTGGCCCGGCCAA	1170
Qy	1141	TGGCACTGGGGCAGGGGCAGTCATGGGCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1200
Db	1171	CAGCACCGGGTAGGGGCAAATACAGGTCCCAACACCACCGTTGAGGAGGGCACCCAGTC	1230
Qy	1201	TGCTGCAGCACTGGCCACCCCGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
Db	1231	ACCTGTCACCCAGCCTCTCCGGACACTCTGCAAGGCCAGTGCTCAGCCTTTGTGCAGCT	1290
Qy	1261	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCT	1320
Db	1291	CTGGGCTGGCTTGACAGCCCATCTTGTGTGGCAACAACCGTACCATTGAGCCTGAAGCACT	1350
Qy	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380

Db	1351	CCGGAGGGGCAACATGAGCTCACTGGGCTTTACGAGCAAAGAACAACGGAACCTGGGCCT	1410
Qy	1381	CCTCGTGCACCTCATGACCAGCAACCCCAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
Db	1411	TCTTGTGCACCTCATGACCAGCAACCCCAAATCCTGTATGACCCGCAGGCTCTGAAGC	1470
Qy	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1500
Db	1471	TGACCATGTTATCCTCAAGGCAAATGAGACCTTTGCCTTTGTGGGCAACGTGACGCACTA	1530
Qy	1501	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1531	CGCCCAGGTCTGGCTCAACATCTCCGCAGAGATCCGGAGCTTCCTGGAGCAGGGCAGGCT	1590
Qy	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCAGGGC	1620
Db	1591	GCAGCAGCATCTGCACTGGCTGCAGCAGTACGTGGCTGACCTCCGGCTACACCCTGAAGC	1650
Qy	1621	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1680
Db	1651	AATGAACCTGTCACTGGACGAGCTGCCCCCTGCTCTGCGCCTGGACTACTTTTCTCTGCC	1710
Qy	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACCGGGCCTGCGGCTGGAT	1740
Db	1711	CAATGGCACAGCCCTTCTGCAGCAGCTAGACACAATAGACAATGCAGCCTGTGGCTGGAT	1770
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1800
Db	1771	CCAGTTCATGTCCAAGGTGAGTGTGGACATCTTCAAGGGGTTTCTGATGAGGAGAGCAT	1830
Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCAGTGTGTTTGGCCAGTGTGAT	1860
Db	1831	CGTGAACCTACACTCTCAATCAGGCCTACCAGGACAATGTTACAGTATTTGCCAGCGTGAT	1890
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1920
Db	1891	TTTCCAGACACGGAAGGATGGTTCCCTCCCCCACATGTCCATTACAAGATTCGCCAGAA	1950
Qy	1921	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1980
Db	1951	CTCAAGCTTCACCGAGAAAACCAACGAGATCCGTGCTGCTTACTGGCGTCCAGGGCCCAA	2010
Qy	1981	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Db	2011	CACTGGTGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATAGAACG	2070
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Db	2071	TGCCATCATCAACACGTTTGTGGGGCACGACGTGGTGAACCCGGCAACTACGTGCAGAT	2130
Qy	2101	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTGATTGAGCACATGATGCC	2160
Db	2131	GTTCCCGTACCCCTGCTACACCCGTGACGACTTCCTGTTTGTGATTGAGCACATGATGCC	2190
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Db	2191	ACTGTGCATGGTGATCTCCTGGGTTTACTCTGTGGCCATGACCATACAGCACATCGTGGC	2250

Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280
Db	2251	GGAGAAAGAGCATCGGCTAAAGGAGGTGATGAAGACGATGGGCCTGAACAACGCCGTGCA	2310
Qy	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2340
Db	2311	CTGGGTGGCCTGGTTCATCACGGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCCCTGAC	2370
Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2400
Db	2371	CGCCATCCTCAAGTATGGCCAGGTCCTCATGCACAGCCACGTGCTCATCATATGGCTCTT	2430
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2460
Db	2431	CCTTGCTGTCTATGCTGTGGCCACTATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2490
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Db	2491	TAAGGCCAAGTTGGCCTCGGCCTGCGGCGGCATCATCTACTTCCTGAGCTACGTTCCCTA	2550
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
Db	2551	CATGTATGTAGCAATCCGTGAGGAAGTAGCCACGATAAGATCACTGCCTTCGAGAAGTG	2610
Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640
Db	2611	CATTGCGTCCCTGATGTCCACAACAGCCTTCGGCCTGGGTTCCAAGTACTTTGCTCTGTA	2670
Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2700
Db	2671	TGAAGTGGCAGGTGTGGGCATCCAGTGGCACACGTTTCAGCCAGTCCCCAGTGAAGGGGA	2730
Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760
Db	2731	TGACTTCAACCTGCTCCTTGCTGTCACCATGCTGATGGTGGACACAGTGGTCTATGGCGT	2790
Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2791	ACTCACTTGGTACATTGAGGCTGTGCACCCAGGTATGTATGGGCTGCCCCGGCCCTGGTA	2850
Qy	2821	CTTCCCCTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2851	CTTCCCCTACAGAAGTCCTATTGGCTGGGCAGTGGGCGGACAGAGACCTGGGAGTGGAG	2910
Qy	2881	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2911	CTGGCCATGGGCACACGCACCCACGCCTCAGCGTTATGGAGGAGGACCAGGCCTGTGCCAT	2970
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACCCACCTGCCTCT	3000
Db	2971	GGAGAGCCGGCACTTCAGGAGACTCGCGGTATGGAGGAGGAGCCCACCCACCTGCCTTT	3030
Qy	3001	GGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3031	GGTCGTCTGCGTGGACAAGCTCACCAAGGTCTATAAAATGACAAGAAGCTGGCCTTAAA	3090

Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3091	CAAACCTGAGCCTCAATCTCTACGAGAACCAGGTGGTCTCTTTCTAGGCCATAACGGGGC	3150
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCG	3180
Db	3151	TGGCAAGACCACTACCATGTCTATCCTGACTGGACTGTTCCACCCACGTCGGGCTCAGC	3210
Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3211	CACATCTATGGCCACGACATCCGCACAGAGATGGATGAGATCCGTAAGAACCTGGGCAT	3270
Qy	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3271	GTGCCCACAGCACAACGTGCTCTTTGACCAGCTCACTGTGGAGGAACACCTCTGGTTCTA	3330
Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3331	CTCACGCCTCAAAGCATGGCACAAGAGGAGATCCGCAAAGAGATGGACAAGATGATCGA	3390
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCTGGGTGGCATGAA	3420
Db	3391	GGACCTGGAGCTCTCCAACAAGCGCCACTCGCTGGTACAGACGCTGTCTGGAGGCATGAA	3450
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3480
Db	3451	GCGCAAGCTTTAGTAGCCATTGCCTTCGTGGGTGGCTCTAGAGCCATTATCTTAGATGA	3510
Qy	3481	GCCACGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3540
Db	3511	GCCACAGCTGGCGTGGACCCCTATGCTCGACGTGCCATCTGGGACCTCATCTGAAGTA	3570
Qy	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3571	CAAGCCGGGTGCGACTATCCTCCTGTCCACCCATCACATGGATGAGGCCGACCTGCTGGG	3630
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3631	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAATGCTGCGGCTCTCCCCTCTTCCT	3690
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCGCGGAGCCGGG	3720
Db	3691	CAAGGGTGCCTACGGCGATGGCTACCGCCTCACACTGGTCAAGCGGCCTGCGGAGCCTGG	3750
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTG	3780
Db	3751	CACCTCCCAAGAGCCAGGGATGGCTTCCAGCCCCCTCAGGTCGTCTCAGCTGAGCAACTG	3810
Qy	3781	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCTCCTGCCTGCTGGTCTC	3840
Db	3811	CTCAGAGATGCAAGTGTCCAGTTCATCCGCAAGCATGTGGCTTCTCCTGCTGGTGTCTC	3870
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCAAGAAGGGGGCTTT	3900
Db	3871	AGACACGAGCACCGAGCTCTCCTACATCCTGCCCAGCGAGGCTGTCAAGAAAGGGGCCTT	3930
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960

Db	3931	CGAGCGCCTCTTTCAGCAATTGGAGCACAGCCTGGACGCACTGCATCTGAGCAGTTTGG	3990
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4020
Db	3991	GCTGATGGACACAACCCTGGAGGAGGTGTTCTCAAGGTGTCTGAAGAAGACCAGTCACT	4050
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4051	GGAGAAATAGTGAGGCCGATGTGAAGGAGTCCCGGAAGGATGCACTGCCTGGGGCAGAGGG	4110
Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4111	CCTGACGGCTGTGGAGAGTCAAGCAGGCAACCTGGCTCGGTGCTCAGAGCTGGCACAGTC	4170
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCGTGGCGACGAGGGAGCTGG	4200
Db	4171	CCAGGCTTCACTGCAGTCTGCATCTTCTGTGGGCTCCGCCCGTGGGGATGAGGGTGCTGG	4230
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4231	CTACACCGACGGCTACGGTGACTACCGTCCCCCTCTTGACAACCTTGCAAGACCCAGACAG	4290
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAA	4320
Db	4291	TGTCAGCTTACAAGAGGCTGAAATGGAGGCCCTGGCTCGGGTAGGCCAGGGCAGCCGCAA	4350
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4351	GCTAGAGGGCTGGTGGCTGAAGATGCGGCAGTTCCATGGGCTCCTGGTGAAGCGCTTCCA	4410
Qy	4381	CTGCGCCCGCCGCAACTCCAAGGCACCTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4411	CTGTGCTCGCCGGAACCTCCAAAGCGCTCTGCTCCCAGATTCTGCTGCCTGCCTTCTTCGT	4470
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4471	CTGTGTGGCCATGACTGTGGCATTGTCTGTCCCTGAGATCGGTGACCTGCCTCCACTGGT	4530
Qy	4501	CCTGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCCTACGC	4560
Db	4531	CCTGTGCGCTTCTCAGTACCACAACCTATACCCAGCCCCGTGGCAACTTTATCCCCCTATGC	4590
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCCAGCAGCT	4620
Db	4591	CAATGAGGAACGCCGCGAGTACCGATTACGGCTGTACCTGATGCCAGCCCCCAGCAGTT	4650
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4651	GGTGAGCACATTCCGGCTGCCCTCTGGTGTGGGTGCCACTTGTGTGCTCAAGTCTCCAGC	4710
Qy	4681	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4711	CAACGGCTCCCTGGGGCCCATGCTGAACTTGAGCAGTGGAGAGTCCCGCCTGCTGGCCGC	4770
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800

Db 4771 ACGGTTCTTCGACAGTATGTGCCTGGAGTCCCTTCACACAGGGGCTGCCACTGTCCAACCTT 4830
 Qy 4801 CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGA--- 4857
 |||||
 Db 4831 CGTGCCACCCCCACCCTCGCCCGCCCCCTTCCGACTCACCCCTGTCCCCGGATGAGGATTC 4890
 Qy 4858 CCTGCAGGCCTGGAACGTCTCCCTGCCGCCACCCTGGGCCAGAAATGTGGACGTCCGC 4917
 |||| |||||
 Db 4891 ACTGCTAGCCTGGAATACGTCCCTGCCCCCTACTGCTGGACCAGAGACGTGGACGTGGGC 4950
 Qy 4918 ACCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCAC 4977
 || |||||
 Db 4951 GCCTTCTCTGCCACGCCTGGTTACAGAGCCGGTCCGCTGTACCTGCTCTGCACAGGGCAC 5010
 Qy 4978 CGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGG 5037
 |||||
 Db 5011 GGGCTTCTCGTGCCCCAGCAGTGTGGGTGGGCACCCACCCAGATGAGAGTGGTCACGGG 5070
 Qy 5038 CGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGA 5097
 |||||
 Db 5071 GGACATCCTGACTGACATCACCGGCCACAATGTTTCCGAGTACCTGCTCTTCACCTCTGA 5130
 Qy 5098 CCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAGTCCATCCC 5157
 |||
 Db 5131 CCGTTTCCGACTGCACCGCTATGGAGCCATCACCTTTGGTAATATCCAGAAGTCCATCCC 5190
 Qy 5158 AGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGC 5217
 ||| |
 Db 5191 AGCACCCATTGGTACCCGGACCCCTCTCATGGTCCGGAAGATTGCAGTGCAGGAGGGTGGC 5250
 Qy 5218 CCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAA 5277
 |||||
 Db 5251 CCAGGTGCTCTACAACAACAAGGGCTACCACAGCATGCCCACCTACCTCAACAGCCTCAA 5310
 Qy 5278 CAACGCCATCCTGCGTGCCAACTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCAT 5337
 ||| |||||
 Db 5311 CAATGCCATTCTGCGTGCAAACCTACCCAAAAGCAAGGGCAATCCAGCAGCCTACGGTAT 5370
 Qy 5338 CACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCT 5397
 |||||
 Db 5371 CACCGTCACCAACCACCCCATGAACAAGACCAGTGCTAGCCTCTCCCTGGATTACCTACT 5430
 Qy 5398 GCAGGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGC 5457
 |||||
 Db 5431 GCAGGGCACAGACGTGGTCATCGCCATCTTCATCATTGTGGCCATGTCCTTCGTGCCGGC 5490
 Qy 5458 CAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGT 5517
 |||||
 Db 5491 CAGCTTCGTGGTCTTCCTTGTGGCCGAGAAATCCACCAAGGCCAAACACCTGCAGTTCGT 5550
 Qy 5518 CAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTA 5577
 |||||
 Db 5551 CAGCGGGTGCAACCCTGTCATCTACTGGCTAGCCAACCTACGTGTGGGACATGCTCAATTA 5610
 Qy 5578 CCTGGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACAC 5637
 |||||
 Db 5611 CCTGGTCCCGGCCACCTGCTGCATCATCATCCTCTTCGTGTTTGACTTGCCGGCCTACAC 5670

Qy	5638	GTCGCCCACCAACTTCCCTGCCGTCCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCAC	5697
Db	5671	GTCACCCACCAACTTCCCCGCGGTGCTCTCCTTGTTTCCTGCTCTATGGATGGTCCATCAC	5730
Qy	5698	GCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCT	5757
Db	5731	ACCCATCATGTACCCGGCCTCCTTCTGGTTTGAGGTCCCTAGCTCAGCCTACGTGTTCCCT	5790
Qy	5758	CATTGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCT	5817
Db	5791	CATCGTCATCAACCTCTTCATTGGCATCACGGCCACAGTGGCCACCTTCCTTCTGCAGCT	5850
Qy	5818	CTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCAT	5877
Db	5851	CTTTGAGCATGACAAGGATCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCAT	5910
Qy	5878	TTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAA	5937
Db	5911	CTTCCCCAACTACAACCTGGGCCACGGACTCATGGAGATAGCCTACAACGAATACATCAA	5970
Qy	5938	CGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACAT	5997
Db	5971	CGAATACTATGCCAAGATCGGCCAGTTTGACAAGATGAAGTCCCCGTTTGAGTGGGACAT	6030
Qy	5998	TGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCAT	6057
Db	6031	TGTCACACGTGGACTGGTGGCCATGACAGTCGAGGGCTTCGTGGGATTCTTTCTCACCAT	6090
Qy	6058	CATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGT	6117
Db	6091	CATGTGTCAATATAAAGCTTCCTACGGCAGCCACAGCGTCTGCCTGTGTCTACTAAACCTGT	6150
Qy	6118	GGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAA	6177
Db	6151	GGAAGACGATGTAGACGTGGCCAGTGAGCGGCAAAGAGTGCTCCGTGGCGATGCTGACAA	6210
Qy	6178	TGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTAT	6237
Db	6211	TGACATGGTCAAGATCGAGAACCTGACTAAGGTGTACAAGTCTCGGAAGATCGGCCGCAT	6270
Qy	6238	CCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGG	6297
Db	6271	CCTGGCAGTGGACCGCCTTTGCCTGGGTGTGCGCCCCGAGAGTGCTTTGGGCTCCTCGG	6330
Qy	6298	CGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGAC	6357
Db	6331	GGTCAATGGTGCCGGGAAGACCAGCACCTTCAAGATGTTGACTGGAGATGAGAGCACAAC	6390
Qy	6358	GGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCA	6417
Db	6391	AGGGGGCGAGGCCTTTGTCAATGGACACAGTGTGCTCAAGGACCTGCTCCAGGTTTCAGCA	6450
Qy	6418	GAGCCTCGGCTACTGCCCCAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCA	6477
Db	6451	GAGCCTTGGCTACTGCCCCAGTTCGACGCCCTGTTTCGATGAGCTCACGGCTCGCGAACA	6510

Qy	6478	CCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAA	6537
Db	6511	CCTGCAGCTGTATACTCGGCTTCGAGGCATCCCCTGGAAGGATGAGGCGCAGGTGGTGAG	6570
Qy	6538	GTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAG	6597
Db	6571	GTGGGCCCTGGAGAAGCTGGAGCTGACGAAGTGTGCAGACAAGCCAGCCGGTAGCTACAG	6630
Qy	6598	CGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCAT	6657
Db	6631	TGGGGGCAACAAACGGAAACTTTCCACAGCCATCGCTCTCATTGGGTACCCTGCCTTCAT	6690
Qy	6658	CTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCT	6717
Db	6691	CTTTCTAGACGAGCCCACCACTGGCATGGACCTAAGGCCCGGCGCTTCCTGTGGAACCT	6750
Qy	6718	CATCCTCGACCTCATCAAGACAGGGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGA	6777
Db	6751	CATTCTGGACCTCATCAAGACAGGACGTTCAGTGGTGCTGACCTCACACAGCATGGAGGA	6810
Qy	6778	GTGCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGG	6837
Db	6811	ATGCGAGGCTGTGTGCACACGGCTGGCCATCATGGTGAATGGACGGCTGCGCTGCCTGGG	6870
Qy	6838	CAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAA	6897
Db	6871	GAGTATCCAGCACCTCAAGAACAGGTTTGGGGACGGCTACATGATCACTGTAAGGACCAA	6930
Qy	6898	GAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCAT	6957
Db	6931	AAGCAGCCAGAACGTGAAGGATGTGGTGCGGTTCTTCAACCGCAACTTCCAGAGGCCAT	6990
Qy	6958	GCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCT	7017
Db	6991	GCTCAAGGAACGCCACCATACGAAGGTGCAGTATCAGCTCAAGTCGGAGCACATCTCGCT	7050
Qy	7018	GGCCCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTC	7077
Db	7051	GGCTCAGGTGTTTCAGCAAGATGGAGCACGTGGTGGTGACTGGGCATCGAGGACTACTC	7110
Qy	7078	GGTCAGCCAGACCACACTGGACAATGTGTTCGTGAACCTTGGCCAAGAAGCAGAGTGACAA	7137
Db	7111	AGTCAGCCAGACCCTCTGGATAACGTGTTTGTGAACCTTCGCCAAGAAGCAAAGTGACAA	7170
Qy	7138	CCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCT	7197
Db	7171	TGTGGAGCAGCAAGAGGCTGA---GCCATCCACCTTGCCGTCCCCCTTG---GACTACT	7224
Qy	7198	CAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCC	7257
Db	7225	TAGCCTGCTGCGGCCCGCCCTGCACCCACAGAGCTCCGGGCACTGGTGGCCGATGAGCC	7284
Qy	7258	CGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCT	7317
Db	7285	TGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAAGAGCGGGCCCAGCT	7344
Qy	7318	GTCCTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTC	7377

Db	7345	CTCCTTCAACACCGATACGCTCTGCTGACGTTCAAGAGTCACATCAGGGATG-----	7396
Qy	7378	CACTGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCAGTGCC	7437
Db	7397	-----CAGCTGTTTGGGGCAGAAGTCAGGCGGTGGCCGTAGCCCCAGTCACACA	7445
Qy	7438	TGCCAGGGCCTGGAGTGG-AGGTTCAGGACCAAGGGGCTTCTGGTCTCCAGCCCCTGTA	7496
Db	7446	TGCCAGGCCCTGGAAAGGCAGGTTCAGGACCAAGGGCTCCCGCCCTCC-----	7494
Qy	7497	CTCGGCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAAAGGCTGACCCG	7556
Db	7495	-----TCCCAACTACCATCCTCCCCGATCGTGCCAAAGGCTGGGCTG	7536
Qy	7557	GCCC-GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCCGCC	7615
Db	7537	GCCCTGGGCTGCACACACCCTCACCTGCTTTGCCTTAAAGCCTTGGGTCTGCCCCAGC	7596
Qy	7616	CCTCGCCCCCTGCCTGGCACTGCTCACC-GCCCAAGGCGACGCCGGCTGGACCAGGCA-CT	7673
Db	7597	CCCTTACCCTGCCCAGCACCATCCACCTTCCCAGGGTGACATGGGCTGCCCCAAGTATCC	7656
Qy	7674	GCTGGCCTTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGAT	7733
Db	7657	TGTGACCCTTCTCTGCAGCGGCCACCAGTCTACCCAGGCCAGCATCTGCACAGATGTCT	7716
Qy	7734	GCCGAGAGCGGGCTGTGGGCGGAGCTGGGTGAG-TCCCGTATTTATTTTGCTTTGAGAAG	7792
Db	7717	TTCATGAAAAGACTGCAGTTGGGGAGGTGGCAGCTTGCCCTACTTATTTTGCTTTAAGA--	7774
Qy	7793	AGGCTCCTCTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCT	7852
Db	7775	----GCCTCCCTCACTCTGCTGTTGTGAAGAAGTTAGGCTACCATGGGAAGCCATGAATG	7830
Qy	7853	TGGGCCAGCTGGCAGG-----TGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCA	7905
Db	7831	TGGCTGCCTCAGCCCTGGTGGGAATGGCAGGAACGGAGAAGCTGGGCTTGCTGGCTAGGTG	7890
Qy	7906	AGGGGCCA-----GACCCCCCCCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGC	7960
Db	7891	AGGGGCCACTGCTCCCTCCCTGCCCCCTCAAGCTGCCTTTGCTCTCCCGCTCAGCTTGG-	7949
Qy	7961	CCCCTGCCCCGCCACCTCCCTGGGAGCCGGGCTGTACATAGCGCACAGATGTTTGTTTT	8020
Db	7950	-CCCTCCTGCCACCCATGTGGGAGTAGGACCTTGTATATAGCACACAGATGTTTGTTTT	8008
Qy	8021	AAATAAATAAACAAAATG	8038
Db	8009	CAATAAATAAGCAAAAAG	8026

RESULT 9

ABT42135

ID ABT42135 standard; DNA; 8040 BP.

XX

AC ABT42135;

XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Toxicity modelling related rat gene SEQ ID No 1837.
 XX
 KW Toxic effect; gene expression profile; renal toxicity; toxicity marker;
 KW database; drug screening; toxicity assay; rat; ds.
 XX
 OS Rattus norvegicus.
 XX
 PN WO200295000-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 22-MAY-2002; 2002WO-US016173.
 XX
 PR 22-MAY-2001; 2001US-0292335P.
 PR 13-JUN-2001; 2001US-0297523P.
 PR 19-JUN-2001; 2001US-0298925P.
 PR 10-JUL-2001; 2001US-0303807P.
 PR 10-JUL-2001; 2001US-0303808P.
 PR 10-JUL-2001; 2001US-0303810P.
 PR 28-AUG-2001; 2001US-0315047P.
 PR 27-SEP-2001; 2001US-0324928P.
 PR 22-OCT-2001; 2001US-0330462P.
 PR 01-NOV-2001; 2001US-0330867P.
 PR 21-NOV-2001; 2001US-0331805P.
 PR 06-DEC-2001; 2001US-0336144P.
 PR 19-DEC-2001; 2001US-0340873P.
 PR 21-FEB-2002; 2002US-0357842P.
 PR 21-FEB-2002; 2002US-0357843P.
 PR 21-FEB-2002; 2002US-0357844P.
 PR 15-MAR-2002; 2002US-0364134P.
 PR 08-APR-2002; 2002US-0370144P.
 PR 08-APR-2002; 2002US-0370206P.
 PR 08-APR-2002; 2002US-0370247P.
 PR 17-APR-2002; 2002US-0372794P.
 PR 21-APR-2002; 2002US-0371679P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;
 XX
 DR WPI; 2003-148464/14.
 XX
 PT Predicting at least one toxic effect of a compound, useful for toxicity
 PT modeling, comprises preparing a gene expression profile of a tissue or
 PT cell sample exposed to the compound, and comparing the gene expression
 PT profile to a database.
 XX
 PS Example 4; Page; 446pp; English.
 XX
 CC The invention relates to a novel method of predicting at least one toxic
 CC effect of a compound. The method comprises a gene expression profile of a
 CC tissue or cell sample exposed to the compound, and comparing the gene
 CC expression profile to a database comprising at least part of the data or
 CC information given in the specification. The methods are useful for

CC predicting at least one toxic effect of a compound, predicting the
CC progression of a toxic effect of a compound, predicting the renal
CC toxicity of a compound, or identifying toxicity markers in tissues or
CC cells exposed to known renal toxin. The genes are useful as toxicity
CC markers in drug screening and toxicity assays, in monitoring disease or
CC physiological states, or disease progression. This polynucleotide
CC represents a rat DNA sequence relating to the toxic effect database
CC described in the specification. NOTE: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from the World Intellectual Property
CC Organization

XX

SQ Sequence 8040 BP; 1673 A; 2464 C; 2199 G; 1704 T; 0 U; 0 Other;

Query Match 72.3%; Score 5810; DB 7; Length 8040;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 6768; Conservative 0; Mismatches 1205; Indels 85; Gaps 15;

Qy	1	CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT	60
Db	34	CCGCGGCGCTGAGGCGGCGGAGCGCGGCCCGGCCATGGGCTTCCTGCACCAGCTGCAGCT	93
Qy	61	GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGAT	120
Db	94	GCTGCTCTGGAAGAACGTGACGCTGAAGCGCCGGAGCCCGTGGGTCTTGGCGTTTGAGAT	153
Qy	121	CTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT	180
Db	154	CTTCATCCCCCTTGTCCTCTTCTTCATCCTGTTGGGACTGCGGCAGAAGAAGCCCACCAT	213
Qy	181	CTCCGTGAAGGAAGTCCCTTCTACACAGCGGCGCCCTGACGTCTGCCGGCATCCTGCC	240
Db	214	CTCTGTGAAGGAAG---CTTTCTACACGGCAGCACCGCTGACATCGGCCGGCATCCTGCC	270
Qy	241	TGTCATGCAATCGCTGTGCGCGGACGGCCAGCGAGACGAGTTCTGGCTTCCTGCAGTACGC	300
Db	271	TGTCATGCAGTCGCTTTGCCCTGATGGCCAGCGTGATGAGTTTGGCTTCCTGCAGTATGC	330
Qy	301	CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT	360
Db	331	CAACTCCACGGTCACCCAGCTTCTGGAACGCCTCAACCGTGTAGTGGAAGAGAGCAACTT	390
Qy	361	GTTTGACCCAGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA	420
Db	391	GTTTGACCCAGAGCGACCTAGCCTGGGCTCAGAGCTTGAGGCACTGCACCAACGTCTGGA	450
Qy	421	GGCCCTCAGTGCGGGCCCGGGCACCTCGGGAGCCACCTGGACAGATCCACAGTGCTTC	480
Db	451	GGCCCTCAGCTCGGGCCCTGGCACCTGGGAGAGCCACTCAGCTAGACCTGCAGTTTCATC	510
Qy	481	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGAGGAGCTCTGGCGTTTCTGACGCAAAA	540
Db	511	CTTCTCTCTGGACTCGGTGGCCAGGGACAAAAGAGAGCTTTGGCGTTTCTGATGCAGAA	570
Qy	541	CTTGTCGCTGCCCAATAGCACGGCCCAAGCACTCTTGCCGCCCGTGTGGACCCGCCGA	600
Db	571	CCTGTCACTGCCCAACAGCACGGCCAGGCCCTCCTGGCTGCCCGTGTAGACCTTCTGA	630

Qy	601	GGTCTACCACTGCTCTTTGGTCCCTCATCTGCCCTGGATTCACAGTCTGGCCTCCACAA	660
Db	631	GGTCTATCGCTTGCTTTTTGGTCCTTTACCTGACCTGGATGGAAAGTTGGGGTTCCTCAG	690
Qy	661	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	720
Db	691	GAAGCAGGAGCCCTGGAGTCACCTGGGTAGCAATCCTCTGTTCCAAATGGAGGAGCTGCT	750
Qy	721	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	780
Db	751	GCTGGCTCCTGCCCTTTTGGAGCAACTCACATGTGCTCCAGGCTCTGGGGAGCTGGGCCG	810
Qy	781	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	840
Db	811	GATTCTTACCATGCCTGAGGGTCATCAGGTAGACCTTCAGGGCTACCGGGATGCTGTCTG	870
Qy	841	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	900
Db	871	CAGCGGGCAGGCTACAGCTCGTGCCAGCATTTTCAGTGATCTAGCCACTGAGCTCCGGAA	930
Qy	901	CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	960
Db	931	CCAGCTGGACATAGCCAAGATTGCCAGCAGCTGGGCTTCAATGTCCCCAACGGCTCAGA	990
Qy	961	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1020
Db	991	TCCACAGCCGACGGCACCCTCCCCACAGAGTCTGCAGGCACTCTTAGGGGACCTGCTGGA	1050
Qy	1021	TGCCCAGAAAGTTCTGCAGGATGTGGATGTCTGTGCGCCCTGGCCCTGCTACTGCCCCA	1080
Db	1051	TGTCCAGAAAGTTCTACAGGATGTGGATGTCTATCAGCCCTTGCCCTGCTGCTGCCTCA	1110
Qy	1081	GGGTGCCTGCACTGGCCGGACCCCCGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Db	1111	AGGTGCCTGTGCTGGCCGGGCCCCCGCACCTCAAGCTGGCAGCCCCAGTGGCCCCGCCAA	1170
Qy	1141	TGGCACTGGGGCAGGGGAGTGCATGGGGCCCCAACGCCACCGCTGAGGAGGGCGACCCCTC	1200
Db	1171	CAGCACCGGGTAGGGGCAAATACAGGTCCCAACACCACCGTTGAGGAGGGCACCCAGTC	1230
Qy	1201	TGCTGCAGCACTGGCCACCCCGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
Db	1231	ACCTGTCACCCAGCCTCTCCGGACACTCTGCAAGGCCAGTGCTCAGCCTTTGTGCAGCT	1290
Qy	1261	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCT	1320
Db	1291	CTGGGCTGGCTTGCAGCCCATCTTGTGTGGCAACAACCGTACCATTGAGCCTGAAGCACT	1350
Qy	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380
Db	1351	CCGGAGGGGCAACATGAGCTCACTGGGCTTTACGAGCAAAGAACACGAACCTGGGCCT	1410
Qy	1381	CCTCGTGCACCTCATGACCAGCAACCCCAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
Db	1411	TCTTGTGCACCTCATGACCAGCAACCCCAAATCCTGTATGCACCCGACGGCTCTGAAGC	1470

Qy	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGGCTTTTGTGGGCAACGTGACTCACTA	1500
Db	1471	TGACCATGTTATCCTCAAGGCAAATGAGACCTTTGCCTTTGTGGGCAACGTGACGCACTA	1530
Qy	1501	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1531	CGCCCAGGTCTGGCTCAACATCTCCGCAGAGATCCGGAGCTTCCTGGAGCAGGGCAGGCT	1590
Qy	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620
Db	1591	GCAGCAGCATCTGCACTGGCTGCAGCAGTACGTGGCTGACCTCCGGCTACACCCTGAAGC	1650
Qy	1621	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1680
Db	1651	AATGAACCTGTCACTGGACGAGCTGCCCCCTGCTCTGCGCCTGGACTACTTTTCTCTGCC	1710
Qy	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGAT	1740
Db	1711	CAATGGCACAGCCCTTCTGCAGCAGCTAGACACAATAGACAATGCAGCCTGTGGCTGGAT	1770
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1800
Db	1771	CCAGTTCATGTCCAAGGTGAGTGTGGACATCTTCAAGGGGTTTCTTGATGAGGAGAGCAT	1830
Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCAGTGTGAT	1860
Db	1831	CGTGAACTACACTCTCAATCAGGCCTACCAGGACAATGTTACAGTATTTGCCAGCGTGAT	1890
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCCGCTCACGTGCACTACAAGATCCGCCAGAA	1920
Db	1891	TTTCCAGACACGGAAGGATGGTTCCCTCCCCCACATGTCCATTACAAGATTCCGCCAGAA	1950
Qy	1921	CTCCAGCTTCACCGAGAAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1980
Db	1951	CTCAAGCTTCACCGAGAAAAACCAACGAGATCCGTCGTGCTTACTGGCGTCCAGGGCCCAA	2010
Qy	1981	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Db	2011	CACTGGTGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATAGAACG	2070
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Db	2071	TGCCATCATCAACACGTTTGTGGGGCACGACGTGGTGAACCCGGCAACTACGTGCAGAT	2130
Qy	2101	GTTCCCTTACCCCTGCTACACACGCGATGACTTCCTGTTTGTCAATTGAGCACATGATGCC	2160
Db	2131	GTTCCCGTACCCCTGCTACACCCGTGACGACTTCCTGTTTGTCAATTGAGCACATGATGCC	2190
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Db	2191	ACTGTGCATGGTGATCTCCTGGGTTTACTCTGTGGCCATGACCATACAGCACATCGTGGC	2250
Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280
Db	2251	GGAGAAAGAGCATCGGCTAAAGGAGGTGATGAAGACGATGGGCCTGAACAACGCCGTGCA	2310
Qy	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2340

Db	2311	 CTGGGTGGCCTGGTTCATCACGGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCCCTGAC	2370
Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2400
Db	2371	CGCCATCCTCAAGTATGGCCAGGTCCTCATGCACAGCCACGTGCTCATCATATGGCTCTT	2430
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2460
Db	2431	CCTTGCTGTCTATGCTGTGGCCACTATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2490
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Db	2491	TAAGGCCAAGTTGGCCTCGGCCTGCGGCGGCATCATCTACTTCCTGAGCTACGTTCCTA	2550
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
Db	2551	CATGTATGTAGCAATCCGTGAGGAAGTAGCCACGATAAGATCACTGCCTTCGAGAAGTG	2610
Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640
Db	2611	CATTGCGTCCCTGATGTCCACAACAGCCTTCGGCCTGGGTTCGAAGTACTTTGCTCTGTA	2670
Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2700
Db	2671	TGAAGTGGCAGGTGTGGGCATCCAGTGGCACACGTTTCAGCCAGTCCCCAGTGAAGGGGA	2730
Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760
Db	2731	TGACTTCAACCTGCTCCTTGCTGTCACCATGCTGATGGTGGACACAGTGGTCTATGGCGT	2790
Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2791	ACTCACTTGGTACATTGAGGCTGTGCACCCAGGTATGTATGGGCTGCCCCGGCCCTGGTA	2850
Qy	2821	CTTCCCCTGCAGAACTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2851	CTTCCCCTACAGAACTCCTATTGGCTGGGCAGTGGGCGGACAGAGACCTGGGAGTGGAG	2910
Qy	2881	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2911	CTGGCCATGGGCACACGCACCCACGCCTCAGCGTTATGGAGGAGGACCAGGCCTGTGCCAT	2970
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACCCACCTGCCTCT	3000
Db	2971	GGAGAGCCGGCACTTCGAGGAGACTCGCGGTATGGAGGAGGAGCCCACCCACCTGCCTTT	3030
Qy	3001	GGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3031	GGTCGTCTGCGTGGACAAGCTCACCAAGGTCTATAAAAATGACAAGAAGCTGGCCTTAA	3090
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3091	CAAACCTGAGCCTCAATCTCTACGAGAACCAGGTGGTCTCTTCTTAGGCCATAACGGGGC	3150
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCCGC	3180

Db	3151	TGGCAAGACCACTACCATGTCTATCCTGACTGGACTGTTCCCACCCACGTCGGGCTCAGC	3210
Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3211	CACTATCTATGGCCACGACATCCGCACAGAGATGGATGAGATCCGTAAGAACCTGGGCAT	3270
Qy	3241	GTGCCCCGACGACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3271	GTGCCCACAGCACAACGTGCTCTTTGACCAGCTCACTGTGGAGGAACACCTCTGGTTCTA	3330
Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3331	CTCACGCCTCAAAGCATGGCACAAGAGGAGATCCGCAAAGAGATGGACAAGATGATCGA	3390
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3420
Db	3391	GGACCTGGAGCTCTCCAACAAGCGCCACTCGCTGGTACAGACGCTGTCTGGAGGCATGAA	3450
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3480
Db	3451	GCGCAAGCTTTCAGTAGCCATTGCCTTCGTGGGTGGCTCTAGAGCCATTATCTTAGATGA	3510
Qy	3481	GCCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3540
Db	3511	GCCCCACAGCTGGCGTGGACCCCTATGCTCGACGTGCCATCTGGGACCTCATTCTGAAGTA	3570
Qy	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3571	CAAGCCGGGTGCGACTATCCTCCTGTCCACCCATCACATGGATGAGGCCGACCTGCTGGG	3630
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3631	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAATGCTGCGGCTCTCCCCTCTTCCT	3690
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3720
Db	3691	CAAGGGTGCTTACGGCGATGGCTACCGCCTCACACTGGTCAAGCGGCCTGCGGAGCCTGG	3750
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGGCCCCGCTGAGCAGCTG	3780
Db	3751	CACCTCCCAAGAGCCAGGGATGGCTTCCAGCCCCCTCAGGTGCTCCTCAGCTGAGCAACTG	3810
Qy	3781	CTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3811	CTCAGAGATGCAAGTGTCCCAGTTCATCCGCAAGCATGTGGCTTCCTCCCTGCTGGTGTG	3870
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3871	AGACACGAGCACCGAGCTCTCCTACATCCTGCCCAGCGAGGCTGTCAAGAAAGGGGCCTT	3930
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3931	CGAGCGCCTCTTTCAGCAATTGGAGCACAGCCTGGACGCACTGCATCTGAGCAGTTTTGG	3990
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTCTGAGGAGGATCAGTCGCT	4020
Db	3991	GCTGATGGACACAACCCTGGAGGAGGTGTTCTCAAGGTGTCTGAAGAAGACCAGTCACT	4050

Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4051	GGAGAATAGTGAGGCCGATGTGAAGGAGTCCCGGAAGGATGCACTGCCTGGGGCAGAGGG	4110
Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4111	CCTGACGGCTGTGGAGAGTCAAGCAGGCAACCTGGCTCGGTGCTCAGAGCTGGCACAGTC	4170
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4200
Db	4171	CCAGGCTTCACTGCAGTCTGCATCTTCTGTGGGCTCCGCCCGTGGGGATGAGGGTGCTGG	4230
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4231	CTACACCGACGGCTACGGTGACTACCGTCCCCTCTTTGACAACTTGACAGACCCAGACAG	4290
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAA	4320
Db	4291	TGTCAGCTTACAAGAGGCTGAAATGGAGGCCCTGGCTCGGGTAGGCCAGGGCAGCCGCAA	4350
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4351	GCTAGAGGGCTGGTGGCTGAAGATGCGGCAGTTCCATGGGCTCCTGGTGAAGCGCTTCCA	4410
Qy	4381	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4411	CTGTGCTCGCCGGAACCTCAAAGCGCTCTGCTCCCAGATTCTGCTGCCTGCCTTCTTCGT	4470
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4471	CTGTGTGGCCATGACTGTGGCATGTCTGTCCCTGAGATCGGTGACCTGCCTCCACTGGT	4530
Qy	4501	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4531	CCTGTCGCCTTCTCAGTACCACAACCTATACCCAGCCCCGTGGCAACTTTATCCCCTATGC	4590
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCCAGCAGCT	4620
Db	4591	CAATGAGGAACGCCGCGAGTACCGATTACGGCTGTACCTGATGCCAGCCCCCAGCAGTT	4650
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4651	GGTGAGCACATTCCGGCTGCCCTCTGGTGTGGGTGCCACTTGTGTGCTCAAGTCTCCAGC	4710
Qy	4681	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4711	CAACGGCTCCCTGGGGCCCATGCTGAACCTTGAGCAGTGAGAGTCCCGCCTGCTGGCCGC	4770
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4771	ACGGTTCTTCGACAGTATGTGCCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4830
Qy	4801	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGA---	4857
Db	4831	CGTGCCACCCCCACCCTCGCCCGCCCCCTCCGACTCACCCCTGTCCCCGGATGAGGATTC	4890

QY	4858	CCTGCAGGCCTGGAACGTCTCCCTGCCGCCCCACCGCTGGGCCAGAAATGTGGACGTCCGG	4917
Db	4891	ACTGCTAGCCTGGAATACGTCCCTGCCCCCTACTGCTGGACCAGAGACGTGGACGTGGGC	4950
QY	4918	ACCCTCCCTGCCGCGCCTGGTACGGGAGCCCCGTCCGCTGCACCTGCTCTGCGCAGGGGCAC	4977
Db	4951	GCCTTCTCTGCCACGCCTGGTTCACGAGCCGGTCCGCTGTACCTGCTCTGCACAGGGGCAC	5010
QY	4978	CGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTTCACAGG	5037
Db	5011	GGGCTTCTCGTGCCCCAGCAGTGTGGGTGGGCACCCACCCAGATGAGAGTGGTTCACGGG	5070
QY	5038	CGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGA	5097
Db	5071	GGACATCCTGACTGACATCACCGGCCACAATGTTTCCGAGTACCTGCTCTTCACCTCTGA	5130
QY	5098	CCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCC	5157
Db	5131	CCGTTTCCGACTGCACCGCTATGGAGCCATCACCTTTGGTAATATCCAGAAGTCCATCCC	5190
QY	5158	AGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGGCTGC	5217
Db	5191	AGCACCCATTGGTACCCGGACCCCTCTCATGGTCCGGAAGATTGCAGTGCGGAGGGTGGC	5250
QY	5218	CCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTCAA	5277
Db	5251	CCAGGTGCTCTACAACAACAAGGGCTACCACAGCATGCCACCTACCTCAACAGCCTCAA	5310
QY	5278	CAACGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCAT	5337
Db	5311	CAATGCCATTCTGCGTGCAAACCTACCCAAAAGCAAGGGCAATCCAGCAGCCTACGGTAT	5370
QY	5338	CACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCT	5397
Db	5371	CACCGTCACCAACCACCCCATGAACAAGACCAGTGTAGCCTCTCCCTGGATTACCTACT	5430
QY	5398	GCAGGGCACGGATGTCGTTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGC	5457
Db	5431	GCAGGGCACAGACGTGGTCATCGCCATCTTCATCATTGTGGCCATGTCCTTCGTGCCGGC	5490
QY	5458	CAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGT	5517
Db	5491	CAGCTTCGTGGTCTTCCTTGTGGCCGAGAAATCCACCAAGGCCAAACACCTGCAGTTCGT	5550
QY	5518	CAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTA	5577
Db	5551	CAGCGGGTGCAACCTGTCATCTACTGGCTAGCCAACCTACGTGTGGGACATGCTCAATTA	5610
QY	5578	CCTGGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACAC	5637
Db	5611	CCTGGTCCCGGCCACCTGCTGCATCATCATCCTCTTCGTGTTTGACTTGCCGGCCTACAC	5670
QY	5638	GTCGCCCACCAACTTCCCTGCCGTCCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCAC	5697
Db	5671	GTCACCCACCAACTTCCCCGCGGTGCTCTCCTTGTTTCCTGCTCTATGGATGGTCCATCAC	5730
QY	5698	GCCCATCATGTACCCGGCCTCCTTCTGGTTTCGAGGTCCCCAGCTCCGCTACGTGTTCT	5757

Db	5731	ACCCATCATGTACCCGGCCTCCTTCTGGTTTGAGGTCCTAGCTCAGCCTACGTGTTCTCT	5790
Qy	5758	CATTGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCT	5817
Db	5791	CATCGTCATCAACCTCTTCATTGGCATCACGGCCACAGTGGCCACCTTCCTTCTGCAGCT	5850
Qy	5818	CTTCGAGCAGGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCAT	5877
Db	5851	CTTTGAGCATGACAAGGATCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCAT	5910
Qy	5878	TTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAA	5937
Db	5911	CTTCCCCAACTACAACCTGGGCCACGGACTCATGGAGATAGCCTACAACGAATACATCAA	5970
Qy	5938	CGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACAT	5997
Db	5971	CGAATACTATGCCAAGATCGGCCAGTTTGACAAGATGAAGTCCCCGTTTGAGTGGGACAT	6030
Qy	5998	TGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCAT	6057
Db	6031	TGTCACACGTGGACTGGTGGCCATGACAGTCGAGGGCTTCGTGGGATTCTTCTCACCAT	6090
Qy	6058	CATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGT	6117
Db	6091	CATGTGTCAATATAACTTCCTACGGCAGCCACAGCGTCTGCCTGTGTCTACTAAACCTGT	6150
Qy	6118	GGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAA	6177
Db	6151	GGAAGACGATGTAGACGTGGCCAGTGAGCGGCAGAGAGTGCTCCGTGGCGATGCTGACAA	6210
Qy	6178	TGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTAT	6237
Db	6211	TGACATGGTCAAGATCGAGAACCTGACTAAGGTGTACAAGTCTCGGAAGATCGGCCGCAT	6270
Qy	6238	CCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGG	6297
Db	6271	CCTGGCAGTGGACCGCCTTTGCCTGGGTGTGCGCCCCGAGAGTGCTTTGGGCTCCTCGG	6330
Qy	6298	CGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGAC	6357
Db	6331	GGTCAATGGTGCCGGGAAGACCAGCACCTTCAAGATGTTGACTGGAGATGAGAGCACAAAC	6390
Qy	6358	GGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCA	6417
Db	6391	AGGGGGCGAGGCCTTTGTCAATGGACACAGTGTGCTCAAGGACCTGCTCCAGGTTAGCA	6450
Qy	6418	GAGCCTCGGCTACTGCCCCAGTGTGACGCGCTGTTGACGAGCTCACGGCCCCGGGAGCA	6477
Db	6451	GAGCCTTGGCTACTGCCCCAGTTCGACGCCCTGTTGATGAGCTCACGGCTCGCGAACA	6510
Qy	6478	CCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAA	6537
Db	6511	CCTGCAGCTGTATACTCGGCTTCGAGGCATCCCCTGGAAGGATGAGGCGCAGGTGGTGAG	6570
Qy	6538	GTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAG	6597

Db	6571	GTGGGCCCCTGGAGAAGCTGGAGCTGACGAAGTGTGCAGACAAGCCAGCCGGTAGCTACAG	6630
Qy	6598	CGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCAT	6657
Db	6631	TGGGGGCAACAAACGGAAACTTTCCACAGCCATCGCTCTCATTGGGTACCTGCCTTCAT	6690
Qy	6658	CTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCT	6717
Db	6691	CTTTCTAGACGAGCCCACCACCTGGCATGGACCCTAAGGCCCGGCGCTTCCTGTGGAACCT	6750
Qy	6718	CATCCTCGACCTCATCAAGACAGGGCGTTCACTGGTGCTGACATCACACAGCATGGAGGA	6777
Db	6751	CATTCTGGACCTCATCAAGACAGGACGTTCACTGGTGCTGACCTCACACAGCATGGAGGA	6810
Qy	6778	GTGCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCTGCGGTGCCTGGG	6837
Db	6811	ATGCGAGGCTGTGTGCACACGGCTGGCCATCATGGTGAATGGACGGCTGCGCTGCCTGGG	6870
Qy	6838	CAGCATCCAGCACCTGAAGAACCGGTTTGAGATGGCTACATGATCACGGTGCGGACCAA	6897
Db	6871	GAGTATCCAGCACCTCAAGAACAGGTTTGGGACGGCTACATGATCACTGTAAGGACCAA	6930
Qy	6898	GAGCAGCCAGAGTGTGAAGGACGTGGTGCAGTTCTTCAACCGCAACTTCCCGGAAGCCAT	6957
Db	6931	AAGCAGCCAGAACGTGAAGGATGTGGTGCAGTTCTTCAACCGCAACTTCCAGAGGCCAT	6990
Qy	6958	GCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCT	7017
Db	6991	GCTCAAGGAACGCCACCATACGAAGGTGCAGTATCAGCTCAAGTCGGAGCACATCTCGCT	7050
Qy	7018	GGCCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTC	7077
Db	7051	GGCTCAGGTGTTTCAGCAAGATGGAGCAGGTGGTGGTGCTACTGGGCATCGAGGACTACTC	7110
Qy	7078	GGTCAGCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGACAA	7137
Db	7111	AGTCAGCCAGACCACTCTGGATAACGTGTTTGTGAACCTTCGCCAAGAAGCAAAGTGACAA	7170
Qy	7138	CCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCCTCTCGGCTGCTTGCT	7197
Db	7171	TGTGGAGCAGCAAGAGGCTGA---GCCATCCACCTTGCCGTCCCCCTTG---GACTACT	7224
Qy	7198	CAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACCTTGTGGCAGACGAGCC	7257
Db	7225	TAGCCTGCTGCGGCCCCGCCCTGCACCCACAGAGCTCCGGGCACCTGCTGGCCGATGAGCC	7284
Qy	7258	CGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCAGCT	7317
Db	7285	TGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAAGAGCGGGCCAGCT	7344
Qy	7318	GTCCTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTC	7377
Db	7345	CTCCTTCAACACCGATACGCTCTGCTGACGTTCAAGAGTCACATCAGGGATG-----	7396
Qy	7378	CACTGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCAGTGCC	7437
Db	7397	-----CAGCTGTTTGGGGCAGAAGTCAGGCGGTGGCCGTAGCCCCAGTCACACA	7445

Qy	7438	TGCCAGGGCCTGGAGTGG-AGGTTTCAGGACCAAGGGGCTTCTGGTCCCTCCAGCCCCCTGTA	7496
Db	7446	TGCCAGGCCCTGGAAAGGCAGGTTTCAGGACCAAAGGGCTCCCGCCCTCC-----	7494
Qy	7497	CTCGGCCATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCG	7556
Db	7495	-----TCCCAACTACCATCCTCCCGATCGTGCCAAAGGCTGGGCTG	7536
Qy	7557	GCCC-GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCC	7615
Db	7537	GCCCTGGGCTGCACACACCCTCACCTGCTTTGCCTTAAAGCCTTGGGTCCTGGCCCAGC	7596
Qy	7616	CCTCGCCCCCTGCCTGGCACTGCTCACC-GCCCAAGGCGACGCCGGCTGGACCAGGCA-CT	7673
Db	7597	CCCTTACCCTGCCAGCACCATCCACCTTCCAGGGTGACATGGGCTGCCCCAAGTATCC	7656
Qy	7674	GCTGGCCTTTCTCCTGCCCGGCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGAT	7733
Db	7657	TGTGACCCTTCTCTGCAGCGGCCACCAGTCTACCCAGGCCAGCATCTTGACAGATGTCT	7716
Qy	7734	GCCGAGAGCGGGCTGTGGGCGGAGCTGGGTCAG-TCCCGTATTTATTTTGCTTTGAGAAG	7792
Db	7717	TTCATGAAAAGACTGCAGTTGGGGAGGTGGCAGCTTGCTACTTATTTTGCTTTAAGA--	7774
Qy	7793	AGGCTCCTCTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCT	7852
Db	7775	----GCCTCCCTCACTCTGCTGTGTGAAGAAGTTAGGCTACCATGGGAAGCCATGAATG	7830
Qy	7853	TGGGCCAGCTGGCAGG-----TGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCA	7905
Db	7831	TGGCTGCCTCAGCCCTGGTGGAAATGGCAGGAACGGAGAAGCTGGGCTTGCTGGCTAGGTG	7890
Qy	7906	AGGGGCCA-----GACCCCCCACCACCCAGCTGCCATCGCTCTCCACCCAGCTTGGC	7960
Db	7891	AGGGGCCACTGCTCCCTCCCTGCCCCCTCAAGCTGCCTTTGCTCTCCCGCTCAGCTTGG-	7949
Qy	7961	CCCCTGCCCGCCACCTCCCTGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTT	8020
Db	7950	-CCCTTCCTGCCACCCATGTGGGAGTAGGACCTTGATATAGCACACAGATGTTTGTTTT	8008
Qy	8021	AAATAAATAAACAAAATG	8038
Db	8009	CAATAAATAAGCAAAAAG	8026

RESULT 10

AAD27271

ID AAD27271 standard; cDNA; 5540 BP.

XX

AC AAD27271;

XX

DT 09-APR-2002 (first entry)

XX

DE Human transporter and ion channel-18 (TRICH-18) cDNA.

XX

KW Human; transporter and ion channel-18; TRICH-18; neuroprotective; asthma;

KW nootropic; cytostatic; cardiovascular; immunosuppressive; cardiomyopathy;
KW antiinflammatory; protein therapy; akinesia; cystic fibrosis; leukaemia;
KW Bell's palsy; amyotrophic lateral sclerosis; Alzheimer's disease; cancer;
KW amnesia; dementia; myocarditis; Duchenne's muscular dystrophy; AIDS;
KW Acquired Immune Deficiency Syndrome; Addison's disease; allergy; angina;
KW cell proliferative disorder; psoriasis; cardiac disease; hypertension;
KW bradyarrhythmia; gene expression; drug screening; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 36. .5351

FT /*tag= a

FT /product= "Human TRICH-18 protein"

XX

PN WO200192304-A2.

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PD 06-DEC-2001.

XX

PF 25-MAY-2001; 2001WO-US017065.

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PR 26-MAY-2000; 2000US-0208424P.

PR 01-JUN-2000; 2000US-0209001P.

PR 08-JUN-2000; 2000US-0210588P.

PR 16-JUN-2000; 2000US-0212335P.

PR 22-JUN-2000; 2000US-0213747P.

PR 29-JUN-2000; 2000US-0215391P.

XX

PA (INCY-) INCYTE GENOMICS INC.

XX

PI Thornton M, Walia NK, Yue H, Nguyen DB, Lai P, Gandhi AR;

PI Tribouley CM, Yao MG, Ramkumar J, Au-Young J, Lu Y, Tang YT;

PI Azimzai Y, Bruns CM, Griffin JA, Yang J, Sanjanwala MS, Raumann BE;

PI Lee EA, Hafalia A, Baughn MR, Green BD, Khan FA, Kearney L;

PI Elliot VS, Seilhamer JJ, Policky JL, Borowsky ML, Burford N, Ding L;

PI Lu DAM, Hillman JL;

XX

DR WPI; 2002-122055/16.

DR P-PSDB; AAE16781.

XX

PT New human transporters and ion channels (TRICH) polypeptides useful for
PT diagnosing, treating or preventing disorders associated with aberrant
PT expression of TRICH.

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PS Claim 11; Page 201-202; 210pp; English.

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CC The invention relates to human transporters and ion channels (TRICH)
CC polypeptides and their cDNA molecules. The nucleic acid and polypeptide
CC sequences are useful in the diagnosis, treatment, and prevention of
CC disorders associated with transport (akinesia, cystic fibrosis, Bell's
CC palsy, amyotrophic lateral sclerosis); neurological (Alzheimer's disease,
CC amnesia, dementia); muscle (cardiomyopathy, myocarditis, Duchenne's
CC muscular dystrophy); immunological (AIDS, Addison's disease, allergies,
CC asthma); cell proliferative disorders (cancers, leukaemia, psoriasis);
CC cardiac disease (angina, hypertension, or bradyarrhythmia) and in the
CC assessment of the effects of exogenous compounds on the expression of
CC nucleic acid and amino acid sequences of transporters and ion channels.

CC The polynucleotides may be used to detect and quantify gene expression in
CC biopsied tissues in which TRICH expression may be correlated with a
CC disease, to generate hybridization probes for mapping naturally occurring
CC genomic sequence, and in drug screening. The present sequence is human
CC TRICH-18 cDNA

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SQ Sequence 5540 BP; 1032 A; 1823 C; 1650 G; 1035 T; 0 U; 0 Other;

Query Match 68.9%; Score 5536.8; DB 6; Length 5540;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5538; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1995	TCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACA	2054
Db	1	TCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACA	60
Qy	2055	CTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGATGTTCCCTACCCCT	2114
Db	61	CTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGATGTTCCCTACCCCT	120
Qy	2115	GCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCCGCTGTGCATGGTGA	2174
Db	121	GCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCCGCTGTGCATGGTGA	180
Qy	2175	TCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACC	2234
Db	181	TCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACC	240
Qy	2235	GGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGT	2294
Db	241	GGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGT	300
Qy	2295	TCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCACCGCCATCCTGAAGT	2354
Db	301	TCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCACCGCCATCCTGAAGT	360
Qy	2355	ACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACG	2414
Db	361	ACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACG	420
Qy	2415	CGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGG	2474
Db	421	CGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGG	480
Qy	2475	CCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGA	2534
Db	481	CCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGA	540
Qy	2535	TCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCA	2594
Db	541	TCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCA	600
Qy	2595	TGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCG	2654
Db	601	TGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCG	660
Qy	2655	TGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGACGACTTCAACTTGC	2714

Db	661	 TGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGACGACTTCAACTTGC	720
Qy	2715	TCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACA	2774
Db	721	 TCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACA	780
Qy	2775	TTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTACTTCCCCTGCAGA	2834
Db	781	 TTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTACTTCCCCTGCAGA	840
Qy	2835	AGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCAC	2894
Db	841	 AGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCAC	900
Qy	2895	GCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCT	2954
Db	901	 GCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCT	960
Qy	2955	TTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCTGGTTGTCTGCGTGG	3014
Db	961	 TTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCTGGTTGTCTGCGTGG	1020
Qy	3015	ACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGA	3074
Db	1021	 ACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGA	1080
Qy	3075	ACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCA	3134
Db	1081	 ACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCA	1140
Qy	3135	CCATGTCCATCCTGACCGGCTGTTCCCTCCAACGTGCGGTTCCGCCACCATCTACGGGC	3194
Db	1141	 CCATGTCCATCCTGACCGGCTGTTCCCTCCAACGTGCGGTTCCGCCACCATCTACGGGC	1200
Qy	3195	ACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCATGTGCCCGCAGCACA	3254
Db	1201	 ACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCATGTGCCCGCAGCACA	1260
Qy	3255	ATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGA	3314
Db	1261	 ATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGA	1320
Qy	3315	GCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCT	3374
Db	1321	 GCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCT	1380
Qy	3375	CCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAAGCGCAAGCTGTCCG	3434
Db	1381	 CCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAAGCGCAAGCTGTCCG	1440
Qy	3435	TGGCCATCGCCTTCGTGGGCGGCTCTCGGCCATCATCCTGGACGAGCCACGGCGGGCG	3494
Db	1441	 TGGCCATCGCCTTCGTGGGCGGCTCTCGGCCATCATCCTGGACGAGCCACGGCGGGCG	1500
Qy	3495	TGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGCA	3554

Db	1501	TGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGCA	1560
Qy	3555	CCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCA	3614
Db	1561	CCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCA	1620
Qy	3615	TCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCTCAAGGGCACCTATG	3674
Db	1621	TCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCTCAAGGGCACCTATG	1680
Qy	3675	GCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCGAGCCGGGGGGCCCCAAGAGC	3734
Db	1681	GCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCGAGCCGGGGGGCCCCAAGAGC	1740
Qy	3735	CAGGGCTGGCATCCAGCCCCCAGGTGCGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGG	3794
Db	1741	CAGGGCTGGCATCCAGCCCCCAGGTGCGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGG	1800
Qy	3795	TGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGG	3854
Db	1801	TGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGG	1860
Qy	3855	AGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTTCGAGCGCCTCTTCC	3914
Db	1861	AGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTTCGAGCGCCTCTTCC	1920
Qy	3915	AGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGGGCTGATGGACACGA	3974
Db	1921	AGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGGGCTGATGGACACGA	1980
Qy	3975	CCCTGGAGGAAGTGTTCTCAAGGTGTCGGAGGAGGATCAGTCGCTGGAGAACAGTGAGG	4034
Db	1981	CCCTGGAGGAAGTGTTCTCAAGGTGTCGGAGGAGGATCAGTCGCTGGAGAACAGTGAGG	2040
Qy	4035	CCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGGCCCCGGCGTCTGGGG	4094
Db	2041	CCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGGCCCCGGCGTCTGGGG	2100
Qy	4095	AGGGTCACGCTGGCAATCTGGCCCCGGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGC	4154
Db	2101	AGGGTCACGCTGGCAATCTGGCCCCGGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGC	2160
Qy	4155	AGTCGGCGTCATCTGTGGGCTCTGCCCCGTGGCGACGAGGGAGCTGGCTACACCGACGTCT	4214
Db	2161	AGTCGGCGTCATCTGTGGGCTCTGCCCCGTGGCGACGAGGGAGCTGGCTACACCGACGTCT	2220
Qy	4215	ATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAATGTGAGCCTGCAAG	4274
Db	2221	ATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAATGTGAGCCTGCAAG	2280
Qy	4275	AGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAAGCTGGACGGCGGGT	4334
Db	2281	AGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAAGCTGGACGGCGGGT	2340
Qy	4335	GGCTGAAGGTGCGCCAGTTCACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCCGCCGCA	4394
Db	2341	GGCTGAAGGTGCGCCAGTTCACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCCGCCGCA	2400

Qy	4395	ACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGGCCATGA	4454
Db	2401	ACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGGCCATGA	2460
Qy	4455	CCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGTCCTGTACCTTCCC	4514
Db	2461	CCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGTCCTGTACCTTCCC	2520
Qy	4515	AGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGCCAACGAGGAGCGCC	4574
Db	2521	AGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGCCAACGAGGAGCGCC	2580
Qy	4575	GCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCAGCAGCTCGTGAGCACGTTCC	4634
Db	2581	GCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCAGCAGCTCGTGAGCACGTTCC	2640
Qy	4635	GGCTGCCGTCGGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGG	4694
Db	2641	GGCTGCCGTCGGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGG	2700
Qy	4695	GGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACA	4754
Db	2701	GGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACA	2760
Qy	4755	GCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCAC	4814
Db	2761	GCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCAC	2820
Qy	4815	CCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCTGCAGGCCTGGAACG	4874
Db	2821	CCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCTGCAGGCCTGGAACG	2880
Qy	4875	TCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTGGGCACCTCCCTGCCGCGCC	4934
Db	2881	TCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTGGGCACCTCCCTGCCGCGCC	2940
Qy	4935	TGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GGCTTCTCCTGCCCCA	4994
Db	2941	TGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GGCTTCTCCTGCCCCA	3000
Qy	4995	GCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACA	5054
Db	3001	GCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACA	3060
Qy	5055	TCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACC	5114
Db	3061	TCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACC	3120
Qy	5115	GGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCA	5174
Db	3121	GGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCA	3180
Qy	5175	GGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCAGGTTTTCTACAACA	5234
Db	3181	GGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCAGGTTTTCTACAACA	3240

Qy	5235	ACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTG	5294
Db	3241	ACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTG	3300
Qy	5295	CCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACC	5354
Db	3301	CCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACC	3360
Qy	5355	CCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGGGCACGGATGTCG	5414
Db	3361	CCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGGGCACGGATGTCG	3420
Qy	5415	TCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCC	5474
Db	3421	TCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCC	3480
Qy	5475	TCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGTCAGCGGCTGCAACCCCA	5534
Db	3481	TCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGTCAGCGGCTGCAACCCCA	3540
Qy	5535	TCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCT	5594
Db	3541	TCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCT	3600
Qy	5595	GCTGTGTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTCGCCCACCAACTTCC	5654
Db	3601	GCTGTGTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTCGCCCACCAACTTCC	3660
Qy	5655	CTGCCGTCCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGG	5714
Db	3661	CTGCCGTCCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGG	3720
Qy	5715	CCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCATTGTCATCAATCTCT	5774
Db	3721	CCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCATTGTCATCAATCTCT	3780
Qy	5775	TCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGG	5834
Db	3781	TCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGG	3840
Qy	5835	ACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACC	5894
Db	3841	ACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACC	3900
Qy	5895	TGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGA	5954
Db	3901	TGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGA	3960
Qy	5955	TTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGG	6014
Db	3961	TTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGG	4020
Qy	6015	TGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAAC	6074
Db	4021	TGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAAC	4080
Qy	6075	TCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACG	6134

Db	4081	 TCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACG	4140
Qy	6135	TGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGGAGACGCCGACAATGACATGGTCAAGATTG	6194
Db	4141	TGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGGAGACGCCGACAATGACATGGTCAAGATTG	4200
Qy	6195	AGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCC	6254
Db	4201	AGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCC	4260
Qy	6255	TGTGCCTGGGTGTGCGTCTCGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCA	6314
Db	4261	TGTGCCTGGGTGTGCGTCTCGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCA	4320
Qy	6315	AGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTCG	6374
Db	4321	AGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTCG	4380
Qy	6375	TCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCC	6434
Db	4381	TCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCC	4440
Qy	6435	CGCAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCGGGAGCACCTGCAGCTGTACACGC	6494
Db	4441	CGCAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCGGGAGCACCTGCAGCTGTACACGC	4500
Qy	6495	GGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGC	6554
Db	4501	GGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGC	4560
Qy	6555	TGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGA	6614
Db	4561	TGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGA	4620
Qy	6615	AGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCA	6674
Db	4621	AGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCA	4680
Qy	6675	CCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCCTCGACCTCATCA	6734
Db	4681	CCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCCTCGACCTCATCA	4740
Qy	6735	AGACAGGGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCA	6794
Db	4741	AGACAGGGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCA	4800
Qy	6795	CGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCGAGCATCCAGCACCTGA	6854
Db	4801	CGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCGAGCATCCAGCACCTGA	4860
Qy	6855	AGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTGA	6914
Db	4861	AGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTGA	4920
Qy	6915	AGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACC	6974

Db 4921 AGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACC 4980
 Qy 6975 ACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAGCA 7034
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 4981 ACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAGCA 5040
 Qy 7035 AGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTTCAGCCAGACCACAC 7094
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 5041 AGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTTCAGCCAGACCACAC 5100
 Qy 7095 TGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGA 7154
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 5101 TGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGA 5160
 Qy 7155 CGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCC 7214
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 5161 CGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCC 5220
 Qy 7215 GGTCTGCCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGAGGACCTGGACACGG 7274
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 5221 GGTCTGCCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGAGGACCTGGACACGG 5280
 Qy 7275 AGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGGCCAGCTGTCTTCAACACGGACA 7334
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 5281 AGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGGCCAGCTGTCTTCAACACGGACA 5340
 Qy 7335 CGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTGACCACCCAGAGC 7394
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 5341 CGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTGACCACCCAGAGC 5400
 Qy 7395 TGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCTGCCAGGGCCTGGAGTG 7454
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 5401 TGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCTGCCAGGGCCTGGAGTG 5460
 Qy 7455 GAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCCTGTACTCGGCCATGCCCTGCGG 7514
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 5461 GAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCCTGTACTCGGCCATGTCTGCGG 5520
 Qy 7515 TCACTGCGGTTGCCGCCCCCT 7534
 ||||||||||||||||
 Db 5521 TCACTGCGGTTGCCGCCCCCT 5540

RESULT 11

AAS62249

ID AAS62249 standard; cDNA; 2740 BP.

XX

AC AAS62249;

XX

DT 14-FEB-2002 (first entry)

XX

DE cDNA sequence #36 encoding novel human secreted protein.

XX

KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;

KW immune deficiency disorder; blood disorder; inflammatory disorder;

KW infectious disorder; gene therapy; antimicrobial; hepatotropic;

KW immunosuppressive; antirheumatic; ss.

XX
 OS Homo sapiens.
 XX
 PN WO200177291-A2.
 XX
 PD 18-OCT-2001.
 XX
 PF 29-MAR-2001; 2001WO-US010485.
 XX
 PR 06-APR-2000; 2000US-0195604P.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
 PI Gulukota K, Graham JR;
 XX
 DR WPI; 2002-010900/01.
 XX
 PT New polynucleotides encoding secreted proteins useful for treating e.g.
 PT asthma, HIV and Crohn's disease.
 XX
 PS Claim 1; Page 91; 391pp; English.
 XX
 CC The present invention relates to the isolation of novel cDNA sequences
 CC which encode human secreted proteins. The cDNA sequences have been
 CC derived from a variety of human tissues. The invention also provides a
 CC method for producing proteins from these polynucleotide sequences. The
 CC proteins are useful for identifying compounds that modulate their
 CC activity and production, and the cell is also useful for identifying
 CC compounds that modulate expression of the polynucleotide sequences
 CC encoding the secreted proteins. The sequences of the invention are useful
 CC for treating diseases such as hyperproliferative disorders (e.g. cancer),
 CC immune deficiency disorders (e.g. severe combined immunodeficiency
 CC (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders
 CC (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and
 CC infectious disorders (e.g. hepatitis). The polynucleotide sequences of
 CC the invention are also useful in gene therapy. AAS62214-AAS62838
 CC represent the cDNA sequences of the invention that encode for novel human
 CC secreted proteins
 XX
 SQ Sequence 2740 BP; 525 A; 892 C; 804 G; 519 T; 0 U; 0 Other;

Query Match 34.0%; Score 2736.8; DB 6; Length 2740;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2738; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5301 TGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGA 5360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 TGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGA 60

 Qy 5361 ATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGGGCACGGATGTCGTCATCG 5420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 ATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGGGCACGGATGTCGTCATCG 120

 Qy 5421 CCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGG 5480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 CCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGG 180

Qy	5481	CCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGTCAGCGGCTGCAACCCCATCATCT	5540
Db	181	CCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGTCAGCGGCTGCAACCCCATCATCT	240
Qy	5541	ACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCTGCTGTG	5600
Db	241	ACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCTGCTGTG	300
Qy	5601	TCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTCGCCCACCAACTTCCCTGCCG	5660
Db	301	TCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTCGCCCACCAACTTCCCTGCCG	360
Qy	5661	TCCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGGCCTCCT	5720
Db	361	TCCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGGCCTCCT	420
Qy	5721	TCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCATTGTTCATCAATCTCTTCATCG	5780
Db	421	TCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCATTGTTCATCAATCTCTTCATCG	480
Qy	5781	GCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGGACCTGA	5840
Db	481	GCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGGACCTGA	540
Qy	5841	AGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTGGGCC	5900
Db	541	AGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTGGGCC	600
Qy	5901	ACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATTGGCC	5960
Db	601	ACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATTGGCC	660
Qy	5961	AGTTTGACAAGATGAAGTCCCCGTTGAGTGGGACATTGTACCCGCGGACTGGTGGCCA	6020
Db	661	AGTTTGACAAGATGAAGTCCCCGTTGAGTGGGACATTGTACCCGCGGACTGGTGGCCA	720
Qy	6021	TGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTCCTGC	6080
Db	721	TGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTCCTGC	780
Qy	6081	GGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTGGCCA	6140
Db	781	GGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTGGCCA	840
Qy	6141	GTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAGAACC	6200
Db	841	GTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAGAACC	900
Qy	6201	TGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCC	6260
Db	901	TGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCC	960
Qy	6261	TGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCA	6320
Db	961	TGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCA	1020

Qy	6321	GCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTCGTCAATG	6380
Db	1021	GCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTCGTCAATG	1080
Qy	6381	GACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCGAGT	6440
Db	1081	GACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCGAGT	1140
Qy	6441	GTGACGCGCTGTTTCGACGAGCTCACGGCCCGGAGCACCTGCAGCTGTACACGCGGCTGC	6500
Db	1141	GTGACGCGCTGTTTCGACGAGCTCACGGCCCGGAGCACCTGCAGCTGTACACGCGGCTGC	1200
Qy	6501	GTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGC	6560
Db	1201	GTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGC	1260
Qy	6561	TGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCT	6620
Db	1261	TGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCT	1320
Qy	6621	CCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCACCACAG	6680
Db	1321	CCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCACCACAG	1380
Qy	6681	GCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCCTCGACCTCATCAAGACAG	6740
Db	1381	GCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCCTCGACCTCATCAAGACAG	1440
Qy	6741	GGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCACGCGGC	6800
Db	1441	GGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCACGCGGC	1500
Qy	6801	TGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACC	6860
Db	1501	TGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACC	1560
Qy	6861	GGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTGAAGGACG	6920
Db	1561	GGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTGAAGGACG	1620
Qy	6921	TGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACCACACAA	6980
Db	1621	TGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACCACACAA	1680
Qy	6981	AGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAGCAAGATGG	7040
Db	1681	AGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAGCAAGATGG	1740
Qy	7041	AGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTTCAGCCAGACCACACTGGACA	7100
Db	1741	AGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTTCAGCCAGACCACACTGGACA	1800
Qy	7101	ATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGC	7160
Db	1801	ATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGC	1860
Qy	7161	CGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTG	7220

Db	1861	CGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTG	1920
Qy	7221	CCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGAGGACCTGGACACGGAGGACG	7280
Db	1921	CCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGAGGACCTGGACACGGAGGACG	1980
Qy	7281	AGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCCTTCAACACGGACACGCTCT	7340
Db	1981	AGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCCTTCAACACGGACACGCTCT	2040
Qy	7341	GCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTGACCACCCAGAGCTGGGCC	7400
Db	2041	GCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTGACCACCCAGAGCTGGGCC	2100
Qy	7401	AGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCCTGCCAGGGCCTGGAGTGGAGGTT	7460
Db	2101	AGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCCTGCCAGGGCCTGGAGTGGAGGTT	2160
Qy	7461	CAGGACCAAGGGGCTTCTGGTCCCTCCAGCCCCTGTACTCGGCCATGCCCTGCGGTCACTG	7520
Db	2161	CAGGACCAAGGGGCTTCTGGTCCCTCCAGCCCCTGTACTCGGCCATGCCCTGCGGTCACTG	2220
Qy	7521	CGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCCGGGCTGCGTACACCCTTGCC	7580
Db	2221	CGGTTGCCGCCCCCTAATTGTGCCAAAGGTTGACCCGGCCCGGGCTGCGTACACCCTTGCC	2280
Qy	7581	CTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCCGCCCCCTCGCCCCTGCCTGGCACTGCTCA	7640
Db	2281	CTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCCGCCCCCTCGCCCATGCCTGGCACTGCTCA	2340
Qy	7641	CCGCCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCCTTTCTCCTGCCCGGCCTCGG	7700
Db	2341	CCGCCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCCTTTCTCCTGCCCGGCCTCGG	2400
Qy	7701	AACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGAGCGGGCTGTGGGCGGAGCTG	7760
Db	2401	AACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGAGCGGGCTGTGGGCGGAGCTG	2460
Qy	7761	GGTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCTCTGGCCCTGCTCTCCTGCAG	7820
Db	2461	GGTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCTCTGGCCCTGCTCTCCTGCAG	2520
Qy	7821	GGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAGCTGGCAGGTGGCAGGAATGG	7880
Db	2521	GGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAGCTGGCAGGTGGCAGGAATGG	2580
Qy	7881	AGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCCCCCCAACCCCCAGCTGCCATC	7940
Db	2581	AGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCCCCCCAACCCCCAGCTGCCATC	2640
Qy	7941	GCTCTCCACCCAGCTTGGCCCCCTGCCCGCCACCTCCCTGGGAGCCGGGCTGTACAT	8000
Db	2641	GCTCTCCACCCAGCTTGGCCCCCTGCCCGCCACCTCCCTGGGAGCCGGGCTGTACAT	2700
Qy	8001	AGCGCACAGATGTTTGTTTTAAATAAAATAAACAAAATGTC	8040

Db 2701 AGCGCACAGATGTTTGTTTTAAATAAAATAAACAAAATGTC 2740

RESULT 12

AAZ94746

ID AAZ94746 standard; cDNA; 7323 BP.

XX

AC AAZ94746;

XX

DT 01-AUG-2000 (first entry)

XX

DE Human ATP binding cassette ABCA5 cDNA.

XX

KW ABCA5; ATP binding cassette; human; cholesterol; lipid disorder;

KW atherosclerosis; lipid disorder; dyslipidemia; psoriasis;

KW lupus erythematosus; diagnosis; gene therapy; chromosome 17q21-25; ss.

XX

OS Homo sapiens.

XX

PN WO200018912-A2.

XX

PD 06-APR-2000.

XX

PF 21-SEP-1999; 99WO-EP006991.

XX

PR 25-SEP-1998; 98US-0101706P.

XX

PA (FARB) BAYER AG.

XX

PI Schmitz G, Klucken J;

XX

DR WPI; 2000-293151/25.

XX

PT Adenosine triphosphate binding proteins useful for identifying agents for
PT treating atherosclerosis and other inflammatory disorders.

XX

PS Claim 9; Page 126-129; 154pp; English.

XX

CC The present sequence is that of human ATP binding cassette subfamily A
CC protein ABCA5 cDNA. The cDNA was identified using a differential display
CC method in which monocytes from peripheral blood were subjected to
CC macrophage differentiation and cholesterol loading with acetylated low
CC density lipoproteins and subsequent deloading with high density
CC lipoprotein (HDL3) to identify cholesterol sensitive genes. The gene maps
CC to chromosome 17q21-25. The invention provides cholesterol-sensitive ABC
CC genes (see AAZ94734-63). These genes, and polypeptides encoded by them,
CC can be used for diagnostic and therapeutic applications, and for
CC biochemical or cell-based assays to screen for pharmacologically active
CC modulator compounds useful for the treatment of lipid disorders,
CC atherosclerosis or other inflammatory diseases such as psoriasis and
CC lupus erythematosus

XX

SQ Sequence 7323 BP; 1796 A; 1976 C; 1853 G; 1698 T; 0 U; 0 Other;

Query Match 12.3%; Score 991.4; DB 3; Length 7323;

Best Local Similarity 52.9%; Pred. No. 2.3e-154;

Matches 2802; Conservative 0; Mismatches 2261; Indels 234; Gaps 22;

[illegible]

Qy	2713	GCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGGCATCCTCACGTGGTA	2772
Db	2595	CCTGCTGTCCATGCAGATGATGCTCCTTGATGCTGCTGTCTATGGCTTACTCGCTTGGTA	2654
Qy	2773	CATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTACTTCCCACTGCA	2832
Db	2655	CCTTGATCAGGTGTTTCCAGGAGACTATGGAACCCCACTTCCTTGGTACTTTCTTCTACA	2714
Qy	2833	GAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGC	2892
Db	2715	AGAGTCGTATTGGCTTGGCGGTGAAGGTGTTCAACCAGAGAAGAAAGAGCCCTGGAAAA	2774
Qy	2893	ACGCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCG	2952
Db	2775	GACCGAGCCCCTAACAGAGGAAACGGAGGATCCAGAGCACCCAGAAGGAATACACGACTC	2834
Qy	2953	CTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCTGGTTGTCTGCGT	3012
Db	2835	CTT-----CTTTGAACGTGAGCATCCAGGGTGGGTTCTTGGGGTATGCGT	2879
Qy	3013	GGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCT	3072
Db	2880	GAAGAATCTGGTAAAGATTTTGTAGCCCTCCGGCCGGCCAGCTGTGGACCGTCTGAACAT	2939
Qy	3073	GAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCAC	3132
Db	2940	CACCTTCTACGAGAACCAGATCACCGCATTCCTGGGCCACAATGGAGCTGGGAAAACCAC	2999
Qy	3133	CACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTGCGGTTCCGCCACCATCTACGG	3192
Db	3000	CACCTTGTCCATCCTGACGGGTCTGTTGCCACCAACCTCTGGGACTGTGCTCGTTGGGGG	3059
Qy	3193	GCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCATGTGCCCCGAGCA	3252
Db	3060	AAGGGACATTGAAACCAGCCTGGATGCAGTCCGGCAGAGCCTTGGCATGTGTCCACAGCA	3119
Qy	3253	CAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAA	3312
Db	3120	CAACATCCTGTTCCACCACCTCACGGTGGCTGAGCACATGCTGTTCTATGCCAGCTGAA	3179
Qy	3313	GAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCT	3372
Db	3180	AGGAAAGTCCCAGGAGGAGGCCAGCTGGAGATGGAAGCCATGTTGGAGGACACAGGCCT	3239
Qy	3373	CTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAAGCGCAAGCTGTC	3432
Db	3240	CCACCACAAGCGGAATGAAGAGGCTCAGGACCTATCAGGTGGCATGCAGAGAAAGCTGTC	3299
Qy	3433	CGTGGCCATCGCCTTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGG	3492
Db	3300	GGTTGCCATTGCCTTTGTGGGAGATGCCAAGGTGGTGATTCTGGACGAACCCACCTCTGG	3359
Qy	3493	CGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCG	3552
Db	3360	GGTGGACCCCTTACTCGAGACGCTCAATCTGGGATCTGCTCCTGAAGTATCGCTCAGGCAG	3419
Qy	3553	CACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGC	3612

Db	3420	AACCATCATCATGTCCACTCACCACATGGACGAGGCCGACCTCCTTGGGGACCGCATTGC	3479
Qy	3613	CATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCTCAAGGGCACCTA	3672
Db	3480	CATCATTGCCCAGGGAAGGCTCTACTGCTCAGGCACCCCACTCTTCCTGAAGAACTGCTT	3539
Qy	3673	TGGCGACGGGTACCGCCTCACGCTGGT---CAAGCGGCCCGCCGAGCCGGGGGGCCCCCA	3729
Db	3540	TGGCACAGGCTTGTACTTAACCTTGGTGCGCAAGATGAAAAACATCCAGAGCCAAAGGAA	3599
Qy	3730	AGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTGCTCCGAGCT	3789
Db	3600	AGGCAGTGAGGGGACCTGCAGCTGCTCGTCTAAGGGTTTCTCCACCACGTGTCCAGCCCA	3659
Qy	3790	CCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAG	3849
Db	3660	C-----GTCGATGACCTAACTCCAGAACAAGTCCTGGATGGGGATGTAAATGAGCTGATG	3714
Qy	3850	CACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTTCGAGCGCCT	3909
Db	3715	GATGTAGTTCTCCACCATGTTCCAGAGGCA-----	3744
Qy	3910	CTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGGGCTGATGGA	3969
Db	3745	-----AAGCTGGTGGAGTGCAATTGGTCAAGAACTTATCTTCCTTCTTCCAAATAAGAA	3797
Qy	3970	CACGACCCTGGAGGAAGTGTTCCCTCAAGGTGTCGGAGGAGGATCAGTCGCTGGAGAACAG	4029
Db	3798	CTTCAAGCACAGAGCATATGCCAGCCTTTTCAGAGAGCTGGAGGAGACGCTGGCTGACCT	3857
Qy	4030	TGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGGCCCCGGCGTC	4089
Db	3858	TGGTCTC-----AGCAGTTTTGGAATT-----TCTGACACTCCCCTGGAAGAGATTT	3904
Qy	4090	TGGGGAGGGTCACGCTGGCAATCTGGCCCCGGTGCTCGGAGCTGACCCAGTCGCAGGCATC	4149
Db	3905	TTCTGAAGGTCACGGAGGATTCTGATTCAAGACCTCTGTTTGCGGGTGGCGCTCAGCAGA	3964
Qy	4150	GCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCGTGGCGACGAGGGAGCTGGCTACACCGA	4209
Db	3965	AAAGAGAAAACGTCAACCCCCGACACCCCTGCTTGGGTCCCAGAGAGAAGGCTGGACAGA	4024
Qy	4210	CGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAATGTCAGCCT	4269
Db	4025	CACCCAGGACTCCAATGTCTGCTC-----CCCAGGGGCGCCGGCTGCTCACCCAGA	4076
Qy	4270	GCAAGAGGTGGAGGCAGAGGCCCTGTGCGAGGTCGGCCAGGGCAGCCGCAAGCTGGACGG	4329
Db	4077	GGGCCAGCCTCCCCCAGAGCCAGAGTGCCCAGGCCCGCAGCTCAAC-----ACGGG	4127
Qy	4330	CGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCCG	4389
Db	4128	GACACAGCTGGTCTCCAGCATGTGCAAGGCGCTGCTGGTCAAGAGATTCCAACACACCAT	4187
Qy	4390	CCGCAACTCCAAGGCACTCTTCTCCAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGGC	4449

Db 4188 CCGCAGCCACAAGGACTTCCTGGCGCAGATCGTGCTCCCGGCTACCTTTGTGTTTTTGGC 4247
 Qy 4450 CATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGTCCCTGTCACC 4509
 ||| | | | ||| ||| | | | ||| ||
 Db 4248 TCTGATGCTTTCTATTGTTATCCCTCCTTTTGGCGAATACCCCGCTTTGACCCTTCACCC 4307
 Qy 4510 TTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGCCAACGAGGA 4569
 | || | | | | | | | | | | |
 Db 4308 CTGGATATATGGGCAGC-----AGTACACCTTCTTCAGCATGGATGA 4349
 Qy 4570 GCGCCGCGAGTACCGGCTGCGGCTATCGCCCCAGCCAGCCCCAGCAGCTCGTGAGCAC 4629
 | | | | | | | | | | | | | | | |
 Db 4350 ACCAGGCAGTGAGCAGTTCACGGTACTTGACAGCGTCCTCCTGAATAAGC-CAGGCTTTG 4408
 Qy 4630 GTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTC 4689
 | | | | | | | | | | | | | | | |
 Db 4409 GCAACCGCTGCCTGAAGGAAGGGTGGCTTCCGGAGTACCCCTGTGGCAACTCAA----- 4462
 Qy 4690 GCTGGGGCCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTT 4749
 | | | | | | | | | | | |
 Db 4463 -----CACCTGGAAGACTCCTTCTGTGTC 4487
 Qy 4750 CGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACC 4809
 | | | | | | | | | | | | | | | |
 Db 4488 CCCAAACATCACCCAGCTGTTCCAGAAGCAGAAATGGACACAGGTCAACCCTTCACCATC 4547
 Qy 4810 CCCACCCTCGCCGCCCCATCTGACTCGCCAGCGTCCCGGATGAGGACCTGCAGGCCTG 4869
 | | | | | | | | | | | | | | | |
 Db 4548 CTGCAGGTGCAGCACCAGGGAGAAGCTCACCATGCTGCCAGAGTGCCCCGAGGGTGCCGG 4607
 Qy 4870 GAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTGCGCACCTCCCTGCC 4929
 | | | | | | | | | | | | | | | |
 Db 4608 GGGCTTCCCGCCCCCCCCAGAGAACACAGCGCAGCACGGAAATTCTACAAGACCTGACGGA 4667
 Qy 4930 GCGCTTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACCGGCTTCTCCTG 4989
 | | | | | | | | | | | | | | | |
 Db 4668 CAGGAACATCTCCGACTTCTTGGTAAAAACGTATCCTGCTCTTATAAGAAGCAGCTTAAA 4727
 Qy 4990 CCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGACATCCTGAC 5049
 || | | | | | | | | | | | | | | |
 Db 4728 GAGCAAATTCTGGGTCAATGAACAGAGGTATGGAGGAATTTCCATTGGAGGAAAGCTCCC 4787
 Qy 5050 CGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCGCTTCCGACT 5109
 | | | | | | | | | | | | | | | |
 Db 4788 AGTCGTCCCCATCACGGGGGAAGCACTTGTTGGGTTTTTAAGCGACCTTGCCCGGATCAT 4847
 Qy 5110 GCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAGTCCATCCCAGCCTCATTTGG 5169
 | | | | | | | | | | | | | | | |
 Db 4848 GAATGTGAGCGGGGGCCCTATCACTAGAGAGGCTCTAAAGAAATACCTGATTTCTT-- 4905
 Qy 5170 CACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCAGGTTTTCTA 5229
 | | | | | | | | | | | | | | | |
 Db 4906 -----AAACATCTAGAACTGAAGACAACATT-----AAGGTGTGGTT 4943
 Qy 5230 CAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTCAACAACGCCATCCT 5289
 || ||||| ||| | | | | | | | | | | | |
 Db 4944 TAATAACAAAGGCTGGCATGCCCTGGTCAGCTTTCTCAATGTGGCCCAACGCCATCTT 5003

Qy	5290	GCGTGCCAAACCTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGGCATCACCGTCACCAA	5349
Db	5004	ACGGGCCAGCCTGCCTAAGGACAGGAG---CCCCGAGGAGTATGGAATCACCGTCATTAG	5060
Qy	5350	CCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGGGCAC---	5406
Db	5061	CCAACCCCTGAACCTGACCAAGGAGCAGCTCTCAGAGATTACAGTGCTGACCACTTCAGT	5120
Qy	5407	GGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCTTCGT	5466
Db	5121	GGATGCTGTGGTTGCCATCTGTGTGATTTTCTCCATGTCCTTCGTCCCAGCCAGCTTTGT	5180
Qy	5467	TGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGACGGCTG	5526
Db	5181	CCTTTATTTGATCCAGGAGCGGGTGAACAAATCCAAGCACCTCCAGTTTATCAGTGGAGT	5240
Qy	5527	CAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCTGGTCCC	5586
Db	5241	GAGCCCCACCACCTACTGGGTGACCAACTTCCTCTGGGACATCGTGAATTATTCCGTGAG	5300
Qy	5587	CGCTACCTGCTGTGTTCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTCGCCCAC	5646
Db	5301	TGCTGGGCTGGTGGTGCGCATCTTCATCGGGTTTCAGAAGAAAGCCTACACTTCTCCAGA	5360
Qy	5647	CAACTTCCCTGCCGTCCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCCCATCAT	5706
Db	5361	AAACCTTCCCTGCCCTTGTGGCACTGCTCCTGCTGTATGGATGGGCGGTCAATCCCATGAT	5420
Qy	5707	GTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCATTTGTCAT	5766
Db	5421	GTACCCAGCATCCTTCCTGTTTGATGTCCCAGCACAGCCTATGTGGCTTTATCTTGTGC	5480
Qy	5767	CAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCA	5826
Db	5481	TAATCTGTTTCATCGGCATCAACAGCAGTGCTATTACCTTCATCTTGGAATTATTTGAGAA	5540
Qy	5827	CGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAA	5886
Db	5541	TAACCGGACGCTGCTCAGGTTCAACGCCGTGCTGAGGAAGCTGCTCATTGTCTTCCCCCA	5600
Qy	5887	CTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTA	5946
Db	5601	CTTCTGCCTGGGCCGGGGCTCATTGACCTTGCACTGAGCCAGGCTGTGACAGATGTCTA	5660
Qy	5947	CGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGGGACATTGTCACCCG	6006
Db	5661	TGCCCCGTTTGGTGAGGAGCACTCTGCAA---TCCGTTCCACTGGGACCTGATTGGGAA	5717
Qy	6007	CGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCA	6066
Db	5718	GAACCTGTTTGCCATGGTGGTGGAAGGGTGGTGACTTCCTCCTGACCCTGCTGGTCCA	5777
Qy	6067	GTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCC---TGTGGAGGA	6123
Db	5778	GCGCCACTTCTTCCTCTCCCAATGGATTGCCGAGCCCACTAAGGAGCCCATTGTTGATGA	5837

Qy 6124 TGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACAT 6183
 |||| | | |||| | | | | | | | | | | | | | |
 Db 5838 AGATGATGATGTGGCTGAAGAAAGACAAAGAATTATTACTGGTGGAAATAAAACTGACAT 5897

Qy 6184 GGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGC 6243
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 Db 5898 CTTAAGGCTACATGAACTAACCAAGATTTATCCGGGCAC-----CTCCAGCCCAGC 5948

Qy 6244 CGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAA 6303
 || ||| | |||| | || | | |||| | |||| | | |||| | | ||
 Db 5949 AGTGGACAGGCTGTGTGTGCGAGTTCGCCCTGGAGAGTGCTTTGGCCTCCTGGGAGTGAA 6008

Qy 6304 CGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGG 6363
 |||| | |||| | | | ||| |||| |||| || || || | | ||| ||
 Db 6009 TGGTGCCGGCAAAACAACCACATTCAAGATGCTCACTGGGGACAACACAGTGACCTCAGG 6068

Qy 6364 CGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCT 6423
 || ||| ||| || | || | | | | | | | | | | | | | |
 Db 6069 GGATGCCACCGTAGCAGGCAAGAGTATTTTAACCAATATTTCTGAAGTCCATCAAATAT 6128

Qy 6424 CGGCTACTGCCCGCAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCTGCA 6483
 |||| |||| | |||| ||| || | || |||| | | || | | | |
 Db 6129 GGGCTACTGTCCTCAGTTTGATGCAATCGATGAGCTGCTCACAGGACGAGAACATCTTTA 6188

Qy 6484 GCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGC 6543
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 Db 6189 CCTTTATGCCCGGCTTCGAGGTGTACCAGCAGAAGAAATCGAAAAGGTTGCAAACCTGGAG 6248

Qy 6544 TCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGG 6603
 | | ||| |||| | |||| | |||| ||| | |||| |||| | | ||
 Db 6249 TATTAAGAGCCTGGGCCTGACTGTCTACGCCGACTGCCTGGCTGGCACGTACAGTGGGGG 6308

Qy 6604 CAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTTCCT 6663
 |||| |||| |||| |||| |||| |||| |||| | |||| | | | |
 Db 6309 CAACAAGCGGAACTCTCCACAGCCATCGCACTCATTGGCTGCCCACCGCTGGTGCTGCT 6368

Qy 6664 GGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCCT 6723
 || | |||| |||| |||| |||| |||| || || || || || || ||
 Db 6369 GGATGAGCCCACCACAGGGATGGACCCCAAGGCACGCCGCATGCTGTGGAACGTATCGT 6428

Qy 6724 CGACCTCATCAAGACAGGGCGTTAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGA 6783
 | |||| | |||| | |||| | |||| || |||| |||| || || ||
 Db 6429 GAGCATCATCAGAGAAGGGAGGGCTGTGGTCCTCACATCCCACAGCATGGAAGAATGTGA 6488

Qy 6784 GGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCCTGCGGTGCCTGGGCAGCAT 6843
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 Db 6489 GGCCTGTGTACCCGGCTGGCCATCATGGTAAAGGGCGCCTTTTCGATGTATGGGCACCAT 6548

Qy 6844 CCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCAG 6903
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 Db 6549 TCAGCATCTCAAGTCCAAATTTGGAGATGGCTATATCGTCACAATGAAGATCAAATCCCC 6608

Qy 6904 CCAGAGTG-----TGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCC 6948
 || | |||| |||| || |||| || || |||| || || |||| ||
 Db 6609 GAAGGACGACCTGCTTCCTGACCTGAACCCTGTGGAGCAGTTCTTCCAGGGGAACTTCCC 6668

Qy 6949 GGAAGCCATGCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCA 7008

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      |      ||| | |||| |||| | | | |||| ||| | |
Db      6669 AGGCAGTGTGCAGAGGGAGAGGCACTACAACATGCTCCAGTTCAGGTCTCCTC----- 6722

Qy      7009 CATCTCGCTGGCCCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGA 7068
      | ||| |||| | ||| | | ||| ||| |||||
Db      6723 CTCCTCCCTGGCGAGGATCTTCCAGCTCCTCCTCTCCCAAGGACAGCCTGCTCATCGA 6782

Qy      7069 GGACTACTCGGTTCAGCCAGACCACACTGGACAATGTGTTCGTGAACCTTGCCAAGAAGCA 7128
      ||| |||| |||| ||||| ||||| | ||| |||| | |||
Db      6783 GGAGTACTCAGTCACACAGACCACACTGGACCAGGTGTTTGTAAATTTTGCTAAACAGCA 6842

Qy      7129 GAGTGACAACCTGGAGC 7145
      || ||| | | || |
Db      6843 GACTGAAAGTCATGACC 6859

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RESULT 13

ABN99317

ID ABN99317 standard; cDNA; 9870 BP.

XX

AC ABN99317;

XX

DT 17-JAN-2003 (first entry)

XX

DE Polymorphic human ABCA1 transporter coding sequence #17.

XX

KW Human; ABCA1; transporter; ATP-binding cassette;

KW high density lipoprotein; HDL; cholesterol; familial HDL deficiency;

KW Tangier disease; myocardial infarction; atherosclerosis;

KW cardiovascular disease; gene; single nucleotide polymorphsim; SNP; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 314..7099

FT /*tag= a

FT /product= "ABCA1 transporter"

FT /transl_except= (pos: 3677..3679,aa:Cys)

XX

PN WO200236770-A2.

XX

PD 10-MAY-2002.

XX

PF 12-OCT-2001; 2001WO-FR003182.

XX

PR 31-OCT-2000; 2000FR-00014037.

PR 11-DEC-2000; 2000US-0254108P.

XX

PA (AVET) AVENTIS PHARMA SA.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX

PI Denefle P, Rosier M, Arnould-Reguigne I, Duverger N, Cambien F;

XX

DR WPI; 2002-435691/46.

DR P-PSDB; ABB83121.

XX

PT New polymorphisms in the human ABCA1 gene, useful for diagnosing

Db 2351 ATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTCTTGTGAGCGCTGGCCTG 2410
 Qy 2336 CTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGG 2395
 || | ||||| || | ||| ||| | | |
 Db 2411 CTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGT 2470
 Qy 2396 CTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTG 2455
 ||||| | || | || ||| || ||| || ||||| | ||
 Db 2471 GTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTC 2530
 Qy 2456 TACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTG 2515
 | |||| | ||| |||| | |||| | ||||| ||||| | ||| ||
 Db 2531 TTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTG 2590
 Qy 2516 CCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAG 2575
 ||||| ||| | || ||| || | | |
 Db 2591 CCCTAC-----GTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTC 2638
 Qy 2576 AAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCG 2635
 ||| | ||| ||| ||| | ||| |||| | |||| | ||||| ||
 Db 2639 AAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCC 2698
 Qy 2636 CTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAG 2695
 || | |||| | ||| | ||| |||| || | || || |||||
 Db 2699 CTTTTTGAGGAGCAGGGCATTTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCTGTGGAG 2758
 Qy 2696 GGGGACGACTTCAACTTGCTCCTGGCTGTCAACATGCTGATGGTGGACGCCGTGGTCTAT 2755
 | || | |||| | | ||| |||| || | || | ||||
 Db 2759 GAAGATGGCTTCAATCTCAACACTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTAT 2818
 Qy 2756 GGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCC 2815
 || | || ||||| ||||| ||||| ||||| | ||| |||||
 Db 2819 GGGGTGATGACCTGGTACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATTCACAGGCC 2878
 Qy 2816 TGGTACTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAG 2875
 |||| || || ||||| |||| | || |
 Db 2879 TGGTATTTTCCTTGCACCAAGTCCTACTGGTTTGGCGAGGAAAG----- 2922
 Qy 2876 TGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGT 2935
 ||| || ||| | ||
 Db 2923 -----TGATGAGAAGAGCCACCCTGGT 2944
 Qy 2936 GCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACCCACCTG 2995
 ||| ||| | || || ||||| ||||| ||||| ||
 Db 2945 TCCAACCAGAAGAGAATATCAGA-----AATCTGCATGGAGGAGGAACCCACCCACTTG 2998
 Qy 2996 CCTCTGGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCC 3055
 |||| || | || | || || ||||| || | ||||| ||||
 Db 2999 AAGCTGGGCGTGTCCATTGAGAACCCTGGTAAAAGTCTACCGAGATGGGATGAAGGTGGCT 3058
 Qy 3056 CTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAAC 3115
 | | ||| |||| | || ||| |||| | ||||| ||||| |||||
 Db 3059 GTCGATGGCCTGGCACTGAATTTTTATGAGGGCCAGATCACCTCCTTCTTGGGCCACAAT 3118
 Qy 3116 GGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGT 3175
 || ||||| |||| | ||||| ||||| ||||| || |||||
 Db 3119 GGAGCGGGGAAGACGACCACCATGTCAATCCTGACCGGGTTGTTCCCCCGACCTCGGGC 3178

Qy 3176 TCCGCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTG 3235
 ||||| |||| | | ||||| || | ||||| ||||| ||||| ||||| |||||
 Db 3179 ACCGCCTACATCCTGGGAAAAGACATTGCTCTGAGATGAGCACCATCCGGCAGAACCTG 3238

Qy 3236 GGCATGTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGG 3295
 || | || || ||||| || ||||| ||||| || | || || ||||| |||||
 Db 3239 GGGGTCTGTCCCCAGCATAACGTGCTGTTTGACATGCTGACTGTGAAGAACACATCTGG 3298

Qy 3296 TTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATG 3355
 ||||| || | | | | | | | | | | | | | | | | ||||| |||||
 Db 3299 TTCTATGCCCCGCTTGAAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATG 3358

Qy 3356 ATCGAGGACCTGG---AGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTGCGGGT 3412
 | ||| | | || | | | | | | | | ||||| |||
 Db 3359 GCCCTGGATGTTGGTTTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTGAGGT 3418

Qy 3413 GGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATC 3472
 || ||| || | ||||| || ||||| || ||||| || || || || | |||||
 Db 3419 GGAATGCAGAGAAAGCTATCTGTGGCCTTGCCCTTTGTGCGGGGATCTAAGGTTGTCATT 3478

Qy 3473 CTGGACGAGCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATC 3532
 ||||| || ||||| || || ||||| || || || || || || || || || || || ||
 Db 3479 CTGGATGAACCCACAGCTGGTGTGGACCCCTACTCCCGCAGGGGAATATGGGAGCTGCTG 3538

Qy 3533 CTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGAC 3592
 ||||| || | ||||| ||||| ||||| || || || ||||| || || || || || ||
 Db 3539 CTGAAATACCGACAAGGCCGACCATTATTCTCTACACACCACATGGATGAAGCGGAC 3598

Qy 3593 CTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCG 3652
 | || ||||| | ||||| ||||| ||||| ||||| || || ||||| |
 Db 3599 GTCCTGGGGGACAGGATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCC 3658

Qy 3653 CTCTTCCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCC 3712
 || || || || | | | | | || || || || || || || || || || || || ||
 Db 3659 CTGTTTCTGAAGAACCAGTTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTG 3718

Qy 3713 GAGCCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTG 3772
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 3719 G-----AATCCTCCCTCAGTTCCTGCAGAAACAGTAGTACACTGTGTCA 3763

Qy 3773 AGCAGCTGCTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTG 3832
 | | | |||| | | | || || || || || || || || || || || || || || ||
 Db 3764 TACCTGAAAAAGGAGGACAGTGTCTCTCAGAGCAGTTCTGATGCTGGCCTGGGCAGCGAC 3823

Qy 3833 CTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAG 3892
 | | | |||| | | | || || || || || || || || || || || || || || ||
 Db 3824 CATGAGAGTGACACGCTGACCATCGATGTCTCTGCTATCTCCAACCTCATCAGGAAGCAT 3883

Qy 3893 GGGGCTTTGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGC 3952
 | || | | || || || | | || || || || || || || || || || || || || ||
 Db 3884 GTGTCTGAAGCCCGGCTGGTGAAGACATAGGGCATGAGCTGACCTATGTGCTGCCATAT 3943

Qy 3953 AGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTCGGAGGAGGAT 4012
 | | | | || || | | || || || || || || || || || || || || || || ||
 Db 3944 GAA---GCTGCTAAGGAGGGAGCCTTTGTGGAAGTCTTTCATGAGATTGATGACCGGCTC 4000

Qy 4013 CAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGG 4072
 Db 4001 TCAGACCTGGGCATTCTAGTTATGGCATCTCAGAGACGACCCCTGGAAGAAATATTCCTC 4060
 Qy 4073 GCGGAGGGCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCCGGTGCTCGGAGCTG 4132
 Db 4061 AAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAGACCTCAGATGGTACCTTGCCAGCAAGA 4120
 Qy 4133 ACCCAGTCGCAGGCATCGCTGCAGTTCGGCGTCATCTGTGGGCTCTGCCCCGTGGCGACGAG 4192
 Db 4121 CGAAACAGGCGGGCCTTCGGGGACAAGCAGAGCTGTCTTCGCCCCGTCACTGAAGATGAT 4180
 Qy 4193 GGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGAC 4252
 Db 4181 GCTGCTG-----ATCCAAATGAT 4198
 Qy 4253 CCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTCCGCCAGGGC 4312
 Db 4199 TCTGACATAGACCCAGAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGG 4258
 Qy 4313 AGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAA 4372
 Db 4259 TCCTACCAGGTGAAAGGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAG 4318
 Qy 4373 CGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCAGATCTTGCTGCCAGCC 4432
 Db 4319 AGACTGCTAATTGCCAGACGGAGTCGGAAGGATTTTTGCTCAGATTGTCTTGCCAGCT 4378
 Qy 4433 TTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCC 4492
 Db 4379 GTGTTTGTCTGCATTGCCCTTGTGTTTCAGCCTGATCGTGCCACCCCTTTGGCAAGTACCCC 4438
 Qy 4493 CCGCTGGTCCTGTCACCTTCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATC 4552
 Db 4439 AGCCTGGAACCTCAGCCCTGGATGTACAACGAACAGTACACATTTGTGAGCAATGATGCT 4498
 Qy 4553 CCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCC 4612
 Db 4499 CCTGA-----GGACACGGGAACC 4516
 Qy 4613 CAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAG 4672
 Db 4517 CTGGAACCTCTAAACGCCCTCACCAAAGACCCTGGCTTCGGGACCCGCTGTATGGAAGGA 4576
 Qy 4673 TCTCCCGCCAACGGCTCGCTGGGGCCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTG 4732
 Db 4577 AACCCAATCCAGACACGCCCTG--CCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCAG 4634
 Qy 4733 CTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCCTTCACACAGGGGCTGCCACTG 4792
 Db 4635 -----TTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAAGTGGACAA 4679
 Qy 4793 TCCAATTTTCGTGCCACCCCAACCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGAT 4852
 Db 4680 TGCAGAACCTTCACCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTG 4739
 Qy 4853 GAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACG 4912

Db	4740	TGTGTCCCCCAGGGGCAGGGGGGCTGCCTCCTCCACAAAGAAAACAAAACACTGCAGATA	4799
Qy	4913	TCGGCACCCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAG	4972
Db	4800	TCCTTCAGGACCTGACAGGAAGAAACATTTTCGGATTATCTGGTGAAGACG-TATGTGCAG	4858
Qy	4973	GGCACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAG-ATGCGGGTGGT	5031
Db	4859	ATCATAGCCAAAAGCTTAAAGAACAAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTT	4918
Qy	5032	CACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCAC	5091
Db	4919	TCCCTGGGTGTCAGTAATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGAT----GC	4974
Qy	5092	CTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAGTC	5151
Db	4975	CACCAAAACAAATGAAGAAACACCTAAAGCTGGCCA-----AGGACAG	5016
Qy	5152	CATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAG	5211
Db	5017	TTCTGCAGATCGATTTCCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCAGAAA	5076
Qy	5212	GGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAG	5271
Db	5077	TAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATGT	5136
Qy	5272	CCTCAACAACGCCATCCTGCGTGCCAACCTGCCAAGAGCAAGGGCAACCCGGCGGCTTA	5331
Db	5137	CATCAACAATGCCATTCTCCGGGCCAACCTGCAAAGGGAGAG---AACCCTAGCCATTA	5193
Qy	5332	CGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTA	5391
Db	5194	TGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGC	5253
Qy	5392	CCTGCTGCAGGGCAC---GGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTT	5448
Db	5254	TCCGATGACCACATCAGTGGATGTCCTTGTGTCCATCTGTGTCATCTTTGCAATGTCCTT	5313
Qy	5449	CGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGCCGAGAAGTCCACCAAGGCCAAGCATCT	5508
Db	5314	CGTCCCAGCCAGCTTTGTCTGTTTCCTGATCCAGGAGCGGGTCAGCAAAGCAAAACACCT	5373
Qy	5509	GCAGTTTGTGTCAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACAT	5568
Db	5374	GCAGTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTCTCTAATTTTGTCTGGGATAT	5433
Qy	5569	GCTCAACTACCTGGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTTCGACCTGCC	5628
Db	5434	GTGCAATTACGTTGTCCCTGCCACACTGGTCATTATCATCTTCATCTGCTTCCAGCAGAA	5493
Qy	5629	GGCCTACACGTCGCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTG	5688
Db	5494	GTCTATGTGTCTCCACCAATCTGCCTGTGCTAGCCCTTCTACTTTTGTGTATGGGTG	5553
Qy	5689	GTCCATCACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTA	5748

Db 5554 GTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTCAGATCCCCAGCACAGCCTA 5613

Qy 5749 CGTGTTCCTCATTGTTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCT 5808
 ||| | ||| | | | | ||| ||| | | | | ||| ||| |

Db 5614 TGTGGTGCTCACCAGCGTGAACCTCTTCATTGGCATTAAATGGCAGCGTGGCCACCTTTGT 5673

Qy 5809 GCTACAGCTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTG 5868
 ||| ||| ||| | | | | | | | | | | | | | |

Db 5674 GCTGGAGCTGTTCT---ACCGACAATAAGCTGAATAATATCAATGATATCCTGAAGTCCGT 5730

Qy 5869 CTTCTCATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGA 5928
 ||| | | | | | | | | | | | | | | | | |

Db 5731 GTTCTTGATCTTCCACATTTTGCCTGGGACGAGGGCTCATCGACATGGTGAAAAACCA 5790

Qy 5929 GTACATCAACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCA 5988
 | || | | | | | | | | | | | | | | | | |

Db 5791 GGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAATCGCTTTGT---GTCACCATTATC 5847

Qy 5989 GTGGGACATTGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCT 6048
 ||||| | | | | | | | | | | | | | | | |

Db 5848 TTGGGACTTGTTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGGGTGGTGTTCCTCCT 5907

Qy 6049 CCTGACCATCATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTAC 6108
 | | | | | | | | | | | | | | | | | |

Db 5908 CATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCCAGACCTGTAAATGCAAAGCT 5967

Qy 6109 CAAGCCTGTG---GAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGG 6165
 ||| || | | | | | | | | | | | | | | | |

Db 5968 ATCTCCTCTGAATGATGAAGATGAAGATGTGAGGCGGGAAAGACAGAGAATTCTTGATGG 6027

Qy 6166 AGACGCCGACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAA 6225
 | | | | | | | | | | | | | | | | | | |

Db 6028 TGGAGGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATATA-----TAG 6078

Qy 6226 GATTGGCCGTATCCTGGCCGTTGACCGCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTT 6285
 | | | | | | | | | | | | | | | | | | |

Db 6079 AAGGAAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCATTCTCCTGGTGAGTGCTT 6138

Qy 6286 CGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGA 6345
 ||||| ||| | | | | | | | | | | | | | |

Db 6139 TGGGCTCCTGGGAGTTAATGGGGCTGGAATAATCACTTTCAAGATGTTAACAGGAGA 6198

Qy 6346 CGAGAGCACGACGGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCT 6405
 | | | | | | | | | | | | | | | | | |

Db 6199 TACCACTGTTACCAGAGGAGATGCTTTCTTAACAGAAATAGTATCTTATCAAACATCCA 6258

Qy 6406 CCAGGTGCAGCAGAGCCTCGGCTACTGCCCGCAGTGTGACGCGCTGTTGACGAGCTCAC 6465
 | | | | | | | | | | | | | | | | | |

Db 6259 TGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTGTTGAC 6318

Qy 6466 GGCCCGGGAGCACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGC 6525
 | | | | | | | | | | | | | | | | | |

Db 6319 TGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAAGTTGG 6378

Qy 6526 CCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGC 6585
 | | | | | | | | | | | | | | | | | |

Db 6379 CAAGGTTGGTGAGTGGGCGATTTCGAAACTGGGCCTCGTGAAGTATGGAGAAAAATATGC 6438

Qy	6586	TGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTTGGGTA	6645
Db	6439	TGGTAACCTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATCGGCGG	6498
Qy	6646	CCCAGCCTTCATCTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCGGCGCTT	6705
Db	6499	GCCTCCTGTGGTGTTCCTGGATGAACCCACCACAGGCATGGATCCCAAAGCGGCGGTT	6558
Qy	6706	CCTCTGGAACCTCATCCTCGACCTCATCAAGACAGGGCGTTTCAAGTGGTGCTGACATCACA	6765
Db	6559	CTTGTGGAATTGTGCCCTAAGTGTGTCAAGGAGGGGAGATCAGTAGTGCTTACATCTCA	6618
Qy	6766	CAGCATGGAGGAGTGCAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCT	6825
Db	6619	TAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGAAGGTT	6678
Qy	6826	GCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCAC	6885
Db	6679	CAGGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGGAGATGGTTATACAATAGT	6738
Qy	6886	GGTGCGGA---CCAAGAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAA	6942
Db	6739	TGTACGAATAGCAGGGTCCAACCCGGACCTGAAGCCTGTCCAGGATTTCTTTGGACTTGC	6798
Qy	6943	CTTCCCGGAAGCCATGCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTC	7002
Db	6799	ATTTCTTGGAGTGTTCAAAAGAGAAACACCGGAACATGCTACAATACCAGCTTCCATC	6858
Qy	7003	GGAGCACATCTCGCTGGCCCAGGTGTTTCAAGATGGAGCAGGTGTCTGGCGTGCTGGG	7062
Db	6859	TTCATTATCTTCTCTGGCCAGGATATTTCAGCATCCTCTCCCAGAGCAAAAAGCGACTCCA	6918
Qy	7063	CATCGAGGACTACTCGGTCTAGCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAA	7122
Db	6919	CATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACCTTTGCCAA	6978
Qy	7123	GAAGCAGAGTGA	7134
Db	6979	GGACCAAAGTGA	6990

RESULT 14

ABN99311

ID ABN99311 standard; cDNA; 9870 BP.

XX

AC ABN99311;

XX

DT 17-JAN-2003 (first entry)

XX

DE Polymorphic human ABCA1 transporter coding sequence #11.

XX

KW Human; ABCA1; transporter; ATP-binding cassette;

KW high density lipoprotein; HDL; cholesterol; familial HDL deficiency;

KW Tangier disease; myocardial infarction; atherosclerosis;

KW cardiovascular disease; gene; single nucleotide polymorphsim; SNP; ss.

XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 314..7099
 FT /*tag= a
 FT /product= "ABCA1 transporter"
 XX
 PN WO200236770-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 12-OCT-2001; 2001WO-FR003182.
 XX
 PR 31-OCT-2000; 2000FR-00014037.
 PR 11-DEC-2000; 2000US-0254108P.
 XX
 PA (AVET) AVENTIS PHARMA SA.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX
 PI Deneffe P, Rosier M, Arnould-Reguigne I, Duverger N, Cambien F;
 XX
 DR WPI; 2002-435691/46.
 DR P-PSDB; ABB83116.
 XX
 PT New polymorphisms in the human ABCA1 gene, useful for diagnosing
 PT predisposition to myocardial infarct and other cardiovascular diseases.
 XX
 PS Claim 1; Page 155-158; 297pp; French.
 XX
 CC The present sequence is a polymorphic coding sequence for human ATP-
 CC binding cassette (ABCA1) transporter. This sequence can be used for
 CC diagnosing (predisposition to) diseases associated with the plasma level
 CC of high density lipoprotein (HDL) cholesterol, especially familial HDL
 CC deficiency conditions such as Tangier disease, myocardial infarction,
 CC atherosclerosis and other cardiovascular diseases. This sequence
 CC comprises mutation s-196e15, also given in ABN99256, and the alternative
 CC form of the polymorphism is shown in ABL58154
 XX
 SQ Sequence 9870 BP; 2671 A; 2221 C; 2339 G; 2638 T; 0 U; 1 Other;

Query Match 12.3%; Score 988; DB 6; Length 9870;
 Best Local Similarity 52.8%; Pred. No. 8.6e-154;
 Matches 2855; Conservative 0; Mismatches 2300; Indels 257; Gaps 23;

Qy 1745 TTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCATTGTC 1804
 ||||| || | | || | | | | | | | | | | | | |
 Db 1814 TTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCCATAGCAACAGAAGTCTGGCTCATC 1873
 Qy 1805 AACTACACCCTCAACCAGGCCTACCAGGACAACGTCAGTGTGTTTGGCAGTGTGATCTTC 1864
 || | | | | | | | | | | | | | | | | | | | |
 Db 1874 AACAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTGTGTTCAGTGA 1933
 Qy 1865 CAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAACTCC 1924
 || | | | | | | | | | | | | | | | | | | | |
 Db 1934 ATTACTCCAGGCAGCATTGAGCTGCCCCATCATGTCAAGTACAAGATCCGAATGGACATT 1993
 Qy 1925 AGCTTCACCGAGAAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCCAATACT 1984

Db	1994	GACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACCTGGTCCTCGAGCT	2053
Qy	1985	GGCGGCCGCTTCTACTTCCTCTAC-----GGCTTCGTCTGGATCCAGGACATGATG	2035
Db	2054	GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG	2113
Qy	2036	GAGCGCGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTG	2095
Db	2114	GAGCAGGCAATCAT---CAGGGTGCTGACGGGCACCGAGAAGAAAACCTGGTGTCTATATG	2170
Qy	2096	CAGATGTTCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTCAATTGAGCACATG	2155
Db	2171	CAACAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGATGAGCCGGTCA	2230
Qy	2156	ATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATC	2215
Db	2231	ATGCCCCCTCTTCATGACGCTGGCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATC	2290
Qy	2216	GTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCG	2275
Db	2291	GTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACAGC	2350
Qy	2276	GTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGTCAGCTGTCCATCTCCGTGACAGCA	2335
Db	2351	ATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTCTGTGAGCGCTGGCCTG	2410
Qy	2336	CTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGG	2395
Db	2411	CTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGT	2470
Qy	2396	CTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTG	2455
Db	2471	GTCTTCCTGTCCGTGTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTC	2530
Qy	2456	TACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTG	2515
Db	2531	TTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTG	2590
Qy	2516	CCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAG	2575
Db	2591	CCCTAC-----GTCTGTGTGTGGCATGGCAGGACTACATGGGCTTCACACTC	2638
Qy	2576	AAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCG	2635
Db	2639	AAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCC	2698
Qy	2636	CTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAG	2695
Db	2699	CTTTTGTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCTGTGGAG	2758
Qy	2696	GGGGACGACTTCAACTTGCTCCTGGCTGTCAACCATGCTGATGGTGGACGCCGTGGTCTAT	2755
Db	2759	GAAGATGGCTTCAATCTCAACCACTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTAT	2818
Qy	2756	GGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCC	2815

Db	2819	GGGGTGATGACCTGGTACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATCCCAGGCC	2878
Qy	2816	TGGTACTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAG	2875
Db	2879	TGGTATTTTCCCTTGCACCAAGTCCTACTGGTTTGGCGAGGAAAG-----	2922
Qy	2876	TGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGT	2935
Db	2923	-----TGATGAGAAGAGCCACCCTGGT	2944
Qy	2936	GCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACCCACCTG	2995
Db	2945	TCCAACCAGAAGAGAATATCAGA-----AATCTGCATGGAGGAGGAACCCACCCACTTG	2998
Qy	2996	CCTCTGGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCC	3055
Db	2999	AAGCTGGGCGTGTCCATTGAGAACCTGGTAAAAGTCTACCGAGATGGGATGAAGGTGGCT	3058
Qy	3056	CTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAAC	3115
Db	3059	GTCGATGGCCTGGCACTGAATTTTATGAGGGCCAGATCACCTCCTTCTTGGGCCACAAT	3118
Qy	3116	GGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGT	3175
Db	3119	GGAGCGGGGAAGACGACCACCATGTCAATCCTGACCGGGTGTTCCTCCCGACCTCGGGC	3178
Qy	3176	TCCGCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTG	3235
Db	3179	ACCGCTACATCCTGGGAAAAGACATTGCTCTGAGATGAGCACCATCCGGCAGAACCTG	3238
Qy	3236	GGCATGTGCCCGCAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGG	3295
Db	3239	GGGGTCTGTCCCCAGCATAACGTGCTGTTTGACATGCTGACTGTGGAAGAACACATCTGG	3298
Qy	3296	TTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATG	3355
Db	3299	TTCTATGCCCGCTTGAAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATG	3358
Qy	3356	ATCGAGGACCTGG---AGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGT	3412
Db	3359	GCCCTGGATGTTGGTTTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTCAGGT	3418
Qy	3413	GGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATC	3472
Db	3419	GGAATGCAGAGAAAGCTATCTGTGGCCTTGGCCTTGTGCGGGGATCTAAGGTTGTCATT	3478
Qy	3473	CTGGACGAGCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATC	3532
Db	3479	CTGGATGAACCCACAGCTGGTGTGGACCCCTACTCCCGCAGGGGAATATGGGAGCTGCTG	3538
Qy	3533	CTGAAGTACAAGCCAGGCCGACCATTCTTCTGTCCACCCACCACATGGATGAGGCTGAC	3592
Db	3539	CTGAAATACCGACAAGGCCGACCATTATTCTCTCTACACACCACATGGATGAAGCGGAC	3598
Qy	3593	CTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCG	3652
Db	3599	GTCCTGGGGACAGGATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCC	3658

Qy	3653	CTCTTCCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCC	3712
Db	3659	CTGTTTCTGAAGAACCAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTG	3718
Qy	3713	GAGCCGGGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTTCGGGCCCCGCTG	3772
Db	3719	G-----AATCCTCCCTCAGTTCCTGCAGAAACAGTAGTAGCACTGTGTCA	3763
Qy	3773	AGCAGCTGCTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTG	3832
Db	3764	TACCTGAAAAAGGAGGACAGTGTCTCTCAGAGCAGTTCTGATGCTGGCCTGGGCAGCGAC	3823
Qy	3833	CTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAG	3892
Db	3824	CATGAGAGTGACACGCTGACCATCGATGTCTCTGCTATCTCCAACCTCATCAGGAAGCAT	3883
Qy	3893	GGGGCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGC	3952
Db	3884	GTGTCTGAAGCCCGGCTGGTGGAAACATAGGGCATGAGCTGACCTATGTGCTGCCATAT	3943
Qy	3953	AGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCGGAGGAGGAT	4012
Db	3944	GAA--GCTGCTAAGGAGGGAGCCCTTTGTGGAACCTCTTCATGAGATTGATGACCGGCTC	4000
Qy	4013	CAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGG	4072
Db	4001	TCAGACCTGGGCATTTCTAGTTATGGCATCTCAGAGACGACCCTGGAAGAAATATTCTC	4060
Qy	4073	GCGGAGGGCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTG	4132
Db	4061	AAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAGACCTCAGATGGTACCTTGCCAGCAAGA	4120
Qy	4133	ACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCGTGGCGACGAG	4192
Db	4121	CGAAACAGGCGGGCCTTCGGGGACAAGCAGAGCTGTCTTCGCCCCGTTCACTGAAGATGAT	4180
Qy	4193	GGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGAC	4252
Db	4181	GCTGCTG-----ATCCAAATGAT	4198
Qy	4253	CCAGACAATGTGAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTTCGGCCAGGGC	4312
Db	4199	TCTGACATAGACCCAGAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGG	4258
Qy	4313	AGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAA	4372
Db	4259	TCCTACCAGGTGAAAGGCTGGAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAG	4318
Qy	4373	CGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCC	4432
Db	4319	AGACTGCTAATTGCCAGACGGAGTCGGAAGGATTTTGTGCTCAGATTGTCTTGCCAGCT	4378
Qy	4433	TTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCC	4492
Db	4379	GTGTTTGTCTGCATTGCCCTTGTGTTTCAGCCTGATCGTGCCACCCTTTGGCAAGTACCC	4438

Qy 4493 CCGCTGGTCCTGTACCTTCCCAGTACCACAACTACACCCAGCCCCGTGGCAATTTTCATC 4552
 |||| | | | | | | | | | | | | | | | |
 Db 4439 AGCCTGGAACCTTCAGCCCTGGATGTACAACGAACAGTACACATTTGTGTCAGCAATGATGCT 4498

Qy 4553 CCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGGCTATCGCCCGACGCCAGCCCC 4612
 || | | | | | | | | | | | | | | | |
 Db 4499 CCTGA-----GGACACGGGAACC 4516

Qy 4613 CAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAG 4672
 | | | | | | | | | | | | | | | | | |
 Db 4517 CTGGAACCTCTTAAACGCCCTCACCAAAGACCCTGGCTTCGGGACCCGCTGTATGGAAGGA 4576

Qy 4673 TCTCCCGCCAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTG 4732
 | | | | | | | | | | | | | | | | | |
 Db 4577 AACCCAATCCCAGACACGCCCTG--CCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCAG 4634

Qy 4733 CTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTG 4792
 | | | | | | | | | | | | | | | | | |
 Db 4635 -----TTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAACCTGGACAA 4679

Qy 4793 TCCAATTTTCGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGAT 4852
 | | | | | | | | | | | | | | | | | |
 Db 4680 TGCAGAACCTTCACCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTG 4739

Qy 4853 GAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCACCGCTGGGCCAGAAATGTGGACG 4912
 | | | | | | | | | | | | | | | | | |
 Db 4740 TGTGTCCCCCAGGGGCAGGGGGGCTGCCTCCTCCACAAAGAAAACAAACACTGCAGATA 4799

Qy 4913 TCGGCACCCCTCCCTGCCCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAG 4972
 | | | | | | | | | | | | | | | | | |
 Db 4800 TCCTTCAGGACCTGACAGGAAGAAACATTTTCGGATTATCTGGTGAAGACG-TATGTGCAG 4858

Qy 4973 GGCACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAG-ATGCGGGTGGT 5031
 | | | | | | | | | | | | | | | | | |
 Db 4859 ATCATAGCCAAAAGCTTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTT 4918

Qy 5032 CACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCAC 5091
 | | | | | | | | | | | | | | | | | |
 Db 4919 TCCCTGGGTGTCAGTAATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGAT----GC 4974

Qy 5092 CTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAGTC 5151
 | | | | | | | | | | | | | | | | | |
 Db 4975 CACCAACAAATGAAGAAACACCTAAAGCTGGCCA-----AGGACAG 5016

Qy 5152 CATCCCAGCCTCATTTGGCACCAAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAG 5211
 | | | | | | | | | | | | | | | | | |
 Db 5017 TTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCAGAAA 5076

Qy 5212 GGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAG 5271
 | | | | | | | | | | | | | | | | | |
 Db 5077 TAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTCTCTGAATGT 5136

Qy 5272 CCTCAACAACGCCATCTGCGTGCCAACCTGCCAAGAGCAAGGGCAACCCGGCGGCTTA 5331
 | | | | | | | | | | | | | | | | | |
 Db 5137 CATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAG---AACCTAGCCATTA 5193

Qy 5332 CGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTA 5391

Db	5194	TGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGC	5253
Qy	5392	CCTGCTGCAGGGCAC---GGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTT	5448
Db	5254	TCCGATGACCACATCAGTGGATGTCCTTGTGTCCATCTGTGTCATCTTTGCAATGTCCTT	5313
Qy	5449	CGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCT	5508
Db	5314	CGTCCCAGCCAGCTTTGTGCTATTCTTGATCCAGGAGCGGGTCAGCAAAGCAAAACACCT	5373
Qy	5509	GCAGTTTGTGTCAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACAT	5568
Db	5374	GCAGTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTCTCTAATTTTGTCTGGGATAT	5433
Qy	5569	GCTCAACTACCTGGTCCCCGCTACCTGCTGTGTCATCATCTGTTTGTGTTTCGACCTGCC	5628
Db	5434	GTGCAATTACGTTGTCCCTGCCACACTGGTCATTATCATCTTCATCTGCTTCCAGCAGAA	5493
Qy	5629	GGCCTACACGTCGCCCCACCAACTTCCCTGCCGTCCTCTCCCTCTTCTGCTCTATGGGTG	5688
Db	5494	GTCCTATGTGTCTCCACCAATCTGCCTGTGCTAGCCCTTCTACTTTTGTCTGTATGGGTG	5553
Qy	5689	GTCCATCACGCCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTA	5748
Db	5554	GTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTCAAGATCCCAGCACAGCCTA	5613
Qy	5749	CGTGTTCCCTCATTGTGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCT	5808
Db	5614	TGTGGTGCTCACCAGCGTGAACCTCTTCATTGGCATTAATGGCAGCGTGGCCACCTTTGT	5673
Qy	5809	GCTACAGCTCTTCGAGCAGGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTG	5868
Db	5674	GCTGGAGCTGTTC---ACCGACAATAAGCTGAATAATATCAATGATATCCTGAAGTCCGT	5730
Qy	5869	CTTCCTCATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGA	5928
Db	5731	GTTCTTGATCTTCCCACATTTTTCCTGGGACGAGGGCTCATCGACATGGTGAAAAACCA	5790
Qy	5929	GTACATCAACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTCTGA	5988
Db	5791	GGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAATCGCTTTGT---GTCACCATTATC	5847
Qy	5989	GTGGGACATTGTCAACCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCT	6048
Db	5848	TTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGGGTGGTGTCTTCCT	5907
Qy	6049	CCTGACCATCATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTAC	6108
Db	5908	CATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCCAGACCTGTAAATGCAAAGCT	5967
Qy	6109	CAAGCCTGTG---GAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGG	6165
Db	5968	ATCTCCTCTGAATGATGAAGATGAAGATGTGAGCGGGGAAAGACAGAGAATTCTTGATGG	6027
Qy	6166	AGACGCCGACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAA	6225

Db	6028	TGGAGGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATATA-----TAG	6078
Qy	6226	GATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTT	6285
Db	6079	AAGGAAGCGGAAGCCTGCTGTTGACAGGATTGCGTGGGCATTCTCCTGGTGAGTGCTT	6138
Qy	6286	CGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGA	6345
Db	6139	TGGGCTCCTGGGAGTTAATGGGGCTGGAAAATCATCAACTTTCAAGATGTTAACAGGAGA	6198
Qy	6346	CGAGAGCACGACGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCT	6405
Db	6199	TACCACTGTTACCAGAGGAGATGCTTTCCTTAACAGAAATAGTATCTTATCAAACATCCA	6258
Qy	6406	CCAGGTGCAGCAGAGCCTCGGCTACTGCCCGCAGTGTGACGCGCTGTTTCGACGAGCTCAC	6465
Db	6259	TGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTGTTGAC	6318
Qy	6466	GGCCCGGGAGCACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGC	6525
Db	6319	TGGGAGAGAAACAGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAAGTTGG	6378
Qy	6526	CCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGC	6585
Db	6379	CAAGGTTGGTGAGTGGGCGATTTCGAAACTGGGCCTCGTGAAGTATGGAGAAAAATATGC	6438
Qy	6586	TGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTA	6645
Db	6439	TGGTAACTATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATCGGCGG	6498
Qy	6646	CCCAGCCTTCATCTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCGGCGCTT	6705
Db	6499	GCCTCCTGTGGTGTTTCTGGATGAACCCACCACAGGCATGGATCCCAAAGCCGGCGGTT	6558
Qy	6706	CCTCTGGAACCTCATCCTCGACCTCATCAAGACAGGGCGTTCAGTGGTGCTGACATCACA	6765
Db	6559	CTTGTTGAATTGTGCCCTAAGTGTTGTCAAGGAGGGGAGATCAGTAGTGCTTACATCTCA	6618
Qy	6766	CAGCATGGAGGAGTGCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCCT	6825
Db	6619	TAGTATGGAAGAATGTGAAGCTCTTGCAC TAGGATGGCAATCATGGTCAATGGAAGGTT	6678
Qy	6826	GCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCAC	6885
Db	6679	CAGGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGGAGATGGTTATACAATAGT	6738
Qy	6886	GGTGCGGA---CCAAGAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAA	6942
Db	6739	TGTACGAATAGCAGGGTCCAACCCGGACCTGAAGCCTGTCCAGGATTTCTTTGGACTTGC	6798
Qy	6943	CTTCCCGGAAGCCATGCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTC	7002
Db	6799	ATTTCCTGGAAGTGTTCCAAAAGAGAAACACCGGAACATGCTACAATACCAGCTTCCATC	6858
Qy	7003	GGAGCACATCTCGCTGGCCCAGGTGTTTCAAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGG	7062
Db	6859	TTCATTATCTTCTCTGGCCAGGATATTCAAGCATCCTCTCCAGAGCAAAAAGCGACTCCA	6918

QY 7063 CATCGAGGACTACTCGGTCAGCCAGACCACACTGGACAATGTGTTCGTGAACCTTTGCCAA 7122
 ||| || ||||| || ||||| ||||| ||| | || |||||
 Db 6919 CATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACCTTTGCCAA 6978

QY 7123 GAAGCAGAGTGA 7134
 | | || |||||
 Db 6979 GGACCAAAGTGA 6990

RESULT 15

ABN99318

ID ABN99318 standard; cDNA; 9870 BP.

XX

AC ABN99318;

XX

DT 17-JAN-2003 (first entry)

XX

DE Polymorphic human ABCA1 transporter coding sequence #18.

XX

KW Human; ABCA1; transporter; ATP-binding cassette;

KW high density lipoprotein; HDL; cholesterol; familial HDL deficiency;

KW Tangier disease; myocardial infarction; atherosclerosis;

KW cardiovascular disease; gene; single nucleotide polymorphsim; SNP; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 314..7099

FT /*tag= a

FT /product= "ABCA1 transporter"

XX

PN WO200236770-A2.

XX

PD 10-MAY-2002.

XX

PF 12-OCT-2001; 2001WO-FR003182.

XX

PR 31-OCT-2000; 2000FR-00014037.

PR 11-DEC-2000; 2000US-0254108P.

XX

PA (AVET) AVENTIS PHARMA SA.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX

PI Deneffe P, Rosier M, Arnould-Reguigne I, Duverger N, Cambien F;

XX

DR WPI; 2002-435691/46.

DR P-PSDB; ABB83122.

XX

PT New polymorphisms in the human ABCA1 gene, useful for diagnosing

PT predisposition to myocardial infarct and other cardiovascular diseases.

XX

PS Claim 1; Page 173-175; 297pp; French.

XX

CC The present sequence is a polymorphic coding sequence for human ATP-

CC binding cassette (ABCA1) transporter. This sequence can be used for

CC diagnosing (predisposition to) diseases associated with the plasma level

CC of high density lipoprotein (HDL) cholesterol, especially familial HDL
CC deficiency conditions such as Tangier disease, myocardial infarction,
CC atherosclerosis and other cardiovascular diseases. This sequence
CC comprises mutation s-54e23, also given in ABN99268, and the alternative
CC form of the polymorphism is shown in ABL58157

XX

SQ Sequence 9870 BP; 2670 A; 2222 C; 2339 G; 2638 T; 0 U; 1 Other;

Query Match 12.3%; Score 988; DB 6; Length 9870;
Best Local Similarity 52.8%; Pred. No. 8.6e-154;
Matches 2855; Conservative 0; Mismatches 2300; Indels 257; Gaps 23;

```
Qy      1745 TTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCATTGTC 1804
      |||||      || || || || || || || || || || || || || || || || ||
Db      1814 TTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCCATAGCAACAGAAGTCTGGGCTCATC 1873

Qy      1805 AACTACACCCTCAACCAGGCCTACCAGGACAACGTCACGTGTTTTTGCCAGTGTGATCTTC 1864
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1874 AACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTGTGTTCACCTGGA 1933

Qy      1865 CAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAACTCC 1924
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1934 ATTACTCCAGGCAGCATTGAGCTGCCCCATCATGTCAAGTACAAGATCCGAATGGACATT 1993

Qy      1925 AGCTTCACCGAGAAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAATACT 1984
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1994 GACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACCCTGGTCCTCGAGCT 2053

Qy      1985 GGCGGCCGCTTCTACTTCCTCTAC-----GGCTTCGTCTGGATCCAGGACATGATG 2035
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2054 GACCCCTTTGAGGACATGCGGTACGCTCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG 2113

Qy      2036 GAGCGGCCCATCATCGACACTTTTGTGGGGCAGCAGCTGGTGGAGCCAGGCAGCTACGTG 2095
      |||| | | |||| | | | | | | | | | | | | | | | | | | | |
Db      2114 GAGCAGGCAATCAT---CAGGGTGCTGACGGGCACCGAGAAGAAAACCTGGTGTCTATATG 2170

Qy      2096 CAGATGTTCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATG 2155
      || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2171 CAACAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGATGAGCCGGTCA 2230

Qy      2156 ATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATC 2215
      |||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      2231 ATGCCCTCTTCATGACGCTGGCCTGGATTACTCAGTGGCTGTGATCATCAAGGGCATC 2290

Qy      2216 GTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCCTGAACAACGCG 2275
      || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2291 GTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCCTGGACAACAGC 2350

Qy      2276 GTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCA 2335
      | | |||| | | | | | | | | | | | | | | | | | | | | | |
Db      2351 ATCCTCTGGTTTAGCTGGTTCATTAGTAGCCTCATTCCTCTTCTGTGAGCGCTGGCCTG 2410

Qy      2336 CTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGG 2395
      || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2411 CTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTGTTT 2470

Qy      2396 CTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTG 2455
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Db 2471 GTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTC 2530
 Qy 2456 TACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTG 2515
 Db 2531 TTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTG 2590
 Qy 2516 CCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAG 2575
 Db 2591 CCCTAC-----GTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTC 2638
 Qy 2576 AAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCG 2635
 Db 2639 AAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCC 2698
 Qy 2636 CTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAG 2695
 Db 2699 CTTTTGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCTGTGGAG 2758
 Qy 2696 GGGGACGACTTCAACTTGCTCCTGGCTGTCAACCATGCTGATGGTGGACGCCGTGGTCTAT 2755
 Db 2759 GAAGATGGCTTCAATCTCACCCTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTAT 2818
 Qy 2756 GGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCC 2815
 Db 2819 GGGGTGATGACCTGGTACATTGAGGCTGTCTTCCAGGCCAGTACGGAATTCACAGGCC 2878
 Qy 2816 TGGTACTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAG 2875
 Db 2879 TGGTATTTTCTTGCACCAAGTCCTACTGGTTTGGCGAGGAAAG----- 2922
 Qy 2876 TGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTGCATGGAGGAGGACCAGGCCTGT 2935
 Db 2923 -----TGATGAGAAGAGCCACCCTGGT 2944
 Qy 2936 GCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTG 2995
 Db 2945 TCCAACCAGAAGAGAATATCAGA-----AATCTGCATGGAGGAGGAACCCACCCACTTG 2998
 Qy 2996 CCTCTGGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCC 3055
 Db 2999 AAGCTGGGCGTGTCCATTGAGAACCTGGTAAAGTCTACCGAGATGGGATGAAGGTGGCT 3058
 Qy 3056 CTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAAC 3115
 Db 3059 GTCGATGGCCTGGCACTGAATTTTATGAGGGCCAGATCACCTCCTTCTTGGGCCACAAT 3118
 Qy 3116 GGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTGCGGT 3175
 Db 3119 GGAGCGGGGAAGACGACCACCATGTCAATCCTGACCGGGTTGTCCCCCGACCTCGGGC 3178
 Qy 3176 TCCGCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTG 3235
 Db 3179 ACCGCCTACATCCTGGGAAAAGACATTCGCTCTGAGATGAGCACCATCCGGCAGAACCTG 3238
 Qy 3236 GGCATGTGCCCGCAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGG 3295

Db	3239	GGGGTCTGTCCCCAGCATAACGTGCTGTTTGACATGCTGACTGTTCGAAGAACAACATCTGG	3298
Qy	3296	TTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATG 	3355
Db	3299	TTCTATGCCCGCTTGAAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATG	3358
Qy	3356	ATCGAGGACCTGG---AGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGT 	3412
Db	3359	GCCCTGGATGTTGGTTTGCCATCAAGCAAGCTGAAAAGCAAACAAGCCAGCTGTCAGGT	3418
Qy	3413	GGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATC 	3472
Db	3419	GGAATGCAGAGAAAGCTATCTGTGGCCTTGCCCTTGTGCGGGGATCTAAGGTTGTCATT	3478
Qy	3473	CTGGACGAGCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATC 	3532
Db	3479	CTGGATGAACCACAGCTGGTGTGGACCCCTACTCCCGCAGGGGAATATGGGAGCTGCTG	3538
Qy	3533	CTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGAC 	3592
Db	3539	CTGAAATACCGACAAGGCCGACCATTATTCTCTACACACCACATGGATGAAGCGGAC	3598
Qy	3593	CTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCG 	3652
Db	3599	GTCCTGGGGGACAGGATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCC	3658
Qy	3653	CTCTTCCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCC 	3712
Db	3659	CTGTTTCTGAAGAACCAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTG	3718
Qy	3713	GAGCCGGGGGGCCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGGGGCCCCGCTG -----	3772
Db	3719	G-----AATCCTCCCTCAGTTCCTGCAGAACAGTAGTAGCACTGTGTCA	3763
Qy	3773	AGCAGCTGCTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTG 	3832
Db	3764	TACCTGAAAAAGGAGGACAGTGTCTCAGAGCAGTTCTGATGCTGGCCTGGGCAGCGAC	3823
Qy	3833	CTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCAAGAAG 	3892
Db	3824	CATGACAGTGACACGCTGACCATCGATGTCTGCTATCTCCAACCTCATCAGGAAGCAT	3883
Qy	3893	GGGGCTTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGC 	3952
Db	3884	GTGTCTGAAGCCCGCTGGTGAAGACATAGGGCATGAGCTGACCTATGTGCTGCCATAT	3943
Qy	3953	AGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTGCGAGGAGGAT 	4012
Db	3944	GAAGCTGC---TAAGGAGGGAGCCTTTGTGGAACCTTTTCATGAGATTGATGACCGGCTC	4000
Qy	4013	CAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGG 	4072
Db	4001	TCAGACCTGGGCATTTCTAGTTATGGCATCTCAGAGACGACCCTGGAAGAAATATTCTC	4060
Qy	4073	GCGGAGGGCCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCCGTGCTCGGAGCTG 	4132
Db	4061	AAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAGACCTCAGATGGGTACCTTGCCAGCAAGA	4120

Qy 4133 ACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCGTGGCGACGAG 4192
 | | | | | | | | | | | | | | | | | |
 Db 4121 CGAAACAGGCGGGCCTTCGGGGACAAGCAGAGCTGTCTTCGCCCCGTTCAGTGAAGATGAT 4180

Qy 4193 GGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGAC 4252
 | | | | | | | | | | | | | | | | | |
 Db 4181 GCTGCTG-----ATCCAAATGAT 4198

Qy 4253 CCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTGGGCCAGGGC 4312
 | | | | | | | | | | | | | | | | | |
 Db 4199 TCTGACATAGACCCAGAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGG 4258

Qy 4313 AGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAA 4372
 | | | | | | | | | | | | | | | | | |
 Db 4259 TCCTACCAGGTGAAAGGCTGGAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAG 4318

Qy 4373 CGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCC 4432
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 Db 4319 AGACTGCTAATTGCCAGACGGAGTCGGAAGGATTTTTTGTCTCAGATTGTCTTGCCAGCT 4378

Qy 4433 TTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCC 4492
 | | | | | | | | | | | | | | | | | |
 Db 4379 GTGTTTGTCTGCATTGCCCTTGTGTTTACGCTGATCGTGCCACCCTTTGGCAAGTACCCC 4438

Qy 4493 CCGCTGGTCCTGTACCTTCCCAGTACCACAACTACACCCAGCCCCGTGGCAATTTTCATC 4552
 | | | | | | | | | | | | | | | | | |
 Db 4439 AGCCTGGAACCTTCAGCCCTGGATGTACAACGAACAGTACACATTTGTGCAATGATGCT 4498

Qy 4553 CCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCC 4612
 | | | | | | | | | | | | | | | | | |
 Db 4499 CCTGA-----GGACACGGGAACC 4516

Qy 4613 CAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAG 4672
 | | | | | | | | | | | | | | | | | |
 Db 4517 CTGGAACCTCTTAAACGCCCTCACCAAAGACCCTGGCTTCGGGACCCGCTGTATGGAAGGA 4576

Qy 4673 TCTCCCGCCAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTG 4732
 | | | | | | | | | | | | | | | | | |
 Db 4577 AACCCAATCCCAGACACGCCCTG--CCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCAG 4634

Qy 4733 CTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCTTACACAGGGGCTGCCACTG 4792
 | | | | | | | | | | | | | | | | | |
 Db 4635 -----TTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAAGTGGACAA 4679

Qy 4793 TCCAATTTCTGTGCCACCCCCACCTCGCCCCGCCCATCTGACTCGCCAGCGTCCCCGGAT 4852
 | | | | | | | | | | | | | | | | | |
 Db 4680 TGCAGAACCCTTCACCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTG 4739

Qy 4853 GAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCACCGCTGGGCCAGAAATGTGGACG 4912
 | | | | | | | | | | | | | | | | | |
 Db 4740 TGTGTCCCCCAGGGGAGGGGGCTGCCTCCTCCACAAAGAAAACAAACACTGCAGATA 4799

Qy 4913 TCGGCACCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAG 4972
 | | | | | | | | | | | | | | | | | |
 Db 4800 TCCTTCAGGACCTGACAGGAAGAAACATTTTCGGATTATCTGGTGAAGACG-TATGTGCAG 4858

Qy 4973 GGCACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAG-ATGCGGGTGGT 5031
 | | | | | | | | | | | | | | | | | | | | | |
 Db 4859 ATCATAGCCAAAAGCTTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTT 4918

Qy 5032 CACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCAC 5091
 | | | | | | | | | | | | | | | | | | | | | |
 Db 4919 TCCCTGGGTGTCAGTAATACTCAAGCACTTCCCTCCGAGTCAAGAAGTTAATGAT----GC 4974

Qy 5092 CTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAGTC 5151
 | | | | | | | | | | | | | | | | | | | | | |
 Db 4975 CACCAAACAAATGAAGAAACACCTAAAGCTGGCCA-----AGGACAG 5016

Qy 5152 CATCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAG 5211
 | | | | | | | | | | | | | | | | | | | | | |
 Db 5017 TTCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCAGAAA 5076

Qy 5212 GGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAG 5271
 | | | | | | | | | | | | | | | | | | | | | |
 Db 5077 TAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATGT 5136

Qy 5272 CCTCAACAACGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTA 5331
 | | | | | | | | | | | | | | | | | | | | | |
 Db 5137 CATCAACAATGCCATTCTCCGGGCCAACCTGCAAAGGGAGAG---AACCTAGCCATTA 5193

Qy 5332 CGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTA 5391
 | | | | | | | | | | | | | | | | | | | | | |
 Db 5194 TGGAAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGC 5253

Qy 5392 CCTGCTGCAGGGCAC---GGATGTGCTCATCGCCATCTTCATCATCGTGGCCATGTCCTT 5448
 | | | | | | | | | | | | | | | | | | | | | |
 Db 5254 TCCGATGACCACATCAGTGGATGTCCTTGTGTCCATCTGTGTCATCTTTGCAATGTCCTT 5313

Qy 5449 CGTGCCGGCCAGCTTCGTTGTCTTCCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCT 5508
 | | | | | | | | | | | | | | | | | | | | | |
 Db 5314 CGTCCCAGCCAGCTTTGTCTGATTTCCTGATCCAGGAGCGGGTCAGCAAAGCAAAACACCT 5373

Qy 5509 GCAGTTTGTGTCAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACAT 5568
 | | | | | | | | | | | | | | | | | | | | | |
 Db 5374 GCAGTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTCTCTAATTTTGTCTGGGATAT 5433

Qy 5569 GCTCAACTACCTGGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTGACCTGCC 5628
 | | | | | | | | | | | | | | | | | | | | | |
 Db 5434 GTGCAATTACGTTGTCCCTGCCACACTGGTCATTATCATCTTCATCTGCTTCCAGCAGAA 5493

Qy 5629 GGCCTACACGTCGCCCACCAACTTCCCTGCCGTCCCTCTCCCTCTTCCCTGCTCTATGGGTG 5688
 | | | | | | | | | | | | | | | | | | | | | |
 Db 5494 GTCCTATGTGTCCTCCACCAATCTGCCTGTGCTAGCCCTTCTACTTTTGTGTATGGGTG 5553

Qy 5689 GTCCATCACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTA 5748
 | | | | | | | | | | | | | | | | | | | | | |
 Db 5554 GTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTCAAGATCCCCAGCACAGCCTA 5613

Qy 5749 CGTGTTCCTCATTGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCT 5808
 | | | | | | | | | | | | | | | | | | | | | |
 Db 5614 TGTGGTGCTCACCAGCGTGAACCTCTTCATTGGCATTAATGGCAGCGTGGCCACCTTTGT 5673

Qy 5809 GCTACAGCTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTG 5868

[illegible]

Db	6499	GCCTCCTGTGGTGTTCCTGGATGAACCCACCACAGGCATGGATCCCCAAAGCCCGGCGGTT	6558
Qy	6706	CCTCTGGAACCTCATCCTCGACCTCATCAAGACAGGGCGTTCAAGTGGTGCTGACATCACA	6765
Db	6559	CTTGTGGAATTGTGCCCTAAGTGTGTCAAGGAGGGGAGATCAGTAGTGCTTACATCTCA	6618
Qy	6766	CAGCATGGAGGAGTGCAGGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCT	6825
Db	6619	TAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGAAGGTT	6678
Qy	6826	GCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCAC	6885
Db	6679	CAGGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGGAGATGGTTATACAATAGT	6738
Qy	6886	GGTGC GGA---CCAAGAGCAGCCAGAGTGTGAAGGACGTGGTGC GGTTCCTCAACCGCAA	6942
Db	6739	TGTACGAATAGCAGGGTCCAACCCGGACCTGAAGCCTGTCCAGGATTTCTTTGGACTTGC	6798
Qy	6943	CTTCCCGGAAGCCATGCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTC	7002
Db	6799	ATTTCTGGAAGTGTTCAAAAGAGAAACACCGGAACATGCTACAATACCAGCTTCCATC	6858
Qy	7003	GGAGCACATCTCGCTGGCCCAGGTGTTTACAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGG	7062
Db	6859	TTCATTATCTTCTCTGGCCAGGATATTACAGCATCCTCTCCCAGAGCAAAAAGCGACTCCA	6918
Qy	7063	CATCGAGGACTACTCGGTCAGCCAGACCACACTGGACAATGTGTTTCGTGAACCTTGCCAA	7122
Db	6919	CATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACCTTGCCAA	6978
Qy	7123	GAAGCAGAGTGA	7134
Db	6979	GGACCAAAAGTGA	6990

Search completed: September 8, 2004, 05:10:44
Job time : 2691 secs

OM nucleic - nucleic search, using sw model

Run on: September 8, 2004, 04:27:58 ; Search time 560 Seconds
 (without alignments)
 7967.509 Million cell updates/sec

Title: US-10-088-467-1
 Perfect score: 8040
 Sequence: 1 ccgcggcgctgaggcgggcg.....aaataaataaacaataatgtc 8040

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	986.6	12.3	7860	4	US-09-526-193A-2	Sequence 2, Appli
2	612.6	7.6	3609	4	US-09-833-381-958	Sequence 958, App
3	547	6.8	2075	4	US-09-833-381-962	Sequence 962, App
4	476.8	5.9	515	4	US-09-833-381-1079	Sequence 1079, Ap
5	450.4	5.6	5894	3	US-08-665-259-24	Sequence 24, Appl
6	450.4	5.6	5894	3	US-08-762-500-24	Sequence 24, Appl
7	450.4	5.6	6525	3	US-08-762-500-74	Sequence 74, Appl
8	416.2	5.2	506	4	US-09-833-381-1078	Sequence 1078, Ap
c 9	139.2	1.7	999	4	US-09-252-991A-4588	Sequence 4588, Ap
10	139.2	1.7	1008	4	US-09-252-991A-4266	Sequence 4266, Ap
11	130	1.6	1614	4	US-09-252-991A-4198	Sequence 4198, Ap

	12	129.2	1.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	13	129.2	1.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	14	126.2	1.6	930	4	US-09-252-991A-4633	Sequence 4633, Ap
c	15	126.2	1.6	1179	4	US-09-252-991A-4241	Sequence 4241, Ap
	16	126.2	1.6	1719	4	US-09-252-991A-4534	Sequence 4534, Ap
	17	120.8	1.5	1824	4	US-09-252-991A-1780	Sequence 1780, Ap
	18	120	1.5	36181	4	US-08-311-731A-120	Sequence 120, App
c	19	119.8	1.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	20	119.2	1.5	972	4	US-09-489-039A-5325	Sequence 5325, Ap
c	21	118.4	1.5	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	22	111	1.4	2769	4	US-09-489-039A-1767	Sequence 1767, Ap
c	23	109.6	1.4	762	4	US-09-252-991A-1938	Sequence 1938, Ap
c	24	109.2	1.4	963	4	US-09-252-991A-15453	Sequence 15453, A
	25	109.2	1.4	1038	4	US-09-252-991A-15386	Sequence 15386, A
	26	102.8	1.3	1614	4	US-09-252-991A-6293	Sequence 6293, Ap
	27	102.8	1.3	2790	4	US-09-252-991A-6375	Sequence 6375, Ap
c	28	102.8	1.3	3948	4	US-09-252-991A-6175	Sequence 6175, Ap
	29	101.4	1.3	1767	4	US-09-489-039A-6408	Sequence 6408, Ap
c	30	100.8	1.3	536165	4	US-09-214-808-1	Sequence 1, Appli
	31	98	1.2	1350	4	US-09-833-381-1082	Sequence 1082, Ap
	32	97	1.2	621	4	US-09-266-965-79	Sequence 79, Appl
c	33	97	1.2	18034	4	US-09-266-965-75	Sequence 75, Appl
c	34	92.8	1.2	1116	4	US-09-252-991A-10924	Sequence 10924, A
	35	92.8	1.2	1209	4	US-09-252-991A-11138	Sequence 11138, A
	36	90.8	1.1	20284	4	US-09-526-193A-21	Sequence 21, Appl
	37	90.2	1.1	1239	4	US-09-252-991A-8289	Sequence 8289, Ap
	38	89.2	1.1	1077	4	US-09-252-991A-10970	Sequence 10970, A
c	39	89.2	1.1	1179	4	US-09-252-991A-11273	Sequence 11273, A
	40	87.2	1.1	6289	4	US-09-526-193A-26	Sequence 26, Appl
	41	87	1.1	531	4	US-09-252-991A-8239	Sequence 8239, Ap
	42	87	1.1	1113	4	US-09-252-991A-4148	Sequence 4148, Ap
c	43	87	1.1	1302	4	US-09-252-991A-4458	Sequence 4458, Ap
	44	87	1.1	1314	4	US-09-252-991A-4290	Sequence 4290, Ap
	45	87	1.1	4244	4	US-09-526-193A-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1

US-09-526-193A-2

; Sequence 2, Application US/09526193A

; Patent No. 6617122

; GENERAL INFORMATION:

; APPLICANT: Hayden, Michael R.

; APPLICANT: Brooks-Wilson, Angela R.

; APPLICANT: Pimstone, Simon N.

; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING

; TITLE OF INVENTION: CHOLESTEROL LEVELS

; FILE REFERENCE: 50110/002005

; CURRENT APPLICATION NUMBER: US/09/526,193A

; CURRENT FILING DATE: 2000-03-15

; PRIOR APPLICATION NUMBER: 60/124,702

; PRIOR FILING DATE: 1999-03-15

; PRIOR APPLICATION NUMBER: 60/138,048

; PRIOR FILING DATE: 1999-06-08

; PRIOR APPLICATION NUMBER: 60/139,600

; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-526-193A-2

Query Match 12.3%; Score 986.6; DB 4; Length 7860;
Best Local Similarity 52.6%; Pred. No. 1.5e-177;
Matches 2847; Conservative 0; Mismatches 2309; Indels 255; Gaps 22;

Qy	1745	TTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCATTGTC	1804
Db	1575	TTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCCATAGCAACAGAAGTCTGGCTCATC	1634
Qy	1805	AACTACACCCTCAACCAGGCCTACCAGGACAACGTCACCTGTTTTTGCCAGTGTGATCTTC	1864
Db	1635	AACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTGTGTTCACTGGA	1694
Qy	1865	CAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAACTCC	1924
Db	1695	ATTACTCCAGGCAGCATTGAGCTGCCCCATCATGTCAAGTACAAGATCCGAATGGACATT	1754
Qy	1925	AGCTTCACCCGAGAAAAACCAACGAGATCCGCCCGCCTACTGGCGGCCTGGGCCCCAATACT	1984
Db	1755	GACAAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACCCTGGTCTCGAGCT	1814
Qy	1985	GGCGGCCGCTTCTACTTCCTCTAC-----GGCTTCGTCTGGATCCAGGACATGATG	2035
Db	1815	GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG	1874
Qy	2036	GAGCGCGCCATCATCGACACTTTTGTGGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTG	2095
Db	1875	GAGCAGGCAATCAT---CAGGGTGCTGACGGGCACCGAGAAGAAAACCTGGTGTCTATATG	1931
Qy	2096	CAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTCTATTGAGCACATG	2155
Db	1932	CAACAGATGCCCTATCCCTGTTACGTTGATGACATCTTCTGCGGGTGATGAGCCGGTCA	1991
Qy	2156	ATGCCGCTGTGCAATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATC	2215
Db	1992	ATGCCCCCTTTCATGACGCTGGCCTGGATTTACTCAGTGGCTGTGATCATCAAGGGCATC	2051
Qy	2216	GTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCG	2275
Db	2052	GTGTATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACAGC	2111
Qy	2276	GTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCA	2335
Db	2112	ATCCTCTGGTTAGCTGGTTCATTAGTAGCCTCATTCTCTTCTTGTGAGCGCTGGCCTG	2171
Qy	2336	CTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGG	2395

Db 2172 CTAGTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTTT 2231
 Qy 2396 CTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTG 2455
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 Db 2232 GTCTTCCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCCTGATTAGCACACTC 2291
 Qy 2456 TACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTG 2515
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 Db 2292 TTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTG 2351
 Qy 2516 CCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAG 2575
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 Db 2352 CCCTAC-----GTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTC 2399
 Qy 2576 AAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCG 2635
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 Db 2400 AAGATCTTCGCTAGCCTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCC 2459
 Qy 2636 CTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAG 2695
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 Db 2460 CTTTTTGGAGGAGCAGGGCATTGGAGTGCAGTGGGACAACCTGTTTGAGAGTCTGTGGAG 2519
 Qy 2696 GGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTAT 2755
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 Db 2520 GAAGATGGCTTCAATCTCACCCTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTAT 2579
 Qy 2756 GGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCC 2815
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 Db 2580 GGGGTGATGACCTGGTACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATCCCAGGCC 2639
 Qy 2816 TGGTACTTCCCCTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAG 2875
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 Db 2640 TGGTATTTTCCTTGCACCAAGTCCTACTGGTTTGGCGAGGAAAG----- 2683
 Qy 2876 TGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTGTCATGGAGGAGGACCAGGCCTGT 2935
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 Qy 2936 GCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACCCACCTG 2995
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 Db 2706 TCCAACCAGAAGAGAATATCAGA-----AATCTGCATGGAGGAGGAACCCACCCACTTG 2759
 Qy 2996 CCTCTGGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCC 3055
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 Db 2760 AAGCTGGGCGTGTCCATTGAGAACCTGGTAAAAGTCTACCGAGATGGGATGAAGGTGGCT 2819
 Qy 3056 CTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAAC 3115
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 Db 2820 GTCGATGGCCTGGCACTGAATTTTATGAGGGCCAGATCACCTCCTTCTTGGGCCACAAT 2879
 Qy 3116 GGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGT 3175
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 Db 2880 GGAGCGGGGAAGACGACCACCATGTCAATCCTGACCGGGTGTTCCTCCCGACCTCGGGC 2939
 Qy 3176 TCCGCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTG 3235
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 Db 2940 ACCGCCTACATCCTGGGAAAAGACATTGCTCTGAGATGAGCACCATCCGGCAGAACCTG 2999

Qy	3236	GGCATGTGCCCCGAGCACAAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGG	3295
Db	3000	GGGGTCTGTCCCCAGCATAACGTGCTGTTTGACATGCTGACTGTCTGAAGAACACATCTGG	3059
Qy	3296	TTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATG	3355
Db	3060	TTCTATGCCCGCTTGAAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATG	3119
Qy	3356	ATCGAGGACCTGG---AGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCTGGGT	3412
Db	3120	GCCCTGGATGTTGGTTTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTCTAGGT	3179
Qy	3413	GGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATC	3472
Db	3180	GGAATGCAGAGAAAGCTATCTGTGGCCTTGGCCTTTGTCTGGGGGATCTAAGGTTGTCATT	3239
Qy	3473	CTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATC	3532
Db	3240	CTGGATGAACCCACAGCTGGTGTGGACCCCTACTCCCGCAGGGGAATATGGGAGCTGCTG	3299
Qy	3533	CTGAAGTACAAGCCAGGCCGCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGAC	3592
Db	3300	CTGAAATACCGACAAGGCCGCGACCATATTTCTCTCTACACACCACATGGATGAAGCGGAC	3359
Qy	3593	CTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCG	3652
Db	3360	GTCCTGGGGGACAGGATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCC	3419
Qy	3653	CTCTTCCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCC	3712
Db	3420	CTGTTTCTGAAGAACCAGCTGGGAACAGGCTACTACCTGACCTGGTCAAGAAAGATGTG	3479
Qy	3713	GAGCCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGGCCCCGCTG	3772
Db	3480	G-----AATCCTCCCTCAGTTCCTGCAGAAACAGTAGTAGCACTGTGTCA	3524
Qy	3773	AGCAGCTGCTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTG	3832
Db	3525	TACCTGAAAAAGGAGGACAGTGTTCCTCAGAGCAGTTCCTGATGCTGGCCTGGGCAGCGAC	3584
Qy	3833	CTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCAGCGAGGCCGCCAAGAAG	3892
Db	3585	CATGAGAGTGACACGCTGACCATCGATGTCTCTGCTATCTCCAACCTCATCAGGAAGCAT	3644
Qy	3893	GGGGCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGC	3952
Db	3645	GTGTCTGAAGCCCGGCTGGTGGGAAGACATAGGGCATGAGCTGACCTATGTGCTGCCATAT	3704
Qy	3953	AGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCTGGAGGAGGAT	4012
Db	3705	GAA---GCTGCTAAGGAGGGAGCCTTTGTGGAACCTTTTCATGAGATTGATGACCGGCTC	3761
Qy	4013	CAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGG	4072
Db	3762	TCAGACCTGGGCATTTCTAGTTATGGCATCTCAGAGACGACCCTGGAAGAAATATTCCTC	3821

Qy 4073 GCGGAGGGCCCGCGCTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTG 4132
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 Db 3822 AAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAGACCTCAGATGGTACCTTGCCAGCAAGA 3881
 Qy 4133 ACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAG 4192
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 Db 3882 CGAAACAGGCGGGCCTTCGGGGACAAGCAGAGCTGTCTTCGCCCCTTCACTGAAGATGAT 3941
 Qy 4193 GGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGAC 4252
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 Db 3942 GCTGCTG-----ATCCAAATGAT 3959
 Qy 4253 CCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTTCGGCCAGGGC 4312
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 Db 3960 TCTGACATAGACCCAGAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGG 4019
 Qy 4313 AGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAA 4372
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 Db 4020 TCCTACCAGGTGAAAGGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAG 4079
 Qy 4373 CGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCAGATCTTGCTGCCAGCC 4432
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 Db 4080 AGACTGCTAATTGCCAGACGGAGTCGGAAGGATTTTGTCTCAGATTGTCTTGCCAGCT 4139
 Qy 4433 TTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCC 4492
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 Db 4140 GTGTTTGTCTGCATTGCCCTTGTGTTTCAGCCTGATCGTGCCACCCCTTGGCAAGTACCCC 4199
 Qy 4493 CCGCTGGTCCTGTCACCTTCCCAGTACCACAACACACCCAGCCCCGTGGCAATTTTCATC 4552
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 Db 4200 AGCCTGGAACCTCAGCCCTGGATGTACAACGAACAGTACACATTTGTGAGCAATGATGCT 4259
 Qy 4553 CCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCC 4612
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 Db 4260 CCTGA-----GGACACGGGAACC 4277
 Qy 4613 CAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAG 4672
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 Db 4278 CTGGAACCTCTAAACGCCCTCACCAAAGACCCTGGCTTCGGGACCCGCTGTATGGAAGGA 4337
 Qy 4673 TCTCCCGCCAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTG 4732
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 Db 4338 AACCCAATCCCAGACACGCCCTG--CCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCAG 4395
 Qy 4733 CTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGGCTGCCACTG 4792
 ||| || | | | || || || || || || || || ||
 Db 4396 -----TTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAACCTGGACAA 4440
 Qy 4793 TCCAATTTCTGTGCCACCCCAACCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGAT 4852
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 Db 4441 TGCAGAACCTTCACCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTG 4500
 Qy 4853 GAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCACCGCTGGGCCAGAAATGTGGACG 4912
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 Db 4501 TGTGTCCCCCAGGGGCAGGGGGGCTGCCTCCTCCACAAAAGAAAACAAAACACTGCAGATA 4560
 Qy 4913 TCGGCACCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAG 4972

Db	4561	TCCTTCAGGACCTGACAGGAAGAAACATTTTCGGATTATCTGGTGAAGACG-TATGTGCAG	4619
Qy	4973	GGCACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTC	5032
Db	4620	ATCATAGCCAAAAGCTTAAAGAACAAGATCTGGGTGAATGAG-----TTTAGGTATGGCG	4674
Qy	5033	ACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACC	5092
Db	4675	GCTTTTCCCTGGGTGTCAGTAATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATG	4734
Qy	5093	TCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCC	5152
Db	4735	CCATCAAACAAATGAAGAAACACCTAAAG-----CTGGCCAAGGACAGT	4778
Qy	5153	ATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGG	5212
Db	4779	TCTGCAGATCGATTTCTCAACAGCTTGGGAAGATTTATGACAGGACTGGACACCAGAAAT	4838
Qy	5213	GCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAGC	5272
Db	4839	AATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATGTC	4898
Qy	5273	CTCAACAACGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTAC	5332
Db	4899	ATCAACAATGCCATTCTCCGGGCCAACCTGCAAAAGGGAGAG---AACCTAGCCATTAT	4955
Qy	5333	GGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTAC	5392
Db	4956	GGAATTACTGCTTTCAATCATCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGCT	5015
Qy	5393	CTGCTGCAGGGCAC---GGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCTTTC	5449
Db	5016	CTGATGACCACATCAGTGGATGTCTTGTGTCCATCTGTGTCTCTTTGCAATGTCTTTC	5075
Qy	5450	GTGCCGGCCAGCTTCGTTGTCTTCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTG	5509
Db	5076	GTCCCAGCCAGCTTTGTCGTATTCTCGATCCAGGAGCGGGTCAGCAAAGCAAAACACCTG	5135
Qy	5510	CAGTTTGTGAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATG	5569
Db	5136	CAGTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTCTCTAATTTGTCTGGGATATG	5195
Qy	5570	CTCAACTACCTGGTCCCCGCTACCTGCTGTGTCTCATCATCCTGTTTGTGTTTCGACCTGCCG	5629
Db	5196	TGCAATTACGTTGTCCCTGCCACACTGGTCATTATCATCTTCATCTGCTTCCAGCAGAAG	5255
Qy	5630	GCCTACACGTCGCCCACCAACTTCCCTGCCGTCCTCTCCCTCTTCTGCTCTATGGGTGG	5689
Db	5256	TCCTATGTGTCCTCCACCAATCTGCCTGTGCTAGCCCTTCTACTTTTGCTGTATGGGTGG	5315
Qy	5690	TCCATCACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTAC	5749
Db	5316	TCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTCAAGATCCCCAGCACAGCCTAT	5375
Qy	5750	GTGTTCCCTCATTTGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTG	5809

Db	5376	GTGGTGTCTCACCAGCGTGAACCTCTTCATTGGCATTAAATGGCAGCGTGGCCACCTTTGTG	5435
Qy	5810	CTACAGCTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGC	5869
Db	5436	CTGGAGCTGTTC---ACCGACAATAAGCTGAATAATATCAATGATATCCTGAAGTCCGTG	5492
Qy	5870	TTCCTCATTTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAG	5929
Db	5493	TTCTTGATCTTCCCACATTTTGCCTGGGACGAGGGCTCATCGACATGGTGAAAACCAG	5552
Qy	5930	TACATCAACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAG	5989
Db	5553	GCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAATCGCTTTGT---GTCACCATTATCT	5609
Qy	5990	TGGGACATTGTCAACCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTC	6049
Db	5610	TGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGGGTGGTGTTCCTCCTC	5669
Qy	6050	CTGACCATCATGTGCCAGTACAACCTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACC	6109
Db	5670	ATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCAGACCTGTAAATGCAAAGCTA	5729
Qy	6110	AAGCCTGTG---GAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGA	6166
Db	5730	TCTCCTCTGAATGATGAAGATGAAGATGTGAGGCGGGAAAGACAGAGAATTCTTGATGGT	5789
Qy	6167	GACGCCGACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAG	6226
Db	5790	GGAGGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATATA-----TAGA	5840
Qy	6227	ATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTC	6286
Db	5841	AGGAAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCATTCTCCTGGTGAGTGCTTT	5900
Qy	6287	GGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGAC	6346
Db	5901	GGGCTCCTGGGAGTTAATGGGGCTGGAATAATCATCAACTTTCAAGATGTTAACAGGAGAT	5960
Qy	6347	GAGAGCACGACGGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTC	6406
Db	5961	ACCACTGTTACCAGAGGAGATGCTTTCCTTAACAAAATAGTATCTTATCAAACATCCAT	6020
Qy	6407	CAGGTGCAGCAGAGCCTCGGCTACTGCCCGCAGTGTGACGCGCTGTTGACGAGCTCACG	6466
Db	6021	GAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTGTTGACT	6080
Qy	6467	GCCCGGGAGCACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCC	6526
Db	6081	GGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAAGTTGGC	6140
Qy	6527	CGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCT	6586
Db	6141	AAGGTTGGTGAGTGGGCGATTTCGGAACCTGGGCCTCGTGAAGTATGGAGAAAAATATGCT	6200
Qy	6587	GGCACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTAC	6646
Db	6201	GGTAACTATAGTGGAGGCAACAACGCAAGCTCTCTACAGCCATGGCTTTGATCGGCGGG	6260

Query Match 7.6%; Score 612.6; DB 4; Length 3609;
Best Local Similarity 61.0%; Pred. No. 6.6e-107;
Matches 1151; Conservative 0; Mismatches 694; Indels 42; Gaps 8;

Qy	5218	CCAGGTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAA	5277
Db	1587	CAAGATCTGGTTCAACAACAAAGGCTGGCACTCCATGGTGGCCTTTGTCAACCGAGCCAG	1646
Qy	5278	CAACGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCAT	5337
Db	1647	CAACGCAATCCTCCGTGCTCACCTGCCCCAGGCCCGGCCCGCC---ACGCCACAGCAT	1703
Qy	5338	CACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCT	5397
Db	1704	CACCACACTCAACCACCCCTTGAACCTCACCAAGGAGCAGCTGTCTGAGGGTGCCTGAT	1763
Qy	5398	GCAGGGCAC---GGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCC	5454
Db	1764	GGCCTCCTCGGTGGACGTCCTCGTCTCCATCTGTGTGGTCTTTGCCATGTCCTTTGTCCC	1823
Qy	5455	GGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTT	5514
Db	1824	GGCCAGCTTCACTCTTGTCTCATTGAGGAGCGAGTCACCCGAGCCAAGCACCTGCAGCT	1883
Qy	5515	TGTCAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAA	5574
Db	1884	CATGGGGGGCCTGTCCCCCACCCTCTACTGGCTTGGCAACTTTCTCTGGGACATGTGTAA	1943
Qy	5575	CTACCTGGTCCCCGCTACCTGCTGTGTATCATCTCTGTTGTGTTGACCTGCCGGCCTA	5634
Db	1944	CTACTTGGTGCCAGCATGCATCGTGGTGTCTATCTTTCTGGCCTTCCAGCAGAGGGCATA	2003
Qy	5635	CACGTCGCCCACCAACTTCCCTGCCGTCCTCTCCCTCTTCTCTGCTCTATGGGTGGTCCAT	5694
Db	2004	TGTGGCCCCGTGCAACCTGCCTGCTCTCTGCTGTTGCTACTACTGTATGGCTGGTTCGAT	2063
Qy	5695	CACGCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTT	5754
Db	2064	CACACCGCTCATGTACCCAGCCTCCTTCTTCTCTCCGTGCCAGCACAGCCTATGTGGT	2123
Qy	5755	CCTCATGTGCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCTGTGCTACA	5814
Db	2124	GCTCACCTGCATAAACCTCTTTATTGGCATCAATGGAAGCATGGCCACCTTTGTGCTTGA	2183
Qy	5815	GCTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCT	5874
Db	2184	GCTCTTC---TCTGATCAGAAGCTGCAGGAGGTGAGCCGGATCTTGAAACAGGTCTTCCT	2240
Qy	5875	CATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACAT	5934
Db	2241	TATCTTCCCCACTTCTGCTTGGGCCGGGGGCTCATTGACATGGTGCAGAACAGGCCAT	2300
Qy	5935	CAACGAGTACTACGCCAAGATTGGCCAGTTTGAC-----AAGATGAAGTC	5979
Db	2301	GGCTGATGCCTTTGAGCGCTTGGGTGAGAACTTCTGTCTCAGGAGACAGGCAGTTCCAGTC	2360

Qy 5980 CCCGTTTCGAGTGGGACATTGTACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCTGT 6039
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 Db 2361 ACCCCTGCGCTGGGAGGTGGTTCGGCAAGAACCTCTTGGCCATGGTGATACAGGGGGCCCT 2420

Qy 6040 GGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTTCTGCGGCGGCCACAGCGCATGCC 6099
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 Db 2421 CTTCTTCTCTTCACACTACTGCTGCAGCACCGAAGCCAACTCCTGCCACAGCCCAGGGT 2480

Qy 6100 TGTGTCT---ACCAAGCCTGTGGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGT 6156
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 Db 2481 GAGGTCTCTGCCACTCCTGGGAGAGGAGGACGAGGATGTAGCCCGTGAACGGGAGCGGGT 2540

Qy 6157 GCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAA 6216
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 Db 2541 GGTCCAAGGAGCCACCCAGGGGGATGTGTTGGTGCTGAGGAACCTGACCAAGGTATACCG 2600

Qy 6217 GTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCTCTGG 6276
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 Db 2601 TGGGCAGAGGATG-----CCAGCTGTTGACCGCTTGTGCCTGGGGATTCCCCCTGG 2651

Qy 6277 CGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCT 6336
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 Db 2652 TGAGTGTTTTGGGCTGCTGGGTGTGAATGGAGCAGGGAAGACGTCCACGTTTCGCATGGT 2711

Qy 6337 GACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAA 6396
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 Db 2712 GACGGGGGACACATTGCCAGCAGGGGGCGAGGCTGTGCTGGCAGGCCACAGCGTGCCCCG 2771

Qy 6397 GGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCAGTGACGCGCTGTTCTGA 6456
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 Db 2772 GGAACCCAGTGCTGCGCACCTCAGCATGGGATACTGCCCTCAATCCGATGCCATCTTTGA 2831

Qy 6457 CGAGCTCACGGCCCCGGGAGCACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAA 6516
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 Db 2832 GCTGCTGACGGGCCGCGAGCACCTGGAGCTGCTTGCGCGCCTGCGCGGTGTCCCGGAGGC 2891

Qy 6517 GGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGA 6576
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2892 CCAGGTTGCCAGACCGCTGGCTCGGGCCTGGCGCGTCTGGGACTCTCATGGTACGCAGA 2951

Qy 6577 CAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCT 6636
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2952 CCGGCCCTGCAGGCACCTACAGCGGAGGGAACAAACGCAAGCTGGCGACGGCCCTGGCGCT 3011

Qy 6637 CATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAGGC 6696
 | | | | | | | | | | | | | | | | | | | | | |
 Db 3012 GGTGGGGACCCAGCCGTGGTGTCTTCTGGACGAGCCGACCACAGGCATGGACCCAGCGC 3071

Qy 6697 CCGGCGCTTCCTCTGGAACCTCATCCTCGACCTCATCAAGACAGGGCGTTCAGTGGTGCT 6756
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 Db 3072 GCGGCGCTTCCTTTGGAACAGCCTTTTGCCGTGGTGCGGGAGGGCCGTTCAGTGATGCT 3131

Qy 6757 GACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAA 6816
 | | | | | | | | | | | | | | | | | | | | | |
 Db 3132 CACCTCCCATAGCATGGAGGAGTGTGAAGCGCTCTGCTCGCGCCTGGCCATCATGGTGAA 3191

Qy 6817 CGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTA 6876

Db	159	GTCCCCCACCTCTACTGGCTTGGCAACTTTCTCTGGGACATGTGTAACCTACTTGGTGCC	218
Qy	5587	CGCTACCTGCTGTGTCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTCGCCCAC	5646
Db	219	AGCATGCATCGTGGTGCTCATCTTTCTGGCCTTCCAGCAGAGGGCATATGTGGCCCCTGC	278
Qy	5647	CAACTTCCCTGCCGTCCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCCCATCAT	5706
Db	279	CAACCTGCCTGCTCTCCTGCTGTTGCTACTACTGTATGGCTGGTCGATCACACCGCTCAT	338
Qy	5707	GTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCTCATTTGTCAT	5766
Db	339	GTACCCAGCCTCCTTCTTCTTCTCCGTGCCAGCACAGCCTATGTGGTGCTCACCTGCAT	398
Qy	5767	CAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCA	5826
Db	399	AAACCTCTTTATTGGCATCAATGGAAGCATGGCCACCTTTGTGCTTGAGCTCTTC---TC	455
Qy	5827	CGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAA	5886
Db	456	TGATCAGAAGCTGCAGGAGGTGAGCCGGATCTTGAAACAGGTCTTCCTTATCTTCCCCCA	515
Qy	5887	CTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTA	5946
Db	516	CTTCTGCTTGGGCCGGGGGCTCATTGACATGGTGCGGAACCAGGCCATGGCTGATGCCTT	575
Qy	5947	CGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGAGGACATTGTCACCCG	6006
Db	576	TGAGCGCTTGGGAGACAGGC---AGTTCAGTCACCCCTGCGCTGGGAGGTGGTCGGCAA	632
Qy	6007	CGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCA	6066
Db	633	GAACCTCTTGGCCATGGTGATACAGGGGCCCTCTTCTTCTTTCACACTACTGCTGCA	692
Qy	6067	GTACAACTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCT---ACCAAGCCTGTGGAGGA	6123
Db	693	GCACCGAAGCCAACTCCTGCCACAGCCCAGGGTGAGGTCTCTGCCACTCCTGGGAGAGGA	752
Qy	6124	TGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACAT	6183
Db	753	GGACGAGGATGTAGCCCGTGAACGGGAGCGGGTGGTCCAAGGAGCCACCCAGGGGGATGT	812
Qy	6184	GGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGC	6243
Db	813	GTTGGTGCTGAGGAACTTGACCAAGGTATACCGTGGGCAGA-----GGATGCCAGC	863
Qy	6244	CGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAA	6303
Db	864	TGTTGACCGCTTGTGCCTGGGGATTCCCCCTGGTGAGTGTTTGTGCTGGTGGGGGCCAA	923
Qy	6304	CGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGG	6363
Db	924	TGGAGCAGGGAATACGTCGACGCTCCGCATGGTGACGGGGCACACATTCTCCACCAGAGA	983
Qy	6364	CGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCT	6423


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; Sequence 1079, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1079
; LENGTH: 515
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-1079

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Query Match          5.9%; Score 476.8; DB 4; Length 515;
Best Local Similarity 99.0%; Pred. No. 2e-81;
Matches 511; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

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Qy      435  GCCCCGGGCACCTCGGGGAGCCACCTGGAC-AGATCCACAGTGTCTTCCTTCTCTCTGGAC 493
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Db        2  GCCCCCGCACCTCGGGGAGCCACCTGGACAAGATCCACAGTGTCTTCCTTCTCTCTGGAC 61

Qy      494  TCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAACTTGTCGCTGCCC 553
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        62  TCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAACTTGTCGCTGCCC 121

Qy      554  AATAGCACGGCCCAAGCACTCTTGCCGCCCCGTGTGGACCCGCCCGAGGTCTACCACTG 613
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       122  AATAGCACGGCCCAAGCACTCTTGCCGCCCCGTGTGGACCCGCCCGAGGTCTACCACTG 181

Qy      614  CTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAAGGGTCAGGAGCCC 673
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       182  CTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAAGGGTCAGGAGCCC 241

Qy      674  TGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCTGCTGGCTCCTGCC 733
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       242  TGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCTGCTGGCTCCTGCC 301

Qy      734  CTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCGGATCCTCACTGTG 793
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       302  CTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCGGATCCTCACTGTG 361

Qy      794  CCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTGCAGTGGGCAGGCT 853
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       362  CCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTGCAGTGGGCAGGCT 421

Qy      854  GCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAACCAGCTGGACGTG 913
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       422  GCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCT-CGGAACCAGCTGGACGTG 480

Qy      914  GCCAAGGTCTCCAGCAGCTGGGCCTGGATGCCCCC 949
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Db       481  G-CAAGGTCTCCAGCAGCTGGGCCTGGATGCCCCC 515

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RESULT 5
 US-08-665-259-24
 ; Sequence 24, Application US/08665259
 ; Patent No. 6028173
 ; GENERAL INFORMATION:
 ; APPLICANT: Landes, Gregory M.
 ; APPLICANT: Burn, Timothy C.
 ; APPLICANT: Connors, Timothy D.
 ; APPLICANT: Dackowski, William R.
 ; APPLICANT: Van Raay, Terence J.
 ; APPLICANT: Klinger, Katherine W.
 ; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
 ; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
 ; NUMBER OF SEQUENCES: 73
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: GENZYME CORPORATION
 ; STREET: One Mountain Road
 ; CITY: Framingham
 ; STATE: Massachusetts
 ; COUNTRY: United States of America
 ; ZIP: 01701
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/665,259
 ; FILING DATE: 17-JUN-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dugan, Deborah A.
 ; REGISTRATION NUMBER: 37,315
 ; REFERENCE/DOCKET NUMBER: IG5-9.1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (508) 872-8400
 ; TELEFAX: (508) 872-5415
 ; INFORMATION FOR SEQ ID NO: 24:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5894 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 2..5053
 US-08-665-259-24

Query Match 5.6%; Score 450.4; DB 3; Length 5894;
 Best Local Similarity 57.9%; Pred. No. 3.5e-76;
 Matches 948; Conservative 0; Mismatches 606; Indels 84; Gaps 5;

Qy 2092 CGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCA 2151
 | | ||| ||||| |||| | || | |||| | | ||| || |

Db	664	CATCAAGAGGTTCCCGTACCCGCCGTTTCATCGCAGACCCCTTCCTCGTGGCCATCCAGTA	723
Qy	2152	CATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCA	2211
Db	724	CCAGCTGCCCCTGCTGCTGCTGCTCAGCTTCACCTACACCGCGCTCACCATTGCCCGTGC	783
Qy	2212	CATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAA	2271
Db	784	TGTCGTGCAGGAGAAGGAAAGGAGGCTGAAGGAGTACATGCGCATGATGGGGCTCAGCAG	843
Qy	2272	CGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGAC	2331
Db	844	CTGGCTGCACTGGAGTGCCTGGTTCCTTCTGTCTTCTCCTCTCCTCCTCATCGCCGCCTC	903
Qy	2332	AGCACTCACCGCCATCCT-----GAAGTACGGCCAGGTGCTTATGCACAG	2376
Db	904	CTTCATGACCCTGCTCTTCTGTGTCAAGGTGAAGCCAAATGTAGCCGTGCTGTCCCGCAG	963
Qy	2377	CCACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTG	2436
Db	964	CGACCCCTCCCTGGTGCTCGCCTTCCTGCTGTGCTTCGCCATCTCTACCATCTCCTTCAG	1023
Qy	2437	CTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCAT	2496
Db	1024	CTTCATGGTCAGCACCTTCTTCAGCAAAGCCAACATGGCAGCAGCCTTCGGAGGCTTCCT	1083
Qy	2497	CTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGA	2556
Db	1084	CTACTTCTTCACCTACATCCCTACTTCTTCGTGGCCCTCG-----GTACAA	1131
Qy	2557	TAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCT	2616
Db	1132	CTGGATGACTCTGAGCCAGAAGCTCTGCTCCTGCCTCCTGTCTAATGTGCCATGGCAAT	1191
Qy	2617	GGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTT	2676
Db	1192	GGGAGCCCAGCTCATTGGGAAATTTGAGGCGAAAGGCATGGGCATCCAGTGGCGAGACCT	1251
Qy	2677	CAGCCAGTCCCCGGTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTGAT	2736
Db	1252	CCTGAGTCCCGTCAACGTGGACGACGACTTCTGCTTCGGGCAGGTGCTGGGGATGCTGCT	1311
Qy	2737	GGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCAT	2796
Db	1312	GCTGGACTCTGTGCTCTATGGCCTGGTGACCTGGTACATGGAGGCCGTCTTCCAGGGCA	1371
Qy	2797	GTACGGGCTGCCCCGGCCCTGGTACTTCCCACTGCAGAAGTCTACTGGCTGGGCAGTGG	2856
Db	1372	GTTCGGCGTGCCCTCAGCCCTGGTACTTCTTCATCATGCCCTCCTATTGGTGTGGGAAGCC	1431
Qy	2857	GCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGACCCCCCGCCTCAGTGTCAT	2916
Db	1432	AAGGGCGGTTGCAGG-----	1446
Qy	2917	GGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGA	2976
Db	1447	GAAGGAGGAAGAAGACAGTGACCCCGAGAAAGCACTCAGAAACGAG-----TACTTTGA	1500


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; Patent No. 6030806
; GENERAL INFORMATION:
; APPLICANT: Landes, Gregory M.
; APPLICANT: Burn, Timothy C.
; APPLICANT: Connors, Timothy D.
; APPLICANT: Dackowski, William R.
; APPLICANT: Van Raay, Terence J.
; APPLICANT: Klinger, Katherine W.
; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: One Mountain Road
; CITY: Framingham
; STATE: Massachusetts
; COUNTRY: United States of America
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/762,500
; FILING DATE: 09-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,259
; FILING DATE: 17-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10469
; FILING DATE: 17-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dugan, Deborah A.
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: IG5-9.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 872-8400
; TELEFAX: (508) 872-5415
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5894 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..5053
US-08-762-500-24

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Query Match          5.6%; Score 450.4; DB 3; Length 5894;
Best Local Similarity 57.9%; Pred. No. 3.5e-76;
Matches 948; Conservative 0; Mismatches 606; Indels 84; Gaps 5;

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Qy      2092 CGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCA 2151

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Db	664	CATCAAGAGGTTCCCGTACCCGCCGTTTCATCGCAGACCCCTTCCTCGTGCCATCCAGTA	723
Qy	2152	CATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCA	2211
Db	724	CCAGCTGCCCTGCTGCTGCTGCTCAGCTTCACCTACACCGCGCTCACCATTGCCCGTGC	783
Qy	2212	CATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAA	2271
Db	784	TGTCGTGCAGGAGAAGGAAAGGAGGCTGAAGGAGTACATGCGCATGATGGGGCTCAGCAG	843
Qy	2272	CGCGGTGCACTGGGTGGCCTGGTTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGAC	2331
Db	844	CTGGCTGCACTGGAGTGCTGGTTCTCCTCTTCTTCTCCTCCTCATCGCCGCCTC	903
Qy	2332	AGCACTCACCGCCATCCT-----GAAGTACGGCCAGGTGCTTATGCACAG	2376
Db	904	CTTCATGACCCTGCTCTTCTGTGTCAAGGTGAAGCCAAATGTAGCCGTGCTGTCCCGCAG	963
Qy	2377	CCACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTG	2436
Db	964	CGACCCCTCCCTGGTGCTCGCCTTCCTGCTGTGCTTCGCCATCTCTACCATCTCCTTCAG	1023
Qy	2437	CTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCAT	2496
Db	1024	CTTCATGGTCAGCACCTTCTTCAGCAAAGCCAACATGGCAGCAGCCTTCGGAGGCTTCCT	1083
Qy	2497	CTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGA	2556
Db	1084	CTACTTCTTCACCTACATCCCCTACTTCTTCGTGGCCCCCTCG-----GTACAA	1131
Qy	2557	TAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCT	2616
Db	1132	CTGGATGACTCTGAGCCAGAAGCTCTGCTCCTGCCTCCTGTCTAATGTGCCATGGCAAT	1191
Qy	2617	GGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTT	2676
Db	1192	GGGAGCCCAGCTCATTGGGAAATTTGAGGCGAAAGGCATGGGCATCCAGTGGCGAGACCT	1251
Qy	2677	CAGCCAGTCCCCGGTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTGAT	2736
Db	1252	CCTGAGTCCCGTCAACGTGGACGACGACTTCTGCTTCGGGCAGGTGCTGGGGATGCTGCT	1311
Qy	2737	GGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCAT	2796
Db	1312	GCTGGACTCTGTGCTCTATGGCCTGGTGACCTGGTACATGGAGGCCGTCTTCCCAGGGCA	1371
Qy	2797	GTACGGGCTGCCCCGGCCCTGGTACTTCCCACTGCAGAAGTCTACTGGCTGGGCAGTGG	2856
Db	1372	GTCGGCGTGCCCTCAGCCCTGGTACTTCTTCATCATGCCCTCCTATTGGTGTGGGAAGCC	1431
Qy	2857	GCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCAT	2916
Db	1432	AAGGGCGGTTGCAGG-----	1446
Qy	2917	GGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGA	2976


```

; Sequence 74, Application US/08762500
; Patent No. 6030806
; GENERAL INFORMATION:
;   APPLICANT: Landes, Gregory M.
;   APPLICANT: Burn, Timothy C.
;   APPLICANT: Connors, Timothy D.
;   APPLICANT: Dackowski, William R.
;   APPLICANT: Van Raay, Terence J.
;   APPLICANT: Klinger, Katherine W.
;   TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,
;   TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME
;   NUMBER OF SEQUENCES: 83
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: GENZYME CORPORATION
;     STREET: One Mountain Road
;     CITY: Framingham
;     STATE: Massachusetts
;     COUNTRY: United States of America
;     ZIP: 01701
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/762,500
;     FILING DATE: 09-DEC-1996
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/665,259
;     FILING DATE: 17-JUN-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: PCT/US96/10469
;     FILING DATE: 17-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Dugan, Deborah A.
;     REGISTRATION NUMBER: 37,315
;     REFERENCE/DOCKET NUMBER: IG5-9.3
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (508) 872-8400
;     TELEFAX: (508) 872-5415
;   INFORMATION FOR SEQ ID NO: 74:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 6525 base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 573..5684
US-08-762-500-74

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Query Match          5.6%;  Score 450.4;  DB 3;  Length 6525;
Best Local Similarity 57.9%;  Pred. No. 3.6e-76;
Matches 948;  Conservative 0;  Mismatches 606;  Indels 84;  Gaps 5;

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Qy	2092	CGTGCAGATGTTCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTCAATTGAGCA	2151
Db	1295	CATCAAGAGGTTCCCGTACCCGCCGTTTCATCGCAGACCCCTTCCTCGTGGCCATCCAGTA	1354
Qy	2152	CATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCA	2211
Db	1355	CCAGCTGCCCCTGCTGCTGCTGCTCAGCTTCACCTACACCGCGCTCACCATTGCCCGTGC	1414
Qy	2212	CATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAA	2271
Db	1415	TGTCGTGCAGGAGAAGGAAAGGAGGCTGAAGGAGTACATGCGCATGATGGGGCTCAGCAG	1474
Qy	2272	CGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGAC	2331
Db	1475	CTGGCTGCACTGGAGTGCCTGGTTCCTCTTGTCTTCCTCTTCCTCCTCATCGCCGCCTC	1534
Qy	2332	AGCACTCACGCCATCCT-----GAAGTACGGCCAGGTGCTTATGCACAG	2376
Db	1535	CTTCATGACCCTGCTCTTCTGTGTCAAGGTGAAGCCAAATGTAGCCGTGCTGTCCGCGAG	1594
Qy	2377	CCACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTG	2436
Db	1595	CGACCCCTCCCTGGTGCCTCGCCTTCCTGCTGTGCTTCGCCATCTCTACCATCTCCTTCAG	1654
Qy	2437	CTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCAT	2496
Db	1655	CTTCATGGTCAGCACCTTCTTCAGCAAAGCCAACATGGCAGCAGCCTTCGGAGGCTTCCT	1714
Qy	2497	CTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGA	2556
Db	1715	CTACTTCTTCACCTACATCCCCCTACTTCTTCGTGGCCCCCTCG-----GTACAA	1762
Qy	2557	TAAGATCACGGCCTTCGAGAAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCT	2616
Db	1763	CTGGATGACTCTGAGCCAGAAGCTCTGCTCCTGCCTCCTGTCTAATGTCGCCATGGCAAT	1822
Qy	2617	GGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTT	2676
Db	1823	GGGAGCCCAGCTCATTTGGGAAATTTGAGGCGAAAGGCATGGGCATCCAGTGGCGAGACCT	1882
Qy	2677	CAGCCAGTCCCCGGTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTGAT	2736
Db	1883	CCTGAGTCCCGTCAACGTGGACGACGACTTCTGCTTCGGGCAGGTGCTGGGGATGCTGCT	1942
Qy	2737	GGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCAT	2796
Db	1943	GCTGGACTCTGTGCTCTATGGCCTGGTGACCTGGTACATGGAGGCCGTCTTCCCAGGGCA	2002
Qy	2797	GTACGGGCTGCCCCGGCCCTGGTACTTCCCACTGCAGAAAGTCTACTGGCTGGGCAGTGG	2856
Db	2003	GTCGCGCTGCCTCAGCCCTGGTACTTCTTCATCATGCCCTCCTATTGGTGTGGGAAGCC	2062
Qy	2857	GCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCAT	2916
Db	2063	AAGGGCGGTTGCAG-----	2077
Qy	2917	GGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGA	2976

Db	2078	GAAGGAGGAAGAAGACAGTGACCCCGAGAAAGCACTCAGAAACGAG-----TACTTTGA	2131
Qy	2977	GGAGGAGCCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAA	3036
Db	2132	AGCCGAGCCAGAGGACCTGGTGGCGGGGATCAAGATCAAGCACCTGTCCAAGGTGTTGAG	2191
Qy	3037	GGACGACAAGAA-----GCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCA	3090
Db	2192	GGTGGGAAATAAGGACAGGGCGGCCGTGAGAGACCTGAACCTCAACCTGTACGAGGGGACA	2251
Qy	3091	GGTGGTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGAC	3150
Db	2252	GATCACCGTCTCTGCTGGGCCACAACGGTGCCGGGAAGACCACCACCTCTCCATGCTCAC	2311
Qy	3151	CGGCCTGTTCCCTCCAACGTCGGGTTCCGCCACCATCTACGGGCACGACATCCGCACGGA	3210
Db	2312	AGGTCTCTTTCCCCCACCAGTGGACGGGCATACATCAGCGGGTATGAAATTTCCAGGA	2371
Qy	3211	GATGGATGAGATCCGCAAGAACCTGGGCATGTGCCCGCAGCACAATGTGCTCTTTGACCG	3270
Db	2372	CATGGTTCAGATCCGGAAGAGCCTGGGCCGTGTGCCCGCAGCAGACATCCTGTTTGACAA	2431
Qy	3271	GCTCACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGA	3330
Db	2432	CTTGACAGTCGCAGAGCACCTTTATTTCTACGCCAGCTGAAGGGCCTGTCACGTCAGAA	2491
Qy	3331	GATCCGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTC	3390
Db	2492	GTGCCCTGAAGAAGTCAAGCAGATGCTGCACATCATCGGCCTGGAGGACAAGTGGAAGTCA	2551
Qy	3391	ACTGGTGCAGACATTGTGCGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGT	3450
Db	2552	ACGGAGCCGCTTCCTGAGCGGGGGCATGAGGCGCAAGCTCTCCATCGGCATCGCCCTCAT	2611
Qy	3451	GGGCGGCTCTCGGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCG	3510
Db	2612	CGCAGGCTCCAAGGTGCTGATACTGGACGAGCCACCTCGGGCATGGACGCCATCTCCAG	2671
Qy	3511	CCGCGCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCAC	3570
Db	2672	GAGGGCCATCTGGGATCTTCTTCAGCGGCAGAAAAGTGACCGCACCATCGTGCTGACCAC	2731
Qy	3571	CCACCACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAA	3630
Db	2732	CCACTTCATGGACGAGGCTGACCTGCTGGGAGACCGCATCGCCATCATGGCCAAGGGGGA	2791
Qy	3631	GCTCAAGTGCTGCGGCTCCCCGCTCTTCCTCAAGGGCACCTATGGCGACGGGTACCGCCT	3690
Db	2792	GCTGCAGTGCTGCGGGTCTCTGCTGTTCTCAAGCAGAAATACGGTGCCGGCTATCACAT	2851
Qy	3691	CACGCTGGTCAAGCGGCC	3708
Db	2852	GACGCTGGTGAAGGAGCC	2869

```

US-09-833-381-1078
; Sequence 1078, Application US/09833381
; Patent No. 6672186
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. 6672186e1 Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1078
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-1078

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```

Query Match          5.2%; Score 416.2; DB 4; Length 506;
Best Local Similarity 98.9%; Pred. No. 5.7e-70;
Matches 440; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

```

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Qy      1 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 60
          |||
Db      62 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 121

Qy      61 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGAT 120
          |||
Db     122 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGAT 181

Qy     121 CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 180
          |||
Db     182 CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCTACAGAAGAAGCCCACCAT 241

Qy     181 CTCCGTGAAGGAAGTCCCCCTTCTACAC-AGCGGCGCCCCCTGACGTCTGCCGGCATCCTGC 239
          |||
Db     242 CTCCGTGAAGGAAGTCTCCTTCTACACAAGCGGCGCCCCCTGACGTCTGCCGGCATCCTGC 301

Qy     240 CTGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTTCGGCTTCCTGCAGTACG 299
          |||
Db     302 CTGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTTCGGCTTCCTGCAGTACG 361

Qy     300 CCAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACC 359
          |||
Db     362 CCAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACC 421

Qy     360 TGTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATC-TG 418
          |||
Db     422 TGTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTTG 481

Qy     419 GAGGCCCTCAGTGCGGGCCCGGGCA 443
          |||
Db     482 GAGGCCCTTAGTGCGGGCCCGGGCA 506

```

RESULT 9

US-09-252-991A-4588/c
 ; Sequence 4588, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 4588
 ; LENGTH: 999
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-4588

Query Match 1.7%; Score 139.2; DB 4; Length 999;
 Best Local Similarity 52.6%; Pred. No. 1.6e-17;
 Matches 328; Conservative 0; Mismatches 293; Indels 3; Gaps 1;

Qy	3050	CTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGC	3109
Db	942	CAGGCCCTCAAGGGCATCGACCTGGACGTCGCCGAAGGTGATTTCTTCGCCCTTGCTCGGC	883
Qy	3110	CACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACG	3169
Db	882	CCCAACGGCGCGGGCAAGTCCACCACCATCGGGATTCTCTCGACCCTGGTGAACAAGACC	823
Qy	3170	TCGGGTTCGCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAG	3229
Db	822	AGCGGTTTCGGTCTCGGTGTTTCGGCCACGACCTCGACAAGGACCCGGCCGGCCTCAAGCGT	763
Qy	3230	AACCTGGGCATGTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACAC	3289
Db	762	TGCCTTGGCGTGGTGCCGCGAGGATTCAACTTCAACCAGTTCGAGAAGGTCTTCGACATC	703
Qy	3290	CTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGAC	3349
Db	702	GTCGTGACCCAGGCCGGCTACTACGGCATCCCGGCGAAGATCGCCAAGGAGCGCGCCGAG	643
Qy	3350	AAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCTG	3409
Db	642	CGCTACCTGACCCAACCTGGGCCTGTGGGACAAGCGCAACGAAGCCTCGCGGATGCTCTCC	583
Qy	3410	GGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATC	3469
Db	582	GCGGCATGAAGCGGCGCCTGATGATCGCCCGCGCACTGGTCCACCAGCCGCGCCTGCTG	523
Qy	3470	ATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTC	3529
Db	522	ATCCTCGACGAGCCACCGCCGGGGTCGACATCGAGCTGCGTCGTTTCGATGTGGAGCTTC	463

Qy 3290 CTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGAC 3349
 || | | | | | | | | | | | | | | | |
 Db 370 GTCGTGACCCAGGCCGGCTACTACGGCATCCCGGCCGAAGATCGCCAAGGAGCGCGCCGAG 429
 Qy 3350 AAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCTG 3409
 | | | | | | | | | | | | | | | | | | | |
 Db 430 CGCTACCTGACCCAACCTGGGCCTGTGGGACAAGCGCAACGAAGCCTCGCGGATGCTCTCC 489
 Qy 3410 GGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATC 3469
 || ||||| |||| | | | | | | | | | | | | | |
 Db 490 GGCGGCATGAAGCGGCGCCTGATGATCGCCGCGCACTGGTCCACCAGCCGCGCCTGCTG 549
 Qy 3470 ATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTC 3529
 ||||| ||||| |||| | | | | | | | | | | | | | |
 Db 550 ATCCTCGACGAGCCACCGCCGGGGTCGACATCGAGCTGCGTCGTTCGATGTGGAGCTTC 609
 Qy 3530 ATCCTGAA---GTACAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAG 3586
 || | | | | | | | | | | | | | | | | | | | |
 Db 610 CTCACAGAACTCAACCAGGAAGGCATCAGCATCATCTCACCACCCACTACCTGGAAGAG 669
 Qy 3587 GCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGC 3646
 || || | || | | | | | | | | | | | | | | | |
 Db 670 GCGGAGCAGCTCTGCCGCAACATTGCCATCATCGACCACGGCGAGATCGTGCAGAACACC 729
 Qy 3647 TCCCCGCTCTTCCTCAAGGGCACC 3670
 | || | || | ||
 Db 730 AGCATGCGCGACCTGCTGATGACC 753

RESULT 11

US-09-252-991A-4198

; Sequence 4198, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 4198

; LENGTH: 1614

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-4198

Query Match 1.6%; Score 130; DB 4; Length 1614;

Best Local Similarity 52.8%; Pred. No. 1e-15;

Matches 305; Conservative 0; Mismatches 270; Indels 3; Gaps 1;

Qy 3096 TCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCC 3155


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; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
```

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Query Match          1.6%;  Score 129.2;  DB 3;  Length 4403765;
Best Local Similarity 49.7%;  Pred. No. 9.8e-15;
Matches 357;  Conservative 0;  Mismatches 358;  Indels 3;  Gaps 1;
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Qy      2974  GGAGGAGGAGCCCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAAACTCACCAAGGTCTA 3033
          |||||  |  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      3266477 GGAGGATCGGATGCGCAACGACGACATGGCGGTGGTGGTTAACGGGGTTCGCAAGACCTA
3266536

Qy      3034  CAAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGT 3093
          |  |  |||||  |||||  |  |  ||||  ||  |  |  |  ||
Db      3266537 CGGCAAGGGCAAGATTGTGGCCCTCGATGACGTGAGTTTCAAGGTGCGCCGCGGTGAAGT
3266596

Qy      3094  GGTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGG 3153
          |  ||  |  |||||  |||||  |||||  ||||  ||  ||  ||  ||
Db      3266597 GATCGGGCTGCTGGGCCCAACGGGGCCGCAAGACGACCATGGTGGACATCTTGTGCGAC
3266656

Qy      3154  CCTGTTCCTTCCAACGTCGGGTTCCGCCACCATCTACGGGCACGACATCCGCACGGAGAT 3213
          |||  ||  ||  |  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      3266657 GCTGACCCGACCGGATGCCGGCTCGGCGATCATCGCTGGCTACGATGTTGTTTCCGAACC
3266716

Qy      3214  GGATGAGATCCGCAAGAACCTGGGCATGTGCCCCGAGCACAATGTGCTCTTTGACCGGCT 3273
          ||  |  |  |||  |  |  |  |||||  |  ||  |||  |||
Db      3266717 GGCCGGTGTAACGCCGCTCGATCATGGTCAACGGGCAGCAGGTGGCCGTCGACGACGCGCT
3266776

Qy      3274  CACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGAT 3333
          |  |  |||  |  |||  |||  |  |||  |  ||  ||  ||  ||
Db      3266777 TTCCGGTGAGCAGAACCTGGTGTGTTTGGTCGTCTGTGGGGACTGAGCAAGTCCGCGGC
3266836

Qy      3334  CCGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACT 3393
          ||||  |  |  |  ||  |||||  |  |  |||  |  |  |
Db      3266837 GCGCAAACGCGCCGCCGAACCTGCTCGAGCAATTACGCCTCGTACATGCCGGAAGAGGCG
3266896

Qy      3394  GGTGCAGACATTGTCGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGG 3453
          ||||  ||  |  ||  ||  ||  ||  ||  ||  |  |  ||  ||  ||||
Db      3266897 GGTGGGCACCTACTCCGGCGGAATGCGCCGACGAATAGACATCGCGTGCGGATTGGTGGT
3266956

Qy      3454  CGGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCG 3513
          |  |  |  |  ||  |||||  ||  ||  ||  ||  ||  ||
Db      3266957 CCAACCCAGGTGGCGTTCTTAGACGAGCCACACCGGGCTCGATCCCAGGAGCCGGCA
3267016
```

Qy	3514	CGCCATCTGGGACCTCATCTGAAGTAC---AAGCCAGGCCGCACCATCCTTCTGTCCAC	3570
Db	3267017	AGCTATTTGGGATCTGGTGGCCAGCTTCAAGAAGCTGGGCATTGCCACGTTGTTGACCAC	
	3267076		
Qy	3571	CCACCACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAA	3630
Db	3267077	GCAGTATCTCGAGGAGGCGGATGCGCTCAGTGACCGCATCATCCTGATCGATCACGGCAT	
	3267136		
Qy	3631	GCTCAAGTGCTGCGGCTCCCCGCTCTTCCTCAAGGGCACCTATGGCGACGGGTACCGC	3688
Db	3267137	AATCATCGCCGAAGGCACCGCGAATGAACTCAAGCACCGCGCCGGCGACACCTTCTGC	3267194

Query Match 1.6%; Score 129.2; DB 3; Length 4411529;
Best Local Similarity 49.7%; Pred. No. 9.8e-15;
Matches 357; Conservative 0; Mismatches 358; Indels 3; Gaps 1;

Qy		3154	CCTGTTCCCTCCAACGTTCGGGTTCGCGCCACCATCTACGGGCACGACATCCGCACGGAGAT	3213
Db	3272381	GCTGACCCGACCGGATGCCGGCTCGGCGATCATCGCTGGCTACGATGTTGTTTCCGAACC		
		3272440		
Qy		3214	GGATGAGATCCGCAAGAACCTGGGCATGTGCCCGCAGCACAAATGTGCTCTTTGACCGGCT	3273
Db	3272441	GGCCGGTGTAACGCCGCTCGATCATGGTCACCGGGCAGCAGGTGGCCGTCGACGACGCGCT		
		3272500		
Qy		3274	CACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGAT	3333
Db	3272501	TTCCGGTGAGCAGAACCTGGTGTGTTTGGTCGTCTGTGGGGACTGAGCAAGTCCGCGGC		
		3272560		
Qy		3334	CCGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACT	3393
Db	3272561	GCGCAAACGCGCCGCCGAACCTGCTCGAGCAATTACAGCCTCGTACATGCCGGAAGAGGCG		
		3272620		
Qy		3394	GGTGCAGACATTGTTCGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGG	3453
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Qy		3454	CGGCTCTCGCGCCATCATCCTGGACGAGCCCACGGCGGGCGTGGACCCCTACGCGCGCCG	3513
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Db	3272741	AGCTATTTGGGATCTGGTGGCCAGCTTCAAGAAGCTGGGCATTGCCACGTTGTTGACCAC		
		3272800		
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Db	3272801	GCAGTATCTCGAGGAGGCGGATGCGCTCAGTGACCGCATCATCCTGATCGATCACGGCAT		
		3272860		
Qy		3631	GCTCAAGTGCTGCGGCTCCCCGCTCTTCCTCAAGGGCACCTATGGCGACGGGTACCGC	3688
Db	3272861	AATCATCGCCGAAGGCACCGCGAATGAAGTCAAGCACCGCGCGGCGACACCTTCTGC		
		3272918		

; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 4633
 ; LENGTH: 930
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-4633

Query Match 1.6%; Score 126.2; DB 4; Length 930;
 Best Local Similarity 51.1%; Pred. No. 4.6e-15;
 Matches 352; Conservative 0; Mismatches 328; Indels 9; Gaps 2;

Qy	6240	TGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCTGGCGAGTGCTTCGGGCTCCTGGGCG	6299
Db	50	TGGCGGTGGACGACCTGTCTTCCAGGTGGCGACGGGGAGGTACTGGGCTTCCTCGGTC	109
Qy	6300	TCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGACGACGCG	6359
Db	110	CGAACGGCGCCGGCAAGTCCACCACCATGAAGATGCTCACC GGCTTCCTGGCGCCAGCG	169
Qy	6360	GGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGA	6419
Db	170	CCGGCACCGCGAGCATCTTCGGCTTCGACATCCGCAACCGCACGCTGCAGGCGCAGCGGC	229
Qy	6420	GCCTCGGCTACTGCCCGCAGTGACGCGCTGTTCGACGAGCTCACGGCCCCGGGAGCACC	6479
Db	230	TGATCGGCTACCTCCCGGAAGGTTGCGCCTGCTACGCGGAAATGACCGTGACGGGCTTCC	289
Qy	6480	TGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGT	6539
Db	290	TCGATTCATCGCCGAGATCCGTGGCTACCGTGGTGCCGGCAAGCGCGAGCGGGTCGCCC	349
Qy	6540	GGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCG	6599
Db	350	GGGCACTGGGGCTGCTGGAAGTGGACGAGGTGCGCCGGCAGACCATCGAAACCCTCTCCA	409
Qy	6600	GCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCT	6659
Db	410	AGGGCTTCCGCCGGCGTGTCGGCCTGGCCCAGGCGATCCTCCACGAACCGCGGGCGCTGG	469
Qy	6660	TCCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCA	6719
Db	470	TGCTCGACGAGCCCACCGACGGGCTCGATCCGAACCAGAAGCACCAGGTCCGCGAACTGA	529
Qy	6720	TCCTCGACCTCATCAAGACAGGGCGTTAGTGGTGCTGACATCACACAGCATGGAGGAGT	6779
Db	530	TCCGCGGCCTCGCGCAG---GAGCGCATCGTGATCATCTCCACCCATATCTCGAGGAAG	586
Qy	6780	GCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCA	6839
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Qy      6900 GCAGCCAGAGTGTGAAGGACGTGGTGCGG 6928
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RESULT 15

US-09-252-991A-4241/c

; Sequence 4241, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 4241

; LENGTH: 1179

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-4241

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Query Match          1.6%; Score 126.2; DB 4; Length 1179;
Best Local Similarity 51.1%; Pred. No. 4.9e-15;
Matches 352; Conservative 0; Mismatches 328; Indels 9; Gaps 2;

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Qy      6240 TGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCG 6299
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Db      899 TGGCGGTGGACGACCTGTCCTTCCAGGTGGCGACGGGGGAGGTACTGGGCTTCCTCGGTC 840

Qy      6300 TCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGACGACGCG 6359
      |||| | | |||| | | |||| | | |||| | | | | | |
Db      839 CGAACGGCGCCGGCAAGTCCACCACCATGAAGATGCTCACCGGCTTCCTGGCGCCAGCG 780

Qy      6360 GGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGA 6419
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Db      779 CCGGCACCGCGAGCATCTTCGGCTTCGACATCCGCAACCGCACGCTGCAGGCGCAGCGGC 720

Qy      6420 GCCTCGGCTACTGCCCGCAGTGTGACGCGCTGTTGACGAGCTCACGGCCCCGGGAGCACC 6479
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Qy      6480 TGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGT 6539
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Db 599 GGGCACTGGGGCTGCTGGAAGTGGACGAGGTGCGCCGGCAGACCATCGAAACCCTCTCCA 540
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 Db 539 AGGGCTTCCGCCGGCGTGTGCGCCTGGCCCAGGCGATCCTCCACGAACCGCGGGCGCTGG 480
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 Db 479 TGCTCGACGAGCCCACCGACGGGCTCGATCCGAACCAGAAGCACCAGGTCCGCGAACTGA 420
 Qy 6720 TCCTCGACCTCATCAAGACAGGGCGTTTCACTGGTGCTGACATCACACAGCATGGAGGAGT 6779
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 Db 419 TCCGCGGCCTCGCGCAG---GAGCGCATCGTGATCATCTCCACCCATATCCTCGAGGAAG 363
 Qy 6780 GCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCA 6839
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 Db 362 TCTCGGCGCTGTGCAGCCG-----CGCCCTGGTGATCGGCGGCGGGCGGCTGCTGGCGG 309
 Qy 6840 GCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGA 6899
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 Db 308 ACAGCACGCCGCTGGAGCTGGCCAGCCGCTCGCGCTACCACCAGGCGGTGACGCTCTACA 249
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 Job time : 598 secs

OM nucleic - nucleic search, using sw model

Run on: September 8, 2004, 13:23:39 ; Search time 3572 Seconds
(without alignments)
11188.113 Million cell updates/sec

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Perfect score: 8040
Sequence: 1 ccgcggcgctgaggcggcgg.....aaataaataaacaataatgtc 8040

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3267054 seqs, 2485319735 residues

Total number of hits satisfying chosen parameters: 6534108

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

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2	8032	99.9	8195	9	US-09-795-693-7	Sequence 7, Appli
3	8032	99.9	8195	15	US-10-156-239-7	Sequence 7, Appli
4	8032	99.9	8195	15	US-10-199-485-7	Sequence 7, Appli
5	7973.2	99.2	8037	16	US-10-120-988-209	Sequence 209, App
6	7529.2	93.6	7610	17	US-10-380-727-28	Sequence 28, Appl
7	7301.8	90.8	7305	9	US-09-795-693-9	Sequence 9, Appli
8	7301.8	90.8	7305	15	US-10-156-239-9	Sequence 9, Appli
9	7301.8	90.8	7305	15	US-10-199-485-9	Sequence 9, Appli
10	5810	72.3	8040	12	US-10-152-319A-1837	Sequence 1837, Ap
11	5810	72.3	8040	16	US-10-191-803-169	Sequence 169, App
12	5536.8	68.9	5540	16	US-10-297-022-45	Sequence 45, Appl
13	5285	65.7	5285	13	US-10-342-887-47	Sequence 47, Appl
14	5285	65.7	5285	13	US-10-172-118-47	Sequence 47, Appl
15	2736.8	34.0	2740	9	US-09-822-830A-36	Sequence 36, Appl
16	989.8	12.3	7488	15	US-10-340-097-1	Sequence 1, Appli
17	989.8	12.3	7488	15	US-10-336-215-1	Sequence 1, Appli
18	989.8	12.3	7488	15	US-10-336-219-1	Sequence 1, Appli
19	988	12.3	9870	10	US-09-984-827-102	Sequence 102, App
20	988	12.3	9870	10	US-09-984-827-108	Sequence 108, App
21	988	12.3	9870	10	US-09-984-827-109	Sequence 109, App
22	988	12.3	9870	10	US-09-984-827-117	Sequence 117, App
23	986.6	12.3	6786	15	US-10-313-641-8	Sequence 8, Appli
24	986.6	12.3	6786	16	US-10-428-551-8	Sequence 8, Appli
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28	986.6	12.3	7860	17	US-10-744-465-2	Sequence 2, Appli
29	986.4	12.3	9497	13	US-10-170-385-294	Sequence 294, App
30	986.4	12.3	9497	17	US-10-429-160-3	Sequence 3, Appli
31	986.4	12.3	9741	9	US-09-846-456-10	Sequence 10, Appl
32	986.4	12.3	9870	10	US-09-984-827-92	Sequence 92, Appl
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34	986.4	12.3	9870	10	US-09-984-827-94	Sequence 94, Appl
35	986.4	12.3	9870	10	US-09-984-827-95	Sequence 95, Appl
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37	986.4	12.3	9870	10	US-09-984-827-97	Sequence 97, Appl
38	986.4	12.3	9870	10	US-09-984-827-98	Sequence 98, Appl
39	986.4	12.3	9870	10	US-09-984-827-99	Sequence 99, Appl
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42	986.4	12.3	9870	10	US-09-984-827-110	Sequence 110, App
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44	986.4	12.3	9870	10	US-09-984-827-114	Sequence 114, App
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ALIGNMENTS

RESULT 1
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 ; Sequence 3, Application US/10072621
 ; Publication No. US20020169137A1
 ; GENERAL INFORMATION:

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; APPLICANT: Reiner, Peter B.
; APPLICANT: Connop, Bruce P.
; APPLICANT: Pollard, Michelle
; TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION
; TITLE OF INVENTION: BY MODIFICATION OF ABC TRANSPORTER EXPRESSION OR
ACTIVITY
; FILE REFERENCE: 100103.402
; CURRENT APPLICATION NUMBER: US/10/072,621
; CURRENT FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-621-3

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 8040; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy     121 CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 180
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Qy     181 CTCCGTGAAGGAAGTCCCCCTTCTACACAGCGGCGCCCCTGACGTCTGCCGGCATCCTGCC 240
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Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1860
Db	1817	 TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1876
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1920
Db	1877	 CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1936
Qy	1921	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1980
Db	1937	 CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1996
Qy	1981	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Db	1997	 TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2056
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Db	2057	 CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2116
Qy	2101	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2160
Db	2117	 GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2176
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Db	2177	 GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2236
Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280

Db	2237	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2296
Qy	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2340
Db	2297	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2356
Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2400
Db	2357	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2416
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2460
Db	2417	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2476
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Db	2477	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2536
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
Db	2537	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2596
Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640
Db	2597	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2656
Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2700
Db	2657	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2716
Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCAACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760
Db	2717	CGACTTCAACTTGCTCCTGGCTGTCAACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2776
Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2777	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2836
Qy	2821	CTTCCCCTGCAGAAAGTCTTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2837	CTTCCCCTGCAGAAAGTCTTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2896
Qy	2881	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2897	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCATGGAGGAGGACCAGGCCTGTGCCAT	2956
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3000
Db	2957	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3016
Qy	3001	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3017	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3076
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3077	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3136

Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTC	3180
Db	3137	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTC	3196
Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3197	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3256
Qy	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3257	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3316
Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3317	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3376
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCTGGGTGGCATGAA	3420
Db	3377	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCTGGGTGGCATGAA	3436
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3480
Db	3437	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3496
Qy	3481	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3540
Db	3497	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3556
Qy	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3557	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3616
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3617	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3676
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3720
Db	3677	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3736
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCTGGGCCCCGCTGAGCAGCTG	3780
Db	3737	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCTGGGCCCCGCTGAGCAGCTG	3796
Qy	3781	CTCCGAGCTCCAGGTGTCCAGTTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3797	CTCCGAGCTCCAGGTGTCCAGTTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3856
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3857	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3916
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3917	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3976

Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4020
Db	3977	GCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4036
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4037	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4096
Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4097	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4156
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4200
Db	4157	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4216
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4217	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4276
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCTGAGGGTCGGCCAGGGCAGCCGCAA	4320
Db	4277	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCTGAGGGTCGGCCAGGGCAGCCGCAA	4336
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4337	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4396
Qy	4381	CTGCGCCCCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4397	CTGCGCCCCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4456
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4457	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4516
Qy	4501	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4517	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4576
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCAGCAGCT	4620
Db	4577	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCAGCAGCT	4636
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4637	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4696
Qy	4681	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4697	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4756
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4757	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4816
Qy	4801	CGTGCCACCCCCACCCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4860

Db	4817		CGTGCCACCCACCCCTCGCCCGCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4876
Qy	4861		GCAGGCCTGGAACGTCTCCCTGCCGCCACCGCTGGGCCAGAAATGTGGACGTCGGCACC	4920
Db	4877		GCAGGCCTGGAACGTCTCCCTGCCGCCACCGCTGGGCCAGAAATGTGGACGTCGGCACC	4936
Qy	4921		CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	4980
Db	4937		CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	4996
Qy	4981		CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5040
Db	4997		CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5056
Qy	5041		CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5100
Db	5057		CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5116
Qy	5101		CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5160
Db	5117		CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5176
Qy	5161		CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCCA	5220
Db	5177		CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCCA	5236
Qy	5221		GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5280
Db	5237		GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5296
Qy	5281		CGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5340
Db	5297		CGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5356
Qy	5341		CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5400
Db	5357		CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5416
Qy	5401		GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5460
Db	5417		GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5476
Qy	5461		CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAG	5520
Db	5477		CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAG	5536
Qy	5521		CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5580
Db	5537		CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5596
Qy	5581		GGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTC	5640
Db	5597		GGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTC	5656
Qy	5641		GCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCC	5700

Db	5657	GGCCACCAACTTCCCTGCCGTCCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCC	5716
Qy	5701	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCAT	5760
Db	5717	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCAT	5776
Qy	5761	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5820
Db	5777	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5836
Qy	5821	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5880
Db	5837	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5896
Qy	5881	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5940
Db	5897	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5956
Qy	5941	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGGGACATTGT	6000
Db	5957	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGGGACATTGT	6016
Qy	6001	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6060
Db	6017	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6076
Qy	6061	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6120
Db	6077	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6136
Qy	6121	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6180
Db	6137	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6196
Qy	6181	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6240
Db	6197	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6256
Qy	6241	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6300
Db	6257	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6316
Qy	6301	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6360
Db	6317	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6376
Qy	6361	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6420
Db	6377	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6436
Qy	6421	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCGGGAGCACCT	6480
Db	6437	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCGGGAGCACCT	6496
Qy	6481	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6540
Db	6497	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6556

Qy	6541	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6600
Db	6557	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6616
Qy	6601	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTTGGGTACCCAGCCTTCATCTT	6660
Db	6617	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTTGGGTACCCAGCCTTCATCTT	6676
Qy	6661	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6720
Db	6677	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6736
Qy	6721	CCTCGACCTCATCAAGACAGGGCGTTTCAAGTGGTGTGACATCACACAGCATGGAGGAGTG	6780
Db	6737	CCTCGACCTCATCAAGACAGGGCGTTTCAAGTGGTGTGACATCACACAGCATGGAGGAGTG	6796
Qy	6781	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6840
Db	6797	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6856
Qy	6841	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCAGGACCAAGAG	6900
Db	6857	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCAGGACCAAGAG	6916
Qy	6901	CAGCCAGAGTGTGAAGGACGTGGTGCAGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6960
Db	6917	CAGCCAGAGTGTGAAGGACGTGGTGCAGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6976
Qy	6961	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7020
Db	6977	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7036
Qy	7021	CCAGGTGTTTCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7080
Db	7037	CCAGGTGTTTCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7096
Qy	7081	CAGCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGACAACCT	7140
Db	7097	CAGCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGACAACCT	7156
Qy	7141	GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7200
Db	7157	GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7216
Qy	7201	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA	7260
Db	7217	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA	7276
Qy	7261	GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7320
Db	7277	GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7336
Qy	7321	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7380
Db	7337	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7396

Qy	7381	TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGC	7440
Db	7397	TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGC	7456
Qy	7441	CAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCG	7500
Db	7457	CAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCG	7516
Qy	7501	GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAAAGGCTGACCCGGCCC	7560
Db	7517	GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAAAGGCTGACCCGGCCC	7576
Qy	7561	GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCTCG	7620
Db	7577	GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCTCG	7636
Qy	7621	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7680
Db	7637	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7696
Qy	7681	TTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA	7740
Db	7697	TTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA	7756
Qy	7741	GCGGGCTGTGGGCGGAGCTGGGTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCT	7800
Db	7757	GCGGGCTGTGGGCGGAGCTGGGTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCT	7816
Qy	7801	CTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAG	7860
Db	7817	CTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAG	7876
Qy	7861	CTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCC	7920
Db	7877	CTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCC	7936
Qy	7921	CCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCACCTCCC	7980
Db	7937	CCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCACCTCCC	7996
Qy	7981	TGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTAAATAAATAAACAAAATGTC	8040
Db	7997	TGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTAAATAAATAAACAAAATGTC	8056

RESULT 2

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; Sequence 7, Application US/09795693

; Patent No. US20020068710A1

; GENERAL INFORMATION:

; APPLICANT: Glucksmann, Maria A.

; TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and

; TITLE OF INVENTION: 32613, No. US20020068710A1el Human Transporters

; FILE REFERENCE: 35800/209292

; CURRENT APPLICATION NUMBER: US/09/795,693

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; SEQ ID NO 7
; LENGTH: 8195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (132)...(7442)
US-09-795-693-7
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Query Match          99.9%; Score 8032; DB 9; Length 8195;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 8035; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Qy      1 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 60
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Db      98 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 157

Qy      61 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGCTCCTGGCCTTCGAGAT 120
          |||
Db     158 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGCTCCTGGCCTTCGAGAT 217

Qy     121 CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 180
          |||
Db     218 CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 277

Qy     181 CTCCGTGAAGGAAGTCCCCCTTCTACACAGCGGCGCCCTGACGTCTGCCGGCATCCTGCC 240
          |||
Db     278 CTCCGTGAAGGAAGTCTCCTTCTACACAGCGGCGCCCTGACGTCTGCCGGCATCCTGCC 337

Qy     241 TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGC 300
          |||
Db     338 TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGC 397

Qy     301 CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT 360
          |||
Db     398 CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT 457

Qy     361 GTTTGACCCAGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA 420
          |||
Db     458 GTTTGACCCAGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA 517

Qy     421 GGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC 480
          |||
Db     518 GGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC 577

Qy     481 CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCGAGGAGCTCTGGCGTTTCCTGACGCAAAA 540
          |||
Db     578 CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCGAGGAGCTCTGGCGTTTCCTGACGCAAAA 637

Qy     541 CTTGTCGCTGCCCAATAGCACGGCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCCGA 600
          |||
Db     638 CTTGTCGCTGCCCAATAGCACGGCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCCGA 697

Qy     601 GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTTCACAGTCTGGCCTCCACAA 660
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Db	698	 GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	757
Qy	661	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	720
Db	758	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	817
Qy	721	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	780
Db	818	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	877
Qy	781	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	840
Db	878	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	937
Qy	841	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	900
Db	938	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	997
Qy	901	CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCCAACGGCTCGGA	960
Db	998	CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCCAACGGCTCGGA	1057
Qy	961	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1020
Db	1058	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1117
Qy	1021	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTCTGGCCCTGGCCCTGCTACTGCCCCA	1080
Db	1118	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTCTGGCCCTGGCCCTGCTACTGCCCCA	1177
Qy	1081	GGGTGCCTGCACTGGCCGGACCCCCGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Db	1178	GGGTGCCTGCACTGGCCGGACCCCCGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1237
Qy	1141	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1200
Db	1238	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1297
Qy	1201	TGCTGCAGCACTGGCCACCCCGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
Db	1298	TGCTGCAGCACTGGCCACCCCGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1357
Qy	1261	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTTGAACCCGAGGCGCT	1320
Db	1358	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTTGAACCCGAGGCGCT	1417
Qy	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380
Db	1418	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1477
Qy	1381	CCTCGTGCACCTCATGACCAGCAACCCAAAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
Db	1478	CCTCGTGCACCTCATGACCAGCAACCCAAAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1537
Qy	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1500

Db	1538	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1597
Qy	1501	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1598	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1657
Qy	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620
Db	1658	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1717
Qy	1621	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTCTCGCTGCC	1680
Db	1718	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTCTCGCTGCC	1777
Qy	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATAACCATTGACAACGCGGCCCTGCGGCTGGAT	1740
Db	1778	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATAACCATTGACAACGCGGCCCTGCGGCTGGAT	1837
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1800
Db	1838	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1897
Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1860
Db	1898	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1957
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1920
Db	1958	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	2017
Qy	1921	CTCCAGCTTCACCGAGAAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCCTGGGCCCAA	1980
Db	2018	CTCCAGCTTCACCGAGAAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCCTGGGCCCAA	2077
Qy	1981	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Db	2078	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2137
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Db	2138	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2197
Qy	2101	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2160
Db	2198	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2257
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Db	2258	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2317
Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280
Db	2318	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2377
Qy	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2340
Db	2378	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2437

Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2400
Db	2438	CGCCATCCTGAAGTACGGCCAGGTGCTTATACACAGCCACGTGGTCATCATCTGGCTCTT	2497
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2460
Db	2498	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2557
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Db	2558	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2617
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
Db	2618	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2677
Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640
Db	2678	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2737
Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2700
Db	2738	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2797
Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760
Db	2798	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2857
Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2858	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2917
Qy	2821	CTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2918	CTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2977
Qy	2881	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2978	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCATGGAGGAGGACCAGGCCTGTGCCAT	3037
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3000
Db	3038	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3097
Qy	3001	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3098	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3157
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3158	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3217
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTGGGTTCCGC	3180
Db	3218	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTGGGTTCCGC	3277

Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3278	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3337
Qy	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3338	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3397
Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3398	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3457
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3420
Db	3458	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3517
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCTGGACGA	3480
Db	3518	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCTGGACGA	3577
Qy	3481	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCTGAAGTA	3540
Db	3578	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCTGAAGTA	3637
Qy	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3638	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3697
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3698	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3757
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCCGAGCCGGG	3720
Db	3758	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCCGAGCCGGG	3817
Qy	3721	GGGCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCTGGGCCCCGCTGAGCAGCTG	3780
Db	3818	GGGCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCTGGGCCCCGCTGAGCAGCTG	3877
Qy	3781	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3878	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3937
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3938	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3997
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3998	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	4057
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4020
Db	4058	GCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4117
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080

Db	4118	 GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4177
Qy	4081	CCCCGGCTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4178	 CCCCGGCTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4237
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4200
Db	4238	 GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4297
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4298	 CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4357
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTGGGCCAGGGCAGCCGCAA	4320
Db	4358	 TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTGGGCCAGGGCAGCCGCAA	4417
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4418	 GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4477
Qy	4381	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4478	 CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4537
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4538	 CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4597
Qy	4501	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCACGC	4560
Db	4598	 CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCACGC	4657
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCT	4620
Db	4658	 CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCT	4717
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4718	 CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4777
Qy	4681	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4778	 CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4837
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCCTTACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4838	 TCGGTTCTTCGACAGCATGTGTCTGGAGTCCCTTACACAGGGGCTGCCACTGTCCAATTT	4897
Qy	4801	CGTGCCACCCCAACCTCGCCCGCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4860
Db	4898	 CGTGCCACCCCAACCTCGCCCGCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4957
Qy	4861	GCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCGGCACC	4920

Db	4958	GCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCGGCACC	5017
Qy	4921	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	4980
Db	5018	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	5077
Qy	4981	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACC CGCCCCAGATGCGGGTGGT CACAGGCGA	5040
Db	5078	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACC CGCCCCAGATGCGGGTGGT CACAGGCGA	5137
Qy	5041	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5100
Db	5138	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5197
Qy	5101	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5160
Db	5198	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5257
Qy	5161	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCCA	5220
Db	5258	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCCA	5317
Qy	5221	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCCACCTACCTCAACAGCCTCAACAA	5280
Db	5318	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCCACCTACCTCAACAGCCTCAACAA	5377
Qy	5281	CGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5340
Db	5378	CGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5437
Qy	5341	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5400
Db	5438	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5497
Qy	5401	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5460
Db	5498	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5557
Qy	5461	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGT CAG	5520
Db	5558	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGT CAG	5617
Qy	5521	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5580
Db	5618	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5677
Qy	5581	GGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTC	5640
Db	5678	GGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTGACCTGCCGGCCTACACGTC	5737
Qy	5641	GCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCC	5700
Db	5738	GCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCC	5797
Qy	5701	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCTCAT	5760
Db	5798	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCTCAT	5857

Qy	5761	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5820
Db	5858	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5917
Qy	5821	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5880
Db	5918	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5977
Qy	5881	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5940
Db	5978	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	6037
Qy	5941	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGGGACATTGT	6000
Db	6038	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTGAGTGGGACATTGT	6097
Qy	6001	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6060
Db	6098	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6157
Qy	6061	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6120
Db	6158	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6217
Qy	6121	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6180
Db	6218	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6277
Qy	6181	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6240
Db	6278	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6337
Qy	6241	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6300
Db	6338	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6397
Qy	6301	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6360
Db	6398	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6457
Qy	6361	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6420
Db	6458	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6517
Qy	6421	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCCGGGAGCACCT	6480
Db	6518	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCCGGGAGCACCT	6577
Qy	6481	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6540
Db	6578	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6637
Qy	6541	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6600
Db	6638	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6697

Qy	6601	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTTGGGTACCCAGCCTTCATCTT	6660
Db	6698	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTTGGGTACCCAGCCTTCATCTT	6757
Qy	6661	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6720
Db	6758	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6817
Qy	6721	CCTCGACCTCATCAAGACAGGGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTG	6780
Db	6818	CCTCGACCTCATCAAGACAGGGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTG	6877
Qy	6781	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6840
Db	6878	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6937
Qy	6841	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6900
Db	6938	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6997
Qy	6901	CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6960
Db	6998	CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	7057
Qy	6961	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7020
Db	7058	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7117
Qy	7021	CCAGGTGTTTACGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7080
Db	7118	CCAGGTGTTTACGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7177
Qy	7081	CAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT	7140
Db	7178	CAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT	7237
Qy	7141	GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7200
Db	7238	GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7297
Qy	7201	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA	7260
Db	7298	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA	7357
Qy	7261	GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7320
Db	7358	GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7417
Qy	7321	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7380
Db	7418	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7477
Qy	7381	TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCAGTGCCTGC	7440
Db	7478	TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCAGTGCCTGC	7537
Qy	7441	CAGGGCCTGGAGTGGAGGTTTACAGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCG	7500

Db	7538	CAGGGCCTGGAGTGGAGGTT CAGGACCAAGGGGCTTCTGGTCCCTCCAGCCCCTGTACTCG	7597
Qy	7501	GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCC	7560
Db	7598	GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCC	7657
Qy	7561	GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCTCG	7620
Db	7658	GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCTCG	7717
Qy	7621	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7680
Db	7718	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7777
Qy	7681	TTTCTCCTGCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA	7740
Db	7778	TTTCTCCTGCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA	7837
Qy	7741	GCGGGCTGTGGGCGGAGCTGGGTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCT	7800
Db	7838	GCGGGCTGTGGGCGGAGCTGGGTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCT	7897
Qy	7801	CTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAG	7860
Db	7898	CTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAG	7957
Qy	7861	CTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCC	7920
Db	7958	CTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCC	8017
Qy	7921	CCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCACCTCCC	7980
Db	8018	CCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCCCCTCCC	8077
Qy	7981	TGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAATAAAACAAAATGTC	8040
Db	8078	TGGGAGCCGGGCCTGTACATAGGGCACAGATGTTTGTTTTAAATAAATAAAACAAAATGTC	8137

RESULT 3

US-10-156-239-7

; Sequence 7, Application US/10156239

; Publication No. US20030036074A1

; GENERAL INFORMATION:

; APPLICANT: Glucksmann, Maria A.

; APPLICANT: Kapeller-Libermann, Rosana

; TITLE OF INVENTION: No. US20030036074A1el Nucleic Acid Sequences Encoding Human Transporters, A Human

; TITLE OF INVENTION: ATPase Molecule, A Human Ubiquitin Hydrolase-Like Molecule, A Human

; TITLE OF INVENTION: Ubiquitin Conjugating Enzyme-Like Molecule, and Uses Therefor

; FILE REFERENCE: 35800/247645

; CURRENT APPLICATION NUMBER: US/10/156,239

; CURRENT FILING DATE: 2002-05-24

; PRIOR APPLICATION NUMBER: 09/795,693

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; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/809,557
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/192,018
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/808,568
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/191,790
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/808,767
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/191,781
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 8195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (132)...(7442)
US-10-156-239-7

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Query Match          99.9%;  Score 8032;  DB 15;  Length 8195;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 8035;  Conservative 0;  Mismatches 5;  Indels 0;  Gaps 0;

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Qy      1  CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 60
          |||
Db      98  CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 157

Qy      61  GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGAT 120
          |||
Db     158  GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGAT 217

Qy     121  CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 180
          |||
Db     218  CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 277

Qy     181  CTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCCTGACGTCTGCCGGCATCCTGCC 240
          |||
Db     278  CTCCGTGAAGGAAGTCTCCTTCTACACAGCGGCGCCCCTGACGTCTGCCGGCATCCTGCC 337

Qy     241  TGTTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTTCGGCTTCCTGCAGTACGC 300
          |||
Db     338  TGTTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTTCGGCTTCCTGCAGTACGC 397

Qy     301  CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT 360
          |||
Db     398  CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT 457

Qy     361  GTTTGACCCAGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA 420
          |||
Db     458  GTTTGACCCAGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA 517

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Qy	421	GGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC	480
Db	518	GGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC	577
Qy	481	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA	540
Db	578	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA	637
Qy	541	CTTGTCGCTGCCCCAATAGCACGGCCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCGA	600
Db	638	CTTGTCGCTGCCCCAATAGCACGGCCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCGA	697
Qy	601	GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	660
Db	698	GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	757
Qy	661	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	720
Db	758	GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	817
Qy	721	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	780
Db	818	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	877
Qy	781	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	840
Db	878	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	937
Qy	841	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	900
Db	938	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	997
Qy	901	CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	960
Db	998	CCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	1057
Qy	961	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1020
Db	1058	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1117
Qy	1021	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGCCCTGGCCCTGCTACTGCCCCA	1080
Db	1118	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGCCCTGGCCCTGCTACTGCCCCA	1177
Qy	1081	GGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Db	1178	GGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1237
Qy	1141	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1200
Db	1238	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1297
Qy	1201	TGCTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
Db	1298	TGCTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1357

Qy	1261	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCT	1320
Db	1358	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCT	1417
Qy	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380
Db	1418	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1477
Qy	1381	CCTCGTGACCTCATGACCAGCAACCCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
Db	1478	CCTCGTGACCTCATGACCAGCAACCCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1537
Qy	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1500
Db	1538	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1597
Qy	1501	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1598	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1657
Qy	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCCGAGGC	1620
Db	1658	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCCGAGGC	1717
Qy	1621	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1680
Db	1718	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1777
Qy	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTTGACAACGCGGCCTGCGGCTGGAT	1740
Db	1778	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTTGACAACGCGGCCTGCGGCTGGAT	1837
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1800
Db	1838	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1897
Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGTCCAGTGTGAT	1860
Db	1898	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGTCCAGTGTGAT	1957
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1920
Db	1958	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	2017
Qy	1921	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1980
Db	2018	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	2077
Qy	1981	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Db	2078	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2137
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Db	2138	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2197
Qy	2101	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2160

Db	2198	 GTTCCCTTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2257
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Db	2258	 GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2317
Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280
Db	2318	 GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2377
Qy	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2340
Db	2378	 CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2437
Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2400
Db	2438	 CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2497
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2460
Db	2498	 CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2557
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Db	2558	 CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2617
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
Db	2618	 CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2677
Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640
Db	2678	 CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2737
Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2700
Db	2738	 TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2797
Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760
Db	2798	 CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2857
Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2858	 CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2917
Qy	2821	CTTCCCCTGCAGAAGTCCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2918	 CTTCCCCTGCAGAAGTCCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2977
Qy	2881	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2978	 CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCATGGAGGAGGACCAGGCCTGTGCCAT	3037
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3000

Db	3038	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3097
Qy	3001	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3098	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3157
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3158	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3217
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGC	3180
Db	3218	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGC	3277
Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3278	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3337
Qy	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3338	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3397
Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3398	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3457
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3420
Db	3458	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3517
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCTGGACGA	3480
Db	3518	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCTGGACGA	3577
Qy	3481	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCTGAAGTA	3540
Db	3578	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCTGAAGTA	3637
Qy	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3638	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3697
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3698	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3757
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCCGAGCCGGG	3720
Db	3758	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCCGAGCCGGG	3817
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGCCCCGCTGAGCAGCTG	3780
Db	3818	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGCCCCGCTGAGCAGCTG	3877
Qy	3781	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3878	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3937

Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3938	AGACACAAGCACGGAGCTCTCCTACATCCTGCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3997
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3998	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	4057
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4020
Db	4058	GCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4117
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4118	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4177
Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4178	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4237
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4200
Db	4238	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4297
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4298	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4357
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTCGGCCAGGGCAGCCGCAA	4320
Db	4358	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTCGGCCAGGGCAGCCGCAA	4417
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4418	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4477
Qy	4381	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4478	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4537
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4538	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4597
Qy	4501	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4598	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4657
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCAGCAGCT	4620
Db	4658	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCAGCAGCT	4717
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTCGGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4718	CGTGAGCACGTTCCGGCTGCCGTCGGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4777

Qy	4681	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4778	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4837
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4838	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4897
Qy	4801	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4860
Db	4898	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4957
Qy	4861	GCAGGCCTGGAACGTCTCCCTGCCGCCACCCTGGGGCCAGAAATGTGGACGTCGGCACC	4920
Db	4958	GCAGGCCTGGAACGTCTCCCTGCCGCCACCCTGGGGCCAGAAATGTGGACGTCGGCACC	5017
Qy	4921	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	4980
Db	5018	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	5077
Qy	4981	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACC CGCCCCAGATGCGGGTGGTACAGGCGA	5040
Db	5078	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACC CGCCCCAGATGCGGGTGGTACAGGCGA	5137
Qy	5041	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5100
Db	5138	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5197
Qy	5101	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5160
Db	5198	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5257
Qy	5161	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5220
Db	5258	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5317
Qy	5221	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5280
Db	5318	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5377
Qy	5281	CGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5340
Db	5378	CGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5437
Qy	5341	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5400
Db	5438	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5497
Qy	5401	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5460
Db	5498	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5557
Qy	5461	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAG	5520
Db	5558	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAG	5617
Qy	5521	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5580

Db	5618		CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5677
Qy	5581		GGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTC	5640
Db	5678		GGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTC	5737
Qy	5641		GCCCACCAACTTCCCTGCCGTCCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCC	5700
Db	5738		GCCCACCAACTTCCCTGCCGTCCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCC	5797
Qy	5701		CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCAT	5760
Db	5798		CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCAT	5857
Qy	5761		TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCTGCTACAGCTCTT	5820
Db	5858		TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCTGCTACAGCTCTT	5917
Qy	5821		CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5880
Db	5918		CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5977
Qy	5881		CCCCAACTACAACCTGGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5940
Db	5978		CCCCAACTACAACCTGGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	6037
Qy	5941		GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGT	6000
Db	6038		GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGT	6097
Qy	6001		CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCTCCTGACCATCAT	6060
Db	6098		CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCTCCTGACCATCAT	6157
Qy	6061		GTGCCAGTACAACCTTCTGCGGCGGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6120
Db	6158		GTGCCAGTACAACCTTCTGCGGCGGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6217
Qy	6121		GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6180
Db	6218		GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6277
Qy	6181		CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6240
Db	6278		CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6337
Qy	6241		GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGGCTCCTGGGCGT	6300
Db	6338		GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGGCTCCTGGGCGT	6397
Qy	6301		CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6360
Db	6398		CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6457
Qy	6361		GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6420

Db	6458	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6517
Qy	6421	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCT	6480
Db	6518	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCT	6577
Qy	6481	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6540
Db	6578	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6637
Qy	6541	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6600
Db	6638	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6697
Qy	6601	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTT	6660
Db	6698	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTT	6757
Qy	6661	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6720
Db	6758	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6817
Qy	6721	CCTCGACCTCATCAAGACAGGGCGTTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTG	6780
Db	6818	CCTCGACCTCATCAAGACAGGGCGTTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTG	6877
Qy	6781	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6840
Db	6878	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6937
Qy	6841	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6900
Db	6938	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6997
Qy	6901	CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6960
Db	6998	CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	7057
Qy	6961	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7020
Db	7058	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7117
Qy	7021	CCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7080
Db	7118	CCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7177
Qy	7081	CAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT	7140
Db	7178	CAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT	7237
Qy	7141	GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7200
Db	7238	GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7297
Qy	7201	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA	7260
Db	7298	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA	7357

Qy	7261	GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7320
Db	7358	GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7417
Qy	7321	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7380
Db	7418	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7477
Qy	7381	TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGC	7440
Db	7478	TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGC	7537
Qy	7441	CAGGGCCTGGAGTGGAGGTTGAGGACCAAGGGGCTTCTGGTCTCCAGCCCCCTGTACTCG	7500
Db	7538	CAGGGCCTGGAGTGGAGGTTGAGGACCAAGGGGCTTCTGGTCTCCAGCCCCCTGTACTCG	7597
Qy	7501	GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAAAGGCTGACCCGGCCC	7560
Db	7598	GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAAAGGCTGACCCGGCCC	7657
Qy	7561	GGGCTGCGTACACCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCCGGCCCCCTCG	7620
Db	7658	GGGCTGCGTACACCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCCGGCCCCCTCG	7717
Qy	7621	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7680
Db	7718	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7777
Qy	7681	TTTCTCCTGCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA	7740
Db	7778	TTTCTCCTGCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA	7837
Qy	7741	GCGGGCTGTGGGCGGAGCTGGGTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCT	7800
Db	7838	GCGGGCTGTGGGCGGAGCTGGGTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCT	7897
Qy	7801	CTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAG	7860
Db	7898	CTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAG	7957
Qy	7861	CTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCC	7920
Db	7958	CTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCC	8017
Qy	7921	CCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCACCTCCC	7980
Db	8018	CCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCCCCTCCC	8077
Qy	7981	TGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAAAATGTC	8040
Db	8078	TGGGAGCCGGGCCTGTACATAGGGCACAGATGTTTGTTTTAAATAAATAAACAAAATGTC	8137

RESULT 4

US-10-199-485-7

; Sequence 7, Application US/10199485

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; Publication No. US20030077626A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
; TITLE OF INVENTION: 32613, No. US20030077626A1el Human Transporters
; FILE REFERENCE: 35800/249468
; CURRENT APPLICATION NUMBER: US/10/199,485
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 09/795,693
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 8195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (132)...(7442)
US-10-199-485-7

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Query Match          99.9%; Score 8032; DB 15; Length 8195;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 8035; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy      1 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 60
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Db      98 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 157

Qy      61 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGAT 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     158 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGAT 217

Qy     121 CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCCACCAT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     218 CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCCACCAT 277

Qy     181 CTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCTGACGTCTGCCGGCATCCTGCC 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     278 CTCCGTGAAGGAAGTCTCCTTCTACACAGCGGCGCCCTGACGTCTGCCGGCATCCTGCC 337

Qy     241 TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTTCGGCTTCCTGCAGTACGC 300
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Db     338 TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTTCGGCTTCCTGCAGTACGC 397

Qy     301 CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     398 CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT 457

Qy     361 GTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     458 GTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA 517

Qy     421 GGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC 480

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Db	518	 GGCCCTCAGTGC GG GCGCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC	577
Qy	481	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA	540
Db	578	CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA	637
Qy	541	CTTGTCGCTGCCCCAATAGCACGGCCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCCGA	600
Db	638	CTTGTCGCTGCCCCAATAGCACGGCCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCCGA	697
Qy	601	GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	660
Db	698	GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA	757
Qy	661	GGGTCAGGAGCCCTGGAGCCGCCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	720
Db	758	GGGTCAGGAGCCCTGGAGCCGCCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT	817
Qy	721	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	780
Db	818	GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG	877
Qy	781	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	840
Db	878	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	937
Qy	841	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	900
Db	938	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	997
Qy	901	CCAGCTGGACGTGGCCAAGGTCTCCACGACAGCTGGGCCTGGATGCCCCAACGGCTCGGA	960
Db	998	CCAGCTGGACGTGGCCAAGGTCTCCACGACAGCTGGGCCTGGATGCCCCAACGGCTCGGA	1057
Qy	961	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1020
Db	1058	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1117
Qy	1021	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGGCCCTGGCCCTGCTACTGCCCCA	1080
Db	1118	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGGCCCTGGCCCTGCTACTGCCCCA	1177
Qy	1081	GGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Db	1178	GGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1237
Qy	1141	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1200
Db	1238	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1297
Qy	1201	TGCTGCAGCACTGGCCACCCCCGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
Db	1298	TGCTGCAGCACTGGCCACCCCCGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1357
Qy	1261	CTGGGCGCGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTTGAACCCGAGGCGCT	1320

Db	1358	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCT	1417
Qy	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380
Db	1418	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1477
Qy	1381	CCTCGTGACCTCATGACCAGCAACCCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
Db	1478	CCTCGTGACCTCATGACCAGCAACCCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1537
Qy	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1500
Db	1538	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1597
Qy	1501	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1598	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1657
Qy	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620
Db	1658	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1717
Qy	1621	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1680
Db	1718	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1777
Qy	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGAT	1740
Db	1778	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGAT	1837
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1800
Db	1838	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1897
Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1860
Db	1898	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1957
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1920
Db	1958	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	2017
Qy	1921	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1980
Db	2018	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	2077
Qy	1981	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Db	2078	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2137
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Db	2138	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2197
Qy	2101	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2160
Db	2198	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2257

Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Db	2258	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2317
Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280
Db	2318	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2377
Qy	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2340
Db	2378	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2437
Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2400
Db	2438	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2497
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2460
Db	2498	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2557
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Db	2558	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2617
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
Db	2618	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2677
Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640
Db	2678	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2737
Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2700
Db	2738	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2797
Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760
Db	2798	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2857
Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2858	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2917
Qy	2821	CTTCCCCTGTCAGAAAGTCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2918	CTTCCCCTGTCAGAAAGTCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2977
Qy	2881	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTGTCATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2978	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTGTCATGGAGGAGGACCAGGCCTGTGCCAT	3037
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3000
Db	3038	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3097

Qy	3001	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3098	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3157
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3158	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3217
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCCGC	3180
Db	3218	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCCGC	3277
Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3278	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3337
Qy	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3338	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3397
Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3398	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3457
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3420
Db	3458	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGCATGAA	3517
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3480
Db	3518	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3577
Qy	3481	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3540
Db	3578	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3637
Qy	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3638	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3697
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3698	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3757
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3720
Db	3758	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3817
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGGGGCCCCGCTGAGCAGCTG	3780
Db	3818	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGGGGCCCCGCTGAGCAGCTG	3877
Qy	3781	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3878	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3937
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900

Db	3938	 AGACACAAGCACGGAGCTCTCCTACATCCTGCCAGCGAGGCCGCAAGAAGGGGGCTTT	3997
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3998	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	4057
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTCCCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4020
Db	4058	GCTGATGGACACGACCCTGGAGGAAGTGTTCCCTCAAGGTGTCGGAGGAGGATCAGTCGCT	4117
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4118	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4177
Qy	4081	CCCGGCGTCTGGGGAGGGTACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4178	CCCGGCGTCTGGGGAGGGTACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4237
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4200
Db	4238	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4297
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4298	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4357
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTCGGCCAGGGCAGCCGCAA	4320
Db	4358	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTCGGCCAGGGCAGCCGCAA	4417
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4418	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4477
Qy	4381	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4478	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4537
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4538	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4597
Qy	4501	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4598	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4657
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCAGCAGCT	4620
Db	4658	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCGACGCCAGCCCCAGCAGCT	4717
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4718	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4777
Qy	4681	CAACGGCTCGCTGGGGCCCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740

Db	4778	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4837
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4838	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4897
Qy	4801	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4860
Db	4898	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4957
Qy	4861	GCAGGCCTGGAACGTCTCCCTGCCGCCACCCTGGGCCAGAAATGTGGACGTCCGCACC	4920
Db	4958	GCAGGCCTGGAACGTCTCCCTGCCGCCACCCTGGGCCAGAAATGTGGACGTCCGCACC	5017
Qy	4921	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC	4980
Db	5018	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC	5077
Qy	4981	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5040
Db	5078	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5137
Qy	5041	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5100
Db	5138	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5197
Qy	5101	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5160
Db	5198	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5257
Qy	5161	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5220
Db	5258	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5317
Qy	5221	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5280
Db	5318	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5377
Qy	5281	CGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5340
Db	5378	CGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5437
Qy	5341	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5400
Db	5438	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5497
Qy	5401	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5460
Db	5498	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5557
Qy	5461	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAG	5520
Db	5558	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGAG	5617
Qy	5521	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5580
Db	5618	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5677

Qy	5581	GGTCCCCGCTACCTGCTGTGTGCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTC	5640
Db	5678	GGTCCCCGCTACCTGCTGTGTGCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTC	5737
Qy	5641	GCCCACCAACTTCCCTGCCGTCCTCTCCCTCTTCCCTGCTCTATGGGTGGTCCATCACGCC	5700
Db	5738	GCCCACCAACTTCCCTGCCGTCCTCTCCCTCTTCCCTGCTCTATGGGTGGTCCATCACGCC	5797
Qy	5701	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCAT	5760
Db	5798	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCAT	5857
Qy	5761	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5820
Db	5858	TGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5917
Qy	5821	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5880
Db	5918	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5977
Qy	5881	CCCCAACTACAACCTGGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5940
Db	5978	CCCCAACTACAACCTGGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	6037
Qy	5941	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCGTTTCGAGTGGGACATTGT	6000
Db	6038	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCGTTTCGAGTGGGACATTGT	6097
Qy	6001	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6060
Db	6098	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6157
Qy	6061	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6120
Db	6158	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6217
Qy	6121	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6180
Db	6218	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6277
Qy	6181	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6240
Db	6278	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6337
Qy	6241	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6300
Db	6338	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6397
Qy	6301	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6360
Db	6398	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6457
Qy	6361	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6420
Db	6458	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6517

Qy	6421	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCCGGGAGCACCT	6480
Db	6518	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCCGGGAGCACCT	6577
Qy	6481	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6540
Db	6578	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6637
Qy	6541	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6600
Db	6638	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6697
Qy	6601	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTT	6660
Db	6698	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTT	6757
Qy	6661	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCTCTGGAACCTCAT	6720
Db	6758	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCTCTGGAACCTCAT	6817
Qy	6721	CCTCGACCTCATCAAGACAGGGCGTTTCAAGTGGTGTGACATCACACAGCATGGAGGAGTG	6780
Db	6818	CCTCGACCTCATCAAGACAGGGCGTTTCAAGTGGTGTGACATCACACAGCATGGAGGAGTG	6877
Qy	6781	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6840
Db	6878	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6937
Qy	6841	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGC GGACCAAGAG	6900
Db	6938	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGC GGACCAAGAG	6997
Qy	6901	CAGCCAGAGTGTGAAGGACGTGGTGC GGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6960
Db	6998	CAGCCAGAGTGTGAAGGACGTGGTGC GGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	7057
Qy	6961	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7020
Db	7058	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7117
Qy	7021	CCAGGTGTTTCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7080
Db	7118	CCAGGTGTTTCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT	7177
Qy	7081	CAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT	7140
Db	7178	CAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT	7237
Qy	7141	GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7200
Db	7238	GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG	7297
Qy	7201	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA	7260
Db	7298	CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA	7357
Qy	7261	GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7320

Db	7358	 GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTC	7417
Qy	7321	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7380
Db	7418	CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC	7477
Qy	7381	TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGC	7440
Db	7478	TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGC	7537
Qy	7441	CAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCCTCCAGCCCCTGTACTCG	7500
Db	7538	CAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCCTCCAGCCCCTGTACTCG	7597
Qy	7501	GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAAAGGCTGACCCGGCCC	7560
Db	7598	GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAAAGGCTGACCCGGCCC	7657
Qy	7561	GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCTCG	7620
Db	7658	GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCTCG	7717
Qy	7621	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7680
Db	7718	CCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCC	7777
Qy	7681	TTTCTCCTGCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA	7740
Db	7778	TTTCTCCTGCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGA	7837
Qy	7741	GCGGGCTGTGGGCGGAGCTGGGTTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCT	7800
Db	7838	GCGGGCTGTGGGCGGAGCTGGGTTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCT	7897
Qy	7801	CTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAG	7860
Db	7898	CTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAG	7957
Qy	7861	CTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCC	7920
Db	7958	CTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCC	8017
Qy	7921	CCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCCCACCTCCC	7980
Db	8018	CCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCCCCTCCC	8077
Qy	7981	TGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAAAATGTC	8040
Db	8078	TGGGAGCCGGGCCTGTACATAGGGCACAGATGTTTGTTTTAAATAAATAAACAAAATGTC	8137

RESULT 5

US-10-120-988-209

; Sequence 209, Application US/10120988

; Publication No. US20030219745A1

; GENERAL INFORMATION:

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; APPLICANT: Tang, Y. Tom
; APPLICANT: Goodrich, Ryle
; APPLICANT: Liu, Chenghua
; APPLICANT: Ren, Feiyan
; APPLICANT: Wang, Dunrui
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030219745A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 802CON
; CURRENT APPLICATION NUMBER: US/10/120,988
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 09/774,528
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 441
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 209
; LENGTH: 8037
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1654)..(7329)
US-10-120-988-209

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Query Match          99.2%; Score 7973.2; DB 16; Length 8037;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 8003; Conservative 0; Mismatches 3; Indels 18; Gaps 1;

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Qy      35 ATGGGCTTCCTGCACCAGCTGCAGCTGCTGCTCTGGAAGAACGTGACGCTCAAACGCCGG 94
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Db      1  ATGGGCTTCCTGCACCAGCTGCAGCTGCTGCTCTGGAAGAACGTGACGCTCAAACGCCGG 60

Qy      95 AGCCCGTGGGTCTTGGCCTTCGAGATCTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTG 154
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 AGCCCGTGGGTCTTGGCCTTCGAGATCTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTG 120

Qy     155 GGGCTGCGACAGAAGAAGCCCACCATCTCCGTGAAGGAAGTCCCCCTTCTACACAGCGGCG 214
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Db     121 GGGCTGCGACAGAAGAAGCCCACCATCTCCGTGAAGGAAGTCCCCCTTCTACACAGCGGCG 180

Qy     215 CCCCTGACGTCTGCCGGCATCCTGCCTGTCATGCAATCGCTGTGCCCCGACGGCCAGCGA 274
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Db     181 CCCCTGACGTCTGCCGGCATCCTGCCTGTCATGCAATCGCTGTGCCCCGACGGCCAGCGA 240

Qy     275 GACGAGTTCGGCTTCCTGCAGTACGCCAACTCCACGGTCACGCAGCTGCTTGAGCGCCTG 334
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Db     241 GACGAGTTCGGCTTCCTGCAGTACGCCAACTCCACGGTCACGCAGCTGCTTGAGCGCCTG 300

Qy     335 GACCGCGTGGTGGAGGAAGGCAACCTGTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAG 394
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Db     301 GACCGCGTGGTGGAGGAAGGCAACCTGTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAG 360

Qy     395 CTCGAGGCCCTACGCCAGCATCTGGAGGCCCTCAGTGCGGGCCCGGGCACCTCGGGGAGC 454
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 CTCGAGGCCCTACGCCAGCATCTGGAGGCCCTCAGTGCGGGCCCGGGCACCTCGGGGAGC 420

Qy     455 CACCTGGACAGATCCACAGTGTCTTCCTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAG 514

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Db	421		CACCTGGACAGATCCACAGTGTCTTCCTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAG	480
Qy	515		GAGCTCTGGCGTTTCCTGACGCAAAACTTGTGCTGCCAATAGCACGGCCCAAGCACTC	574
Db	481		GAGCTCTGGCGTTTCCTGACGCAAAACTTGTGCTGCCAATAGCACGGCCCAAGCACTC	540
Qy	575		TTGGCCGCCCCGTGTGGACCCGCCCGAGGTCTACCACCTGCTCTTTGGTCCCTCATCTGCC	634
Db	541		TTGGCCGCCCCGTGTGGACCCGCCCGAGGTCTACCACCTGCTCTTTGGTCCCTCATCTGCC	600
Qy	635		CTGGATTACAGTCTGGCCTCCACAAGGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAAT	694
Db	601		CTGGATTACAGTCTGGCCTCCACAAGGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAAT	660
Qy	695		CCCCGTTCGGATGGAGGAGCTGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGC	754
Db	661		CCCCGTTCGGATGGAGGAGCTGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGC	720
Qy	755		ACGCCGGGCTCGGGGGAGCTGGGCCGGATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCC	814
Db	721		ACGCCGGGCTCGGGGGAGCTGGGCCGGATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCC	780
Qy	815		CTGCAGGGCTACCGGGATGCTGTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTC	874
Db	781		CTGCAGGGCTACCGGGATGCTGTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTC	840
Qy	875		TCTGGGCTGTCTGCTGAGCTCCGGAACCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTG	934
Db	841		TCTGGGCTGTCTGCTGAGCTCCGGAACCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTG	900
Qy	935		GGCCTGGATGCCCCCAACGGGCTCGGACTCCTCGCCACAGGCGCCACCCCCACGGAGGCTG	994
Db	901		GGCCTGGATGCCCCCAACGGGCTCGGACTCCTCGCCACAGGCGCCACCCCCACGGAGGCTG	960
Qy	995		CAGGCGCTTCTGGGGGACCTGCTGGATGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTG	1054
Db	961		CAGGCGCTTCTGGGGGACCTGCTGGATGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTG	1020
Qy	1055		TCGGCCCTGGCCCTGCTACTGCCCCAGGGTGCCTGCACTGGCCGGACCCCCGGACCCCCA	1114
Db	1021		TCGGCCCTGGCCCTGCTACTGCCCCAGGGTGCCTGCACTGGCCGGACCCCCGGACCCCCA	1080
Qy	1115		GCCAGTGGTGCGGGTGGGGCGGCCAATGGCACTGGGGCAGGGGCAGTCATGGGCCCCAAC	1174
Db	1081		GCCAGTGGTGCGGGTGGGGCGGCCAATGGCACTGGGGCAGGGGCAGTCATGGGCCCCAAC	1140
Qy	1175		GCCACCGCTGAGGAGGGCGCACCCCTCTGCTGCAGCACTGGCCACCCCCGGACACGCTGCAG	1234
Db	1141		GCCACCGCTGAGGAGGGCGCACCCCTCTGCTGCAGCACTGGCCACCCCCGGACACGCTGCAG	1200
Qy	1235		GGCCAGTGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAAC	1294
Db	1201		GGCCAGTGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAAC	1260
Qy	1295		AACCGCACCATTTGAACCCGAGGCGCTGCGGCGGGGCAACATGAGCTCCCTGGGCTTCACG	1354

Db	1261	AACCGCACCATTGAACCCGAGGCGCTGCGGCGGGGCAACATGAGCTCCTTGGGCTTCACG	1320
Qy	1355	AGCAAGGAGCAGCGGAACCTGGGCCTCCTCGTGCACCTCATGACCAGCAACCCCAAATC	1414
Db	1321	AGCAAGAAGCAGCGGAACCTGGGCCTCCTCGTGCACCTCATGACCAGCAACCCCAAATC	1380
Qy	1415	CTGTACGCGCCTGCGGGCTCTGAGGTCGACCGCGTCATCCTCAAGGCCAACGAGACTTTT	1474
Db	1381	CTGTACGCGCCTGCGGGCTCTGAGGTCGACCGCGTCATCCTCAAGGCCAACGAGACTTTT	1440
Qy	1475	GCTTTTGTGGGCAACGTGACTCACTATGCCCAGGTCTGGCTCAACATCTCGGCGGAGATC	1534
Db	1441	GCTTTTGTGGGCAACGTGACTCACTATGCCCAGGTCTGGCTCAACATCTCGGCGGAGATC	1500
Qy	1535	CGCAGCTTCCTGGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTATGTA	1594
Db	1501	CGCAGCTTCCTGGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTATGTA	1560
Qy	1595	GCAGAGCTGCGGCTGCACCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCGGCC	1654
Db	1561	GCAGAGCTGCGGCTGCACCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCGGCC	1620
Qy	1655	CTGAGACAGGACAACTTCTCGCTGCCAGTGGCATGGCCCTCCTGCAGCAGCTGGATACC	1714
Db	1621	CTGAGACAGGACAACTTCTCGCTGCCAGTGGCATGGCCCTCCTGCAGCAGCTGGATACC	1680
Qy	1715	ATTGACAACGCGGCCTGCGGCTGGATCCAGTTCATGTCCAAGGTGAGCGTGGACATCTTC	1774
Db	1681	ATTGACAACGCGGCCTGCGGCTGGATCCAGTTCATGTCCAAGGTGAGCGTGGACATCTTC	1740
Qy	1775	AAGGGCTTCCCCGACGAGGAGAGCATTGTCAACTACACCCTCAACCAGGCCTACCAGGAC	1834
Db	1741	AAGGGCTTCCCCGACGAGGAGAGCATTGTCAACTACACCCTCAACCAGGCCTACCAGGAC	1800
Qy	1835	AACGTCACTGTTTTTGCAGTGTGATCTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCT	1894
Db	1801	AACGTCACTGTTTTTGCAGTGTGATCTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCT	1860
Qy	1895	CACGTGCACTACAAGATCCGCCAGAACTCCAGCTTCACCGAGAAAACCAACGAGATCCGC	1954
Db	1861	CACGTGCACTACAAGATCCGCCAGAACTCCAGCTTCACCGAGAAAACCAACGAGATCCGC	1920
Qy	1955	CGCGCCTACTGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCCTCTACGGCTTC	2014
Db	1921	CGCGCCTACTGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCCTCTACGGCTTC	1980
Qy	2015	GTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCACGACGTG	2074
Db	1981	GTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCACGACGTG	2040
Qy	2075	GTGGAGCCAGGCAGCTACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTC	2134
Db	2041	GTGGAGCCAGGCAGCTACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTC	2100
Qy	2135	CTGTTTGTTCATTGAGCACATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTG	2194
Db	2101	CTGTTTGTTCATTGAGCACATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTG	2160

Qy	2195	GCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAG	2254
Db	2161	GCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAG	2220
Qy	2255	ACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAG	2314
Db	2221	ACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAG	2280
Qy	2315	CTGTCCATCTCCGTGACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCAC	2374
Db	2281	CTGTCCATCTCCGTGACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCAC	2340
Qy	2375	AGCCACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTT	2434
Db	2341	AGCCACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTT	2400
Qy	2435	TGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATC	2494
Db	2401	TGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATC	2460
Qy	2495	ATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCAT	2554
Db	2461	ATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCAT	2520
Qy	2555	GATAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGT	2614
Db	2521	GATAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGT	2580
Qy	2615	CTGGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACC	2674
Db	2581	CTGGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACC	2640
Qy	2675	TTCAGCCAGTCCCCGGTGGAGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTG	2734
Db	2641	TTCAGCCAGTCCCCGGTGGAGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTG	2700
Qy	2735	ATGGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGC	2794
Db	2701	ATGGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGC	2760
Qy	2795	ATGTACGGGCTGCCCCGGCCCTGGTACTTCCCACTGCAGAAGTCTACTGGCTGGGCAGT	2854
Db	2761	ATGTACGGGCTGCCCCGGCCCTGGTACTTCCCACTGCAGAAGTCTACTGGCTGGGCAGT	2820
Qy	2855	GGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTC	2914
Db	2821	GGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTC	2880
Qy	2915	ATGGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATG	2974
Db	2881	ATGGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATG	2940
Qy	2975	GAGGAGGAGCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAAACTCACCAAGGTCTAC	3034
Db	2941	GAGGAGGAGCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAAACTCACCAAGGTCTAC	3000

Qy	3035	AAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTG	3094
Db	3001	AAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTG	3060
Qy	3095	GTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGC	3154
Db	3061	GTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGC	3120
Qy	3155	CTGTTCCCTCCAACGTCGGGTTCGCCACCATCTACGGGCACGACATCCGCACGGAGATG	3214
Db	3121	CTGTTCCCTCCAACGTCGGGTTCGCCACCATCTACGGGCACGACATCCGCACGGAGATG	3180
Qy	3215	GATGAGATCCGCAAGAACCTGGGCATGTGCCCGCAGCACAATGTGCTCTTTGACCGGCTC	3274
Db	3181	GATGAGATCCGCAAGAACCTGGGCATGTGCCCGCAGCACAATGTGCTCTTTGACCGGCTC	3240
Qy	3275	ACGGTGGAGGAACACCTCTGGTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATC	3334
Db	3241	ACGGTGGAGGAACACCTCTGGTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATC	3300
Qy	3335	CGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTG	3394
Db	3301	CGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTG	3360
Qy	3395	GTGCAGACATTGTCGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGC	3454
Db	3361	GTGCAGACATTGTCGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGC	3420
Qy	3455	GGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGC	3514
Db	3421	GGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGC	3480
Qy	3515	GCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCAC	3574
Db	3481	GCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCAC	3540
Qy	3575	CACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTC	3634
Db	3541	CACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTC	3600
Qy	3635	AAGTGCTGCGGCTCCCCGCTCTTCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACG	3694
Db	3601	AAGTGCTGCGGCTCCCCGCTCTTCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACG	3660
Qy	3695	CTGGTCAAGCGGCCCCGCCGAGCCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCC	3754
Db	3661	CTGGTCAAGCGGCCCCGCCGAGCCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCC	3720
Qy	3755	CCAGGTCGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCAGTTTCATCCGCAAG	3814
Db	3721	CCAGGTCGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCAGTTTCATCCGCAAG	3780
Qy	3815	CATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCC	3874
Db	3781	CATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCC	3840
Qy	3875	AGCGAGGCCGCCAAGAAGGGGGCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTG	3934

Db	3841	AGCGAGGCCGCAAGAAGGGGGCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTG	3900
Qy	3935	GATGCACTGCACCTCAGCAGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCCTC	3994
Db	3901	GATGCACTGCACCTCAGCAGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCCTC	3960
Qy	3995	AAGGTGTCGGAGGAGGATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGG	4054
Db	3961	AAGGTGTCGGAGGAGGATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGG	4020
Qy	4055	AAGGATGTGCTCCCTGGGGCGGAGGGCCCGCGTCTGGGGAGGGTCACGCTGGCAATCTG	4114
Db	4021	AAGGATGTGCTCCCTGGGGCGGAGGGCCCGCGTCTGGGGAGGGTCACGCTGGCAATCTG	4080
Qy	4115	GCCCGGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGC	4174
Db	4081	GCCCGGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGC	4140
Qy	4175	TCTGCCCCGTGGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTC	4234
Db	4141	TCTGCCCCGTGGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTC	4200
Qy	4235	TTTGATAACCCACAGGACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTG	4294
Db	4201	TTTGATAACCCACAGGACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTG	4260
Qy	4295	TCGAGGGTCGGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTC	4354
Db	4261	TCGAGGGTCGGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTC	4320
Qy	4355	CACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCC	4414
Db	4321	CACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCC	4380
Qy	4415	CAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCG	4474
Db	4381	CAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCG	4440
Qy	4475	GAGATTGGTGATCTGCCCCGCTGGTCCTGTACCTTCCCAGTACCACAACCTACACCCAG	4534
Db	4441	GAGATTGGTGATCTGCCCCGCTGGTCCTGTACCTTCCCAGTACCACAACCTACACCCAG	4500
Qy	4535	CCCCGTGGCAATTTTCATCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTA	4594
Db	4501	CCCCGTGGCAATTTTCATCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTA	4560
Qy	4595	TCGCCCCGACGCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGT	4654
Db	4561	TCGCCCCGACGCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGT	4620
Qy	4655	GCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCACGTTGAACCTGAGC	4714
Db	4621	GCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCACGTTGAACCTGAGC	4680
Qy	4715	AGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTC	4774

Db	4681	AGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTC	4740
Qy	4775	ACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCGCCCCATCTGAC	4834
Db	4741	ACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCGCCCCATCTGAC	4800
Qy	4835	TCGCCAGCGTCCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCT	4894
Db	4801	TCGCCAGCGTCCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCT	4860
Qy	4895	GGGCCAGAAATGTGGACGTCGGCACCCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGC	4954
Db	4861	GGGCCAGAAATGTGGACGTCGGCACCCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGC	4920
Qy	4955	TGCACCTGCTCTGCGCAGGGCACC GGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACC CG	5014
Db	4921	TGCACCTGCTCTGCGCAGGGCACC GGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACC CG	4980
Qy	5015	CCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCT	5074
Db	4981	CCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCT	5040
Qy	5075	GAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTT	5134
Db	5041	GAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTT	5100
Qy	5135	GGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGG	5194
Db	5101	GGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGG	5160
Qy	5195	AAGATCGCGGTGCGCAGGGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATG	5254
Db	5161	AAGATCGCGGTGCGCAGGGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATG	5220
Qy	5255	CCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAG	5314
Db	5221	CCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAG	5280
Qy	5315	GGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCC	5374
Db	5281	GGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCC	5340
Qy	5375	AGCCTCTCCCTGGATTACCTGCTGCAGGGCACGGATGTCGTCATCGCCATCTTCATCATC	5434
Db	5341	AGCCTCTCCCTGGATTACCTGCTGCAGGGCACGGATGTCGTCATCGCCATCTTCATCATC	5400
Qy	5435	GTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAAGTCCACC	5494
Db	5401	GTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAAGTCCACC	5460
Qy	5495	AAGGCCAAGCATCTGCAGTTTGTGACGGCTGCAACCCCATCATCTACTGGCTGGCGAAC	5554
Db	5461	AAGGCCAAGCATCTGCAGTTTGTGACGGCTGCAACCCCATCATCTACTGGCTGGCGAAC	5520
Qy	5555	TACGTGTGGGACAT-----GCTCAACTACCTGGTCCCCGCTACCTGC	5596
Db	5521	TACGTGTGGGACATGCCGCCCCACCCCTGCAGCTCAACTACCTGGTCCCCGCTACCTGC	5580

Qy	5597	TGTGTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTCGCCCACCAACTTCCTT	5656
Db	5581	TGTGTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTCGCCCACCAACTTCCTT	5640
Qy	5657	GCCGTCCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGGCC	5716
Db	5641	GCCGTCCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGGCC	5700
Qy	5717	TCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTTCCTCATTGTTCATCAATCTCTTC	5776
Db	5701	TCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTTCCTCATTGTTCATCAATCTCTTC	5760
Qy	5777	ATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGGAC	5836
Db	5761	ATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGGAC	5820
Qy	5837	CTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTG	5896
Db	5821	CTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTG	5880
Qy	5897	GGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATT	5956
Db	5881	GGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATT	5940
Qy	5957	GGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGGTG	6016
Db	5941	GGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGGTG	6000
Qy	6017	GCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTTC	6076
Db	6001	GCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTTC	6060
Qy	6077	CTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTG	6136
Db	6061	CTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTG	6120
Qy	6137	GCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAG	6196
Db	6121	GCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAG	6180
Qy	6197	AACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTG	6256
Db	6181	AACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTG	6240
Qy	6257	TGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAG	6316
Db	6241	TGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAG	6300
Qy	6317	ACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTCGTC	6376
Db	6301	ACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTCGTC	6360
Qy	6377	AATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCG	6436
Db	6361	AATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCG	6420

Qy	6437	CAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCTGCAGCTGTACACGCGG	6496
Db	6421	CAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCTGCAGCTGTACACGCGG	6480
Qy	6497	CTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTG	6556
Db	6481	CTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTG	6540
Qy	6557	GAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAG	6616
Db	6541	GAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAG	6600
Qy	6617	CTCTCCACGGCCATCGCCCTCATTTGGGTACCCAGCCTTCATCTTCTGGACGAGCCCACC	6676
Db	6601	CTCTCCACGGCCATCGCCCTCATTTGGGTACCCAGCCTTCATCTTCTGGACGAGCCCACC	6660
Qy	6677	ACAGGCATGGACCCCAAGGCCCGGCGCTTCTCTGGAACCTCATCCTCGACCTCATCAAG	6736
Db	6661	ACAGGCATGGACCCCAAGGCCCGGCGCTTCTCTGGAACCTCATCCTCGACCTCATCAAG	6720
Qy	6737	ACAGGGCGTTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCACG	6796
Db	6721	ACAGGGCGTTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCACG	6780
Qy	6797	CGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAG	6856
Db	6781	CGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAG	6840
Qy	6857	AACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTGAAG	6916
Db	6841	AACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTGAAG	6900
Qy	6917	GACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACCAC	6976
Db	6901	GACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACCAC	6960
Qy	6977	ACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAGCAAG	7036
Db	6961	ACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAGCAAG	7020
Qy	7037	ATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACACTG	7096
Db	7021	ATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACACTG	7080
Qy	7097	GACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACG	7156
Db	7081	GACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACG	7140
Qy	7157	GAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGG	7216
Db	7141	GAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGG	7200
Qy	7217	TCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCGAGGACCTGGACACGGAG	7276
Db	7201	TCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCGAGGACCTGGACACGGAG	7260
Qy	7277	GACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCCTTCAACACGGACACG	7336

Db	7261		GACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCAGCTGTCTTCAACACGGACACG	7320
Qy	7337		CTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTGACCACCCAGAGCTG	7396
Db	7321		CTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTGACCACCCAGAGCTG	7380
Qy	7397		GGCCAGGGACTCAACAATGGGGACAGAAGTCCCCAGTGCCTGCCAGGGCCTGGAGTGGA	7456
Db	7381		GGCCAGGGACTCAACAATGGGGACAGAAGTCCCCAGTGCCTGCCAGGGCCTGGAGTGGA	7440
Qy	7457		GGTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCGGCCATGCCCTGCGGTC	7516
Db	7441		GGTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCGGCCATGCCCTGCGGTC	7500
Qy	7517		ACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCCCGGGCTGCGTACACCCT	7576
Db	7501		ACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCCCGGGCTGCGTACACCCT	7560
Qy	7577		TGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCTCGCCCCCTGCCTGGCACTG	7636
Db	7561		TGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCCCTCGCCCCCTGCCTGGCACTG	7620
Qy	7637		CTCACCGCCCAAGGCGACCCGGCTGGACCAGGCACTGCTGGCCTTTCTCCTGCCCGGCC	7696
Db	7621		CTCACCGCCCAAGGCGACCCGGCTGGACCAGGCACTGCTGGCCTTTCTCCTGCCCGGCC	7680
Qy	7697		TCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGAGCGGGCTGTGGGCGGA	7756
Db	7681		TCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGAGCGGGCTGTGGGCGGA	7740
Qy	7757		GCTGGGTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCTCTGGCCCTGCTCTCCT	7816
Db	7741		GCTGGGTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCTCTGGCCCTGCTCTCCT	7800
Qy	7817		GCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAGCTGGCAGGTGGCAGGA	7876
Db	7801		GCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAGCTGGCAGGTGGCAGGA	7860
Qy	7877		ATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCCCAACCCCCAGCTGC	7936
Db	7861		ATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCCCAACCCCCAGCTGC	7920
Qy	7937		CATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCCACCTCCCTGGGAGCCGGGCCTGT	7996
Db	7921		CATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCCACCTCCCTGGGAGCCGGGCCTGT	7980
Qy	7997		ACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAAAATGTC	8040
Db	7981		ACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAAAATGTC	8024

RESULT 6

US-10-380-727-28

; Sequence 28, Application US/10380727

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; GENERAL INFORMATION:

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; PRIOR APPLICATION NUMBER: US 60/236,882
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; PRIOR APPLICATION NUMBER: US 60/234,842
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/232,685
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 7610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040024183A1 7078207CB1
US-10-380-727-28

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Query Match          93.6%; Score 7529.2; DB 17; Length 7610;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7531; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 60
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Db      77 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 136
          |||

Qy      61 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGAGCCCGTGGGTCTTGGCCTTCGAGAT 120
          |||
Db     137 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGAGCCCGTGGGTCTTGGCCTTCGAGAT 196
          |||

Qy     121 CTTTCATCCCCCTGGTGTCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 180
          |||

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Db 197 CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 256

Qy 181 CTCCGTGAAGGAAGTCCCCCTTCTACACAGCGGGCGCCCCTGACGTCTGCCGGCATCCTGCC 240
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Db 257 CTCCGTGAAGGAAGTCTCCTTCTACACAGCGGGCGCCCCTGACGTCTGCCGGCATCCTGCC 316

Qy 241 TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTTCGGCTTCCTGCAGTACGC 300
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Db 317 TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTTCGGCTTCCTGCAGTACGC 376

Qy 301 CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT 360
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Db 377 CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT 436

Qy 361 GTTTGACCCAGCGCGGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA 420
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Db 437 GTTTGACCCAGCGCGGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA 496

Qy 421 GGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC 480
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Db 497 GGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC 556

Qy 481 CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA 540
 |||

Db 557 CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAGGAGCTCTGGCGTTTCCTGACGCAAAA 616

Qy 541 CTTGTCGCTGCCCAATAGCACGGCCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCGA 600
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Db 617 CTTGTCGCTGCCCAATAGCACGGCCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCGA 676

Qy 601 GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA 660
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Db 677 GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA 736

Qy 661 GGGTCAGGAGCCCTGGAGCCGCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT 720
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Db 737 GGGTCAGGAGCCCTGGAGCCGCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT 796

Qy 721 GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG 780
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Db 797 GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG 856

Qy 781 GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG 840
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Db 857 GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG 916

Qy 841 CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA 900
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Db 917 CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA 976

Qy 901 CCAGCTGGACGTGGCCAAGGTCTCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA 960
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Db 977 CCAGCTGGACGTGGCCAAGGTCTCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA 1036

Qy 961 CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA 1020
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Db 1037 CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA 1096

Qy	1021	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCTGTCTGGCCCTGGCCCTGCTACTGCCCCA	1080
Db	1097	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCTGTCTGGCCCTGGCCCTGCTACTGCCCCA	1156
Qy	1081	GGGTGCCTGCACTGGCCGGACCCCGGACCCCGAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Db	1157	GGGTGCCTGCACTGGCCGGACCCCGGACCCCGAGCCAGTGGTGCGGGTGGGGCGGCCAA	1216
Qy	1141	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1200
Db	1217	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1276
Qy	1201	TGCTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
Db	1277	TGCTGCAGCACTGGCCACCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1336
Qy	1261	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCT	1320
Db	1337	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCT	1396
Qy	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380
Db	1397	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1456
Qy	1381	CCTCGTGACCTCATGACCAGCAACCCCAAAATCCTGTACGCGCTGCGGGCTCTGAGGT	1440
Db	1457	CCTCGTGACCTCATGACCAGCAACCCCAAAATCCTGTACGCGCTGCGGGCTCTGAGGT	1516
Qy	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1500
Db	1517	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1576
Qy	1501	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1577	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1636
Qy	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620
Db	1637	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1696
Qy	1621	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1680
Db	1697	ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1756
Qy	1681	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGAT	1740
Db	1757	CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCCTGCGGCTGGAT	1816
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1800
Db	1817	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1876
Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1860
Db	1877	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1936

Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1920
Db	1937	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1996
Qy	1921	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	1980
Db	1997	CTCCAGCTTCACCGAGAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGCCCAA	2056
Qy	1981	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Db	2057	TACTGGCGGCCGCTTCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2116
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Db	2117	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2176
Qy	2101	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2160
Db	2177	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTTCATTGAGCACATGATGCC	2236
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Db	2237	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2296
Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280
Db	2297	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2356
Qy	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2340
Db	2357	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2416
Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2400
Db	2417	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2476
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2460
Db	2477	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2536
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Db	2537	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2596
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
Db	2597	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2656
Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640
Db	2657	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2716
Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2700
Db	2717	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2776
Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760

Db	2777	 CGACTTCAACTTGCTCCTGGCTGTCAACATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2836
Qy	2761	 CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2837	 CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2896
Qy	2821	 CTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2897	 CTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2956
Qy	2881	 CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2957	 CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGTGCCAT	3016
Qy	2941	 GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3000
Db	3017	 GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3076
Qy	3001	 GGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3077	 GGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3136
Qy	3061	 CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3137	 CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3196
Qy	3121	 GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCG	3180
Db	3197	 GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCG	3256
Qy	3181	 CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3257	 CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3316
Qy	3241	 GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3317	 GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3376
Qy	3301	 CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3377	 CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3436
Qy	3361	 GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTGCGGTGGCATGAA	3420
Db	3437	 GGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTGCGGTGGCATGAA	3496
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Db	3497	 GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCTGGACGA	3556
Qy	3481	 GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCTGAAGTA	3540
Db	3557	 GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCTGAAGTA	3616
Qy	3541	 CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600

Db	3617	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3676
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3677	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3736
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCCGAGCCGGG	3720
Db	3737	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCCGAGCCGGG	3796
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGCCCCGCTGAGCAGCTG	3780
Db	3797	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGCCCCGCTGAGCAGCTG	3856
Qy	3781	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3857	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3916
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3917	AGACACAAGCACGGAGCTCTCCTACATCCTGCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3976
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3977	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	4036
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTGCGGAGGAGGATCAGTCGCT	4020
Db	4037	GCTGATGGACACGACCCTGGAGGAAGTGTTCTCAAGGTGTGCGGAGGAGGATCAGTCGCT	4096
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4097	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4156
Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4157	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4216
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4200
Db	4217	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4276
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4277	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4336
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTGGGCCAGGGCAGCCGCAA	4320
Db	4337	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTGGGCCAGGGCAGCCGCAA	4396
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4397	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4456
Qy	4381	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4457	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4516

Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4517	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4576
Qy	4501	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4577	CCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4636
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCCAGCAGCT	4620
Db	4637	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCCAGCAGCT	4696
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4697	CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4756
Qy	4681	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4757	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4816
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4817	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4876
Qy	4801	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4860
Db	4877	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCT	4936
Qy	4861	GCAGGCCTGGAACGTCTCCCTGCCGCCCCACCGCTGGGCCAGAAATGTGGACGTGGGCACC	4920
Db	4937	GCAGGCCTGGAACGTCTCCCTGCCGCCCCACCGCTGGGCCAGAAATGTGGACGTGGGCACC	4996
Qy	4921	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	4980
Db	4997	CTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GG	5056
Qy	4981	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5040
Db	5057	CTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGGCGA	5116
Qy	5041	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5100
Db	5117	CATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCG	5176
Qy	5101	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5160
Db	5177	CTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGC	5236
Qy	5161	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5220
Db	5237	CTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCA	5296
Qy	5221	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5280
Db	5297	GGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAA	5356

Qy	5281	CGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5340
Db	5357	CGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCAC	5416
Qy	5341	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5400
Db	5417	CGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCA	5476
Qy	5401	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5460
Db	5477	GGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAG	5536
Qy	5461	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGTCAG	5520
Db	5537	CTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGTCAG	5596
Qy	5521	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5580
Db	5597	CGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCT	5656
Qy	5581	GGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTC	5640
Db	5657	GGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTC	5716
Qy	5641	GCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCC	5700
Db	5717	GCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCC	5776
Qy	5701	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTTCCTCAT	5760
Db	5777	CATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTTCCTCAT	5836
Qy	5761	TGTCATCAATCTCTTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5820
Db	5837	TGTCATCAATCTCTTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTT	5896
Qy	5821	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5880
Db	5897	CGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTT	5956
Qy	5881	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	5940
Db	5957	CCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGA	6016
Qy	5941	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGT	6000
Db	6017	GTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGT	6076
Qy	6001	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6060
Db	6077	CACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCAT	6136
Qy	6061	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6120
Db	6137	GTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGA	6196
Qy	6121	GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6180

Db	6197	 GGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGA	6256
Qy	6181	CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6240
Db	6257	 CATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCT	6316
Qy	6241	GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6300
Db	6317	 GGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGT	6376
Qy	6301	CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6360
Db	6377	 CAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGG	6436
Qy	6361	GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6420
Db	6437	 GGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAG	6496
Qy	6421	CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCCGGGAGCACCT	6480
Db	6497	 CCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCCGGGAGCACCT	6556
Qy	6481	GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6540
Db	6557	 GCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTG	6616
Qy	6541	GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6600
Db	6617	 GGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGG	6676
Qy	6601	CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTT	6660
Db	6677	 CGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTT	6736
Qy	6661	CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6720
Db	6737	 CCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCAT	6796
Qy	6721	CCTCGACCTCATCAAGACAGGGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTG	6780
Db	6797	 CCTCGACCTCATCAAGACAGGGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTG	6856
Qy	6781	CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6840
Db	6857	 CGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAG	6916
Qy	6841	CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6900
Db	6917	 CATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAG	6976
Qy	6901	CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	6960
Db	6977	 CAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCT	7036
Qy	6961	CAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC	7020

Db 7037 CAAGGAGCGGCACCCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGC 7096
 Qy 7021 CCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT 7080
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 Db 7097 CCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGT 7156
 Qy 7081 CAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT 7140
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 Db 7157 CAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGACAACCT 7216
 Qy 7141 GGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAG 7200
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 Qy 7201 CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA 7260
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 Db 7277 CCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGA 7336
 Qy 7261 GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGGCCAGCTGTC 7320
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 Db 7337 GGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGGCCAGCTGTC 7396
 Qy 7321 CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC 7380
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 Db 7397 CTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCAC 7456
 Qy 7381 TGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGC 7440
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 Qy 7441 CAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCCTGTACTCG 7500
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 Db 7517 CAGGGCCTGGAGTGGAGGTTTCAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCCTGTACTCG 7576
 Qy 7501 GCCATGCCCTGCGGTCACTGCGGTTGCCGCCCT 7534
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 Db 7577 GCCATGTCCTGCGGTCACTGCGGTTGCCGCCCT 7610

RESULT 7

US-09-795-693-9

; Sequence 9, Application US/09795693

; Patent No. US20020068710A1

; GENERAL INFORMATION:

; APPLICANT: Glucksmann, Maria A.

; TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and

; TITLE OF INVENTION: 32613, No. US20020068710A1el Human Transporters

; FILE REFERENCE: 35800/209292

; CURRENT APPLICATION NUMBER: US/09/795,693

; CURRENT FILING DATE: 2001-02-28

; PRIOR APPLICATION NUMBER: 60/185,906

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 7305

; TYPE: DNA

; ORGANISM: Homo sapiens
US-09-795-693-9

Query Match 90.8%; Score 7301.8; DB 9; Length 7305;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7303; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      35 ATGGGCTTCCTGCACCAGCTGCAGCTGCTGCTCTGGAAGAACGTGACGCTCAAACGCCGG 94
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Db      1 ATGGGCTTCCTGCACCAGCTGCAGCTGCTGCTCTGGAAGAACGTGACGCTCAAACGCCGG 60

Qy     95 AGCCCGTGGGTCTTGGCCTTCGAGATCTTCATCCCCCTGGTGTGTTCTTTATCCTGCTG 154
      |||
Db     61 AGCCCGTGGGTCTTGGCCTTCGAGATCTTCATCCCCCTGGTGTGTTCTTTATCCTGCTG 120

Qy    155 GGGCTGCGACAGAAGAAGCCCAACCATCTCCGTGAAGGAAGTCCCCCTTCTACACAGCGGCG 214
      |||
Db    121 GGGCTGCGACAGAAGAAGCCCAACCATCTCCGTGAAGGAAGTCTCCTTCTACACAGCGGCG 180

Qy    215 CCCCTGACGTCTGCCGGCATCCTGCCTGTCATGCAATCGCTGTGCCCGGACGGCCAGCGA 274
      |||
Db    181 CCCCTGACGTCTGCCGGCATCCTGCCTGTCATGCAATCGCTGTGCCCGGACGGCCAGCGA 240

Qy    275 GACGAGTTCGGCTTCCTGCAGTACGCCAACTCCACGGTCACGCAGCTGCTTGAGCGCCTG 334
      |||
Db    241 GACGAGTTCGGCTTCCTGCAGTACGCCAACTCCACGGTCACGCAGCTGCTTGAGCGCCTG 300

Qy    335 GACCGCGTGGTGGAGGAAGGCAACCTGTTTGACCCAGCGCGGCCCAGCCTGGGCTCAGAG 394
      |||
Db    301 GACCGCGTGGTGGAGGAAGGCAACCTGTTTGACCCAGCGCGGCCCAGCCTGGGCTCAGAG 360

Qy    395 CTCGAGGCCCTACGCCAGCATCTGGAGGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGC 454
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Db    361 CTCGAGGCCCTACGCCAGCATCTGGAGGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGC 420

Qy    455 CACCTGGACAGATCCACAGTGTCTTCTTCTCTCTGGAAGTCCGGTGGCCAGAAACCCGCAG 514
      |||
Db    421 CACCTGGACAGATCCACAGTGTCTTCTTCTCTCTGGAAGTCCGGTGGCCAGAAACCCGCAG 480

Qy    515 GAGCTCTGGCGTTTCCTGACGCAAACTTGTCGCTGCCCAATAGCACGGCCCAAGCACTC 574
      |||
Db    481 GAGCTCTGGCGTTTCCTGACGCAAACTTGTCGCTGCCCAATAGCACGGCCCAAGCACTC 540

Qy    575 TTGGCCGCCCGTGTGGACCCGCCGAGGTCTACCACCTGCTCTTTGGTCCCTCATCTGCC 634
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Db    541 TTGGCCGCCCGTGTGGACCCGCCGAGGTCTACCACCTGCTCTTTGGTCCCTCATCTGCC 600

Qy    635 CTGGATTACAGTCTGGCCTCCACAAGGGTCAGGAGCCCTGGAGCCGCCCTAGGGGGCAAT 694
      |||
Db    601 CTGGATTACAGTCTGGCCTCCACAAGGGTCAGGAGCCCTGGAGCCGCCCTAGGGGGCAAT 660

Qy    695 CCCCTGTTCCGGATGGAGGAGCTGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGC 754
      |||
Db    661 CCCCTGTTCCGGATGGAGGAGCTGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGC 720

Qy    755 ACGCCGGGCTCGGGGGAGCTGGGCCGGATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCC 814
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Db	721	ACGCCGGGCTCGGGGGAGCTGGGCCGGATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCC	780
Qy	815	CTGCAGGGCTACCGGGATGCTGTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTC	874
Db	781	CTGCAGGGCTACCGGGATGCTGTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTC	840
Qy	875	TCTGGGCTGTCTGCTGAGCTCCGGAACCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTG	934
Db	841	TCTGGGCTGTCTGCTGAGCTCCGGAACCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTG	900
Qy	935	GGCCTGGATGCCCCCAACGGCTCGGACTCCTCGCCACAGGCGCCACCCCCACGGAGGCTG	994
Db	901	GGCCTGGATGCCCCCAACGGCTCGGACTCCTCGCCACAGGCGCCACCCCCACGGAGGCTG	960
Qy	995	CAGGCGCTTCTGGGGACCTGCTGGATGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTG	1054
Db	961	CAGGCGCTTCTGGGGACCTGCTGGATGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTG	1020
Qy	1055	TCGGCCCTGGCCCTGCTACTGCCCCAGGGTGCCTGCACTGGCCGGACCCCCGGACCCCCA	1114
Db	1021	TCGGCCCTGGCCCTGCTACTGCCCCAGGGTGCCTGCACTGGCCGGACCCCCGGACCCCCA	1080
Qy	1115	GCCAGTGGTGCGGGTGGGGCGGCCAATGGCACTGGGGCAGGGGCAGTCATGGGCCCCAAC	1174
Db	1081	GCCAGTGGTGCGGGTGGGGCGGCCAATGGCACTGGGGCAGGGGCAGTCATGGGCCCCAAC	1140
Qy	1175	GCCACCGCTGAGGAGGGCGCACCCCTCTGCTGCAGCACTGGCCACCCCGGACACGCTGCAG	1234
Db	1141	GCCACCGCTGAGGAGGGCGCACCCCTCTGCTGCAGCACTGGCCACCCCGGACACGCTGCAG	1200
Qy	1235	GGCCAGTGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAAC	1294
Db	1201	GGCCAGTGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAAC	1260
Qy	1295	AACCGCACCATTTGAACCCGAGGCGCTGCGGCCGGGGCAACATGAGCTCCCTGGGCTTCACG	1354
Db	1261	AACCGCACCATTTGAACCCGAGGCGCTGCGGCCGGGGCAACATGAGCTCCCTGGGCTTCACG	1320
Qy	1355	AGCAAGGAGCAGCGGAACCTGGGCCTCCTCGTGACCTCATGACCAGCAACCCCAAAATC	1414
Db	1321	AGCAAGGAGCAGCGGAACCTGGGCCTCCTCGTGACCTCATGACCAGCAACCCCAAAATC	1380
Qy	1415	CTGTACGCGCCTGCGGGCTCTGAGGTGACCGCGTCATCCTCAAGGCCAACGAGACTTTT	1474
Db	1381	CTGTACGCGCCTGCGGGCTCTGAGGTGACCGCGTCATCCTCAAGGCCAACGAGACTTTT	1440
Qy	1475	GCTTTTGTGGGCAACGTGACTCACTATGCCCAGGTCTGGCTCAACATCTCGGCGGAGATC	1534
Db	1441	GCTTTTGTGGGCAACGTGACTCACTATGCCCAGGTCTGGCTCAACATCTCGGCGGAGATC	1500
Qy	1535	CGCAGCTTCCTGGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTATGTA	1594
Db	1501	CGCAGCTTCCTGGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTATGTA	1560
Qy	1595	GCAGAGCTGCGGCTGCACCCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCGGCC	1654
Db	1561	GCAGAGCTGCGGCTGCACCCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCGGCC	1620

Qy	1655	CTGAGACAGGACAACCTTCTCGCTGCCAGTGGCATGGCCCTCCTGCAGCAGCTGGATACC	1714
Db	1621	CTGAGACAGGACAACCTTCTCGCTGCCAGTGGCATGGCCCTCCTGCAGCAGCTGGATACC	1680
Qy	1715	ATTGACAACGCGGCCTGCGGCTGGATCCAGTTCATGTCCAAGGTGAGCGTGGACATCTTC	1774
Db	1681	ATTGACAACGCGGCCTGCGGCTGGATCCAGTTCATGTCCAAGGTGAGCGTGGACATCTTC	1740
Qy	1775	AAGGGCTTCCCCGACGAGGAGAGCATTGTCAACTACACCCTCAACCAGGCCTACCAGGAC	1834
Db	1741	AAGGGCTTCCCCGACGAGGAGAGCATTGTCAACTACACCCTCAACCAGGCCTACCAGGAC	1800
Qy	1835	AACGTCACGTGTTTTTGGCAGTGTGATCTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCT	1894
Db	1801	AACGTCACGTGTTTTTGGCAGTGTGATCTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCT	1860
Qy	1895	CACGTGCACTACAAGATCCGCCAGAACTCCAGCTTCACCGAGAAAACCAACGAGATCCGC	1954
Db	1861	CACGTGCACTACAAGATCCGCCAGAACTCCAGCTTCACCGAGAAAACCAACGAGATCCGC	1920
Qy	1955	CGCGCCTACTGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCCTCTACGGCTTC	2014
Db	1921	CGCGCCTACTGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCCTCTACGGCTTC	1980
Qy	2015	GTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCAGCAGTG	2074
Db	1981	GTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCAGCAGTG	2040
Qy	2075	GTGGAGCCAGGCAGCTACGTGCAGATGTTCCCTACCCCTGCTACACACGCGATGACTTC	2134
Db	2041	GTGGAGCCAGGCAGCTACGTGCAGATGTTCCCTACCCCTGCTACACACGCGATGACTTC	2100
Qy	2135	CTGTTTGTCAATTGAGCACATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTG	2194
Db	2101	CTGTTTGTCAATTGAGCACATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTG	2160
Qy	2195	GCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAG	2254
Db	2161	GCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAG	2220
Qy	2255	ACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAG	2314
Db	2221	ACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAG	2280
Qy	2315	CTGTCCATCTCCGTGACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCAC	2374
Db	2281	CTGTCCATCTCCGTGACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATACAC	2340
Qy	2375	AGCCACGTGGTCATCATCTGGCTCTTCTGGCAGTCTACGCGGTGGCCACCATCATGTTC	2434
Db	2341	AGCCACGTGGTCATCATCTGGCTCTTCTGGCAGTCTACGCGGTGGCCACCATCATGTTC	2400
Qy	2435	TGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATC	2494
Db	2401	TGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATC	2460

Qy	2495	ATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCAT	2554
Db	2461	ATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCAT	2520
Qy	2555	GATAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGT	2614
Db	2521	GATAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGT	2580
Qy	2615	CTGGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACC	2674
Db	2581	CTGGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACC	2640
Qy	2675	TTCAGCCAGTCCCCGGTGGAGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTG	2734
Db	2641	TTCAGCCAGTCCCCGGTGGAGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTG	2700
Qy	2735	ATGGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGC	2794
Db	2701	ATGGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGC	2760
Qy	2795	ATGTACGGGCTGCCCCGGCCCTGGTACTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGT	2854
Db	2761	ATGTACGGGCTGCCCCGGCCCTGGTACTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGT	2820
Qy	2855	GGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTC	2914
Db	2821	GGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTC	2880
Qy	2915	ATGGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATG	2974
Db	2881	ATGGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATG	2940
Qy	2975	GAGGAGGAGCCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAAACTCACCAAGGTCTAC	3034
Db	2941	GAGGAGGAGCCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAAACTCACCAAGGTCTAC	3000
Qy	3035	AAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTG	3094
Db	3001	AAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTG	3060
Qy	3095	GTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGC	3154
Db	3061	GTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGC	3120
Qy	3155	CTGTTCCCTCCAACGTCGGGTTCCGCCACCATCTACGGGCACGACATCCGCACGGAGATG	3214
Db	3121	CTGTTCCCTCCAACGTCGGGTTCCGCCACCATCTACGGGCACGACATCCGCACGGAGATG	3180
Qy	3215	GATGAGATCCGCAAGAACCTGGGCATGTGCCCGCAGCACAATGTGCTCTTTGACCGGCTC	3274
Db	3181	GATGAGATCCGCAAGAACCTGGGCATGTGCCCGCAGCACAATGTGCTCTTTGACCGGCTC	3240
Qy	3275	ACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATC	3334
Db	3241	ACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATC	3300
Qy	3335	CGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTG	3394

Db	3301	 CGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTG	3360
Qy	3395	GTGCAGACATTGTCGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGC	3454
Db	3361	 GTGCAGACATTGTCGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGC	3420
Qy	3455	GGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGC	3514
Db	3421	 GGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGC	3480
Qy	3515	GCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCAC	3574
Db	3481	 GCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCAC	3540
Qy	3575	CACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTC	3634
Db	3541	 CACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTC	3600
Qy	3635	AAGTGCTGCGGCTCCCCGCTCTTCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACG	3694
Db	3601	 AAGTGCTGCGGCTCCCCGCTCTTCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACG	3660
Qy	3695	CTGGTCAAGCGGCCCCGCCGAGCCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCC	3754
Db	3661	 CTGGTCAAGCGGCCCCGCCGAGCCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCC	3720
Qy	3755	CCAGGTCGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAG	3814
Db	3721	 CCAGGTCGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAG	3780
Qy	3815	CATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCC	3874
Db	3781	 CATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCC	3840
Qy	3875	AGCGAGGCCGCCAAGAAGGGGGCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTG	3934
Db	3841	 AGCGAGGCCGCCAAGAAGGGGGCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTG	3900
Qy	3935	GATGCACTGCACCTCAGCAGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCCTC	3994
Db	3901	 GATGCACTGCACCTCAGCAGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCCTC	3960
Qy	3995	AAGGTGTCGGAGGAGGATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGG	4054
Db	3961	 AAGGTGTCGGAGGAGGATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGG	4020
Qy	4055	AAGGATGTGCTCCCTGGGGCGGAGGGCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTG	4114
Db	4021	 AAGGATGTGCTCCCTGGGGCGGAGGGCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTG	4080
Qy	4115	GCCCCGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGC	4174
Db	4081	 GCCCCGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGC	4140
Qy	4175	TCTGCCCCGTGGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTC	4234

Db	4141	TCTGCCCCGTGGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTC	4200
Qy	4235	TTTGATAACCCACAGGACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTG	4294
Db	4201	TTTGATAACCCACAGGACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTG	4260
Qy	4295	TCGAGGGTCGGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTC	4354
Db	4261	TCGAGGGTCGGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTC	4320
Qy	4355	CACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCC	4414
Db	4321	CACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCC	4380
Qy	4415	CAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCG	4474
Db	4381	CAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCG	4440
Qy	4475	GAGATTGGTGATCTGCCCCGCTGGTCCTGTACCTTCCCAGTACCACAACCTACACCCAG	4534
Db	4441	GAGATTGGTGATCTGCCCCGCTGGTCCTGTACCTTCCCAGTACCACAACCTACACCCAG	4500
Qy	4535	CCCCGTGGCAATTTTCATCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTA	4594
Db	4501	CCCCGTGGCAATTTTCATCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTA	4560
Qy	4595	TCGCCCAGCGCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGT	4654
Db	4561	TCGCCCAGCGCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGT	4620
Qy	4655	GCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCCCACGTTGAACCTGAGC	4714
Db	4621	GCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCCCACGTTGAACCTGAGC	4680
Qy	4715	AGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTC	4774
Db	4681	AGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTC	4740
Qy	4775	ACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCGCCCCATCTGAC	4834
Db	4741	ACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCGCCCCATCTGAC	4800
Qy	4835	TCGCCAGCGTCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCACCGCT	4894
Db	4801	TCGCCAGCGTCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCACCGCT	4860
Qy	4895	GGGCCAGAAATGTGGACGTGGGCACCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGC	4954
Db	4861	GGGCCAGAAATGTGGACGTGGGCACCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGC	4920
Qy	4955	TGCACCTGCTCTGCGCAGGGCACC GGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCG	5014
Db	4921	TGCACCTGCTCTGCGCAGGGCACC GGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCG	4980
Qy	5015	CCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACATACCGGCCACAATGTCTCT	5074
Db	4981	CCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACATACCGGCCACAATGTCTCT	5040

Qy	5075	GAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTT	5134
Db	5041	GAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTT	5100
Qy	5135	GGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGG	5194
Db	5101	GGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGG	5160
Qy	5195	AAGATCGCGGTGCGCAGGGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATG	5254
Db	5161	AAGATCGCGGTGCGCAGGGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATG	5220
Qy	5255	CCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAG	5314
Db	5221	CCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAG	5280
Qy	5315	GGCAACCCGGCGGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCC	5374
Db	5281	GGCAACCCGGCGGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCC	5340
Qy	5375	AGCCTCTCCCTGGATTACCTGCTGCAGGGCACGGATGTCGTCATCGCCATCTTCATCATC	5434
Db	5341	AGCCTCTCCCTGGATTACCTGCTGCAGGGCACGGATGTCGTCATCGCCATCTTCATCATC	5400
Qy	5435	GTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACC	5494
Db	5401	GTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACC	5460
Qy	5495	AAGGCCAAGCATCTGCAGTTTGTGTCAGGGCTGCAACCCCATCATCTACTGGCTGGCGAAC	5554
Db	5461	AAGGCCAAGCATCTGCAGTTTGTGTCAGGGCTGCAACCCCATCATCTACTGGCTGGCGAAC	5520
Qy	5555	TACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCTGCTGTGTCATCATCCTGTTT	5614
Db	5521	TACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCTGCTGTGTCATCATCCTGTTT	5580
Qy	5615	GTGTTTCGACCTGCCGGCCTACACGTCGCCCACCAACTTCCCTGCCGTCTCTCCCTCTTC	5674
Db	5581	GTGTTTCGACCTGCCGGCCTACACGTCGCCCACCAACTTCCCTGCCGTCTCTCCCTCTTC	5640
Qy	5675	CTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTC	5734
Db	5641	CTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTC	5700
Qy	5735	CCCAGCTCCGCCTACGTGTTCTCATTGTGTCATCAATCTCTTCATCGGCATCACCGCCACC	5794
Db	5701	CCCAGCTCCGCCTACGTGTTCTCATTGTGTCATCAATCTCTTCATCGGCATCACCGCCACC	5760
Qy	5795	GTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGT	5854
Db	5761	GTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGT	5820
Qy	5855	TACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAG	5914
Db	5821	TACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAG	5880

Qy 5915 ATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATG 5974
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 Db 5881 ATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATG 5940

Qy 5975 AAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGC 6034
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 Db 5941 AAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGC 6000

Qy 6035 GTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTCCTGCGGCGGCCACAGCGC 6094
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 Db 6001 GTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTCCTGCGGCGGCCACAGCGC 6060

Qy 6095 ATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGA 6154
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 Db 6061 ATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGA 6120

Qy 6155 GTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTAC 6214
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 Db 6121 GTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTAC 6180

Qy 6215 AAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCT 6274
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 Db 6181 AAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCT 6240

Qy 6275 GGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATG 6334
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 Db 6241 GGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATG 6300

Qy 6335 CTGACCGGCGACGAGAGCACGACGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTG 6394
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 Db 6301 CTGACCGGCGACGAGAGCACGACGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTG 6360

Qy 6395 AAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTC 6454
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 Db 6361 AAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTC 6420

Qy 6455 GACGAGCTCACGGCCCCGGGAGCACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGG 6514
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 Db 6421 GACGAGCTCACGGCCCCGGGAGCACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGG 6480

Qy 6515 AAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCA 6574
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 Db 6481 AAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCA 6540

Qy 6575 GACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCC 6634
 |||||
 Db 6541 GACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCC 6600

Qy 6635 CTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCACCACAGGCATGGACCCCAAG 6694
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 Db 6601 CTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCACCACAGGCATGGACCCCAAG 6660

Qy 6695 GCCCCGGCGCTTCCTCTGGAACCTCATCCTCGACCTCATCAAGACAGGGCGTTCAGTGGTG 6754
 |||||
 Db 6661 GCCCCGGCGCTTCCTCTGGAACCTCATCCTCGACCTCATCAAGACAGGGCGTTCAGTGGTG 6720

Qy 6755 CTGACATCACACAGCATGGAGGAGTGGGAGGCGCTGTGCACGCGGCTGGCCATCATGGTG 6814

Db	6721		CTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTG	6780
Qy	6815		AACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGC	6874
Db	6781		AACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGC	6840
Qy	6875		TACATGATCACGGTTCGGACCAAGAGCAGCCAGAGTGTGAAGGACGTGGTTCGGTTCTTC	6934
Db	6841		TACATGATCACGGTTCGGACCAAGAGCAGCCAGAGTGTGAAGGACGTGGTTCGGTTCTTC	6900
Qy	6935		AACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACACAAAGGTGCAGTACCAG	6994
Db	6901		AACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACACAAAGGTGCAGTACCAG	6960
Qy	6995		CTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGC	7054
Db	6961		CTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGC	7020
Qy	7055		GTGCTGGGCATCGAGGACTACTCGGTTCAGCCAGACCACACTGGACAATGTGTTTCGTGAAC	7114
Db	7021		GTGCTGGGCATCGAGGACTACTCGGTTCAGCCAGACCACACTGGACAATGTGTTTCGTGAAC	7080
Qy	7115		TTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTG	7174
Db	7081		TTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTG	7140
Qy	7175		CAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTC	7234
Db	7141		CAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTC	7200
Qy	7235		CGGGCACTTGTGGCAGACGAGCCCGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGC	7294
Db	7201		CGGGCACTTGTGGCAGACGAGCCCGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGC	7260
Qy	7295		TTCGAGGAGGAGCGGGCCCAGCTGTCCTTCAACACGGACACGCTC	7339
Db	7261		TTCGAGGAGGAGCGGGCCCAGCTGTCCTTCAACACGGACACGCTC	7305

RESULT 8

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; Sequence 9, Application US/10156239

; Publication No. US20030036074A1

; GENERAL INFORMATION:

; APPLICANT: Glucksmann, Maria A.

; APPLICANT: Kapeller-Libermann, Rosana

; TITLE OF INVENTION: No. US20030036074A1el Nucleic Acid Sequences Encoding Human Transporters, A Human

; TITLE OF INVENTION: ATPase Molecule, A Human Ubiquitin Hydrolase-Like Molecule, A Human

; TITLE OF INVENTION: Ubiquitin Conjugating Enzyme-Like Molecule, and Uses Therefor

; FILE REFERENCE: 35800/247645

; CURRENT APPLICATION NUMBER: US/10/156,239

; CURRENT FILING DATE: 2002-05-24

; PRIOR APPLICATION NUMBER: 09/795,693

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; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/809,557
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/192,018
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/808,568
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/191,790
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/808,767
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/191,781
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 7305
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-156-239-9
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 7303; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      35 ATGGGCTTCCTGCACCAGCTGCAGCTGCTGCTCTGGAAGAACGTGACGCTCAAACGCCGG 94
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Db       1 ATGGGCTTCCTGCACCAGCTGCAGCTGCTGCTCTGGAAGAACGTGACGCTCAAACGCCGG 60

Qy      95 AGCCCGTGGGTCTTGGCCTTCGAGATCTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTG 154
          |||
Db       61 AGCCCGTGGGTCTTGGCCTTCGAGATCTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTG 120

Qy     155 GGGCTGCGACAGAAGAAGCCACCATCTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCG 214
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Db     121 GGGCTGCGACAGAAGAAGCCACCATCTCCGTGAAGGAAGTCTCCTTCTACACAGCGGCG 180

Qy     215 CCCCTGACGTCTGCCGGCATCCTGCCTGTCATGCAATCGCTGTGCCCCGACGGCCAGCGA 274
          |||
Db     181 CCCCTGACGTCTGCCGGCATCCTGCCTGTCATGCAATCGCTGTGCCCCGACGGCCAGCGA 240

Qy     275 GACGAGTTCGGCTTCCTGCAGTACGCCAACTCCACGGTCACGCAGCTGCTTGAGCGCCTG 334
          |||
Db     241 GACGAGTTCGGCTTCCTGCAGTACGCCAACTCCACGGTCACGCAGCTGCTTGAGCGCCTG 300

Qy     335 GACCGCGTGGTGGAGGAAGGCAACCTGTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAG 394
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Db     301 GACCGCGTGGTGGAGGAAGGCAACCTGTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAG 360

Qy     395 CTCGAGGCCCTACGCCAGCATCTGGAGGCCCTCAGTGCGGGCCCGGGCACCTCGGGGAGC 454
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Db     361 CTCGAGGCCCTACGCCAGCATCTGGAGGCCCTCAGTGCGGGCCCGGGCACCTCGGGGAGC 420

Qy     455 CACCTGGACAGATCCACAGTGTCTTCCTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAG 514
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Db	421	CACCTGGACAGATCCACAGTGTCTTCTCTCTCTGGACTCGGTGGCCAGAAACCCGCAG	480
Qy	515	GAGCTCTGGCGTTTCCTGACGCAAACTTGTCGCTGCCCAATAGCACGGCCCAAGCACTC	574
Db	481	GAGCTCTGGCGTTTCCTGACGCAAACTTGTCGCTGCCCAATAGCACGGCCCAAGCACTC	540
Qy	575	TTGGCCGCCCCGTGTGGACCCGCCCCGAGGTCTACCACCTGCTCTTTGGTCCCTCATCTGCC	634
Db	541	TTGGCCGCCCCGTGTGGACCCGCCCCGAGGTCTACCACCTGCTCTTTGGTCCCTCATCTGCC	600
Qy	635	CTGGATTACAGTCTGGCCTCCACAAGGGTCAGGAGCCCTGGAGCCGCTAGGGGGCAAT	694
Db	601	CTGGATTACAGTCTGGCCTCCACAAGGGTCAGGAGCCCTGGAGCCGCTAGGGGGCAAT	660
Qy	695	CCCCTGTTCCGGATGGAGGAGCTGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGC	754
Db	661	CCCCTGTTCCGGATGGAGGAGCTGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGC	720
Qy	755	ACGCCGGGCTCGGGGGAGCTGGGCCGGATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCC	814
Db	721	ACGCCGGGCTCGGGGGAGCTGGGCCGGATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCC	780
Qy	815	CTGCAGGGCTACCGGGATGCTGTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTC	874
Db	781	CTGCAGGGCTACCGGGATGCTGTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTC	840
Qy	875	TCTGGGCTGTCTGCTGAGCTCCGGAACCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTG	934
Db	841	TCTGGGCTGTCTGCTGAGCTCCGGAACCAGCTGGACGTGGCCAAGGTCTCCCAGCAGCTG	900
Qy	935	GGCCTGGATGCCCCAACGGCTCGGACTCCTCGCCACAGGCGCCACCCCCACGGAGGCTG	994
Db	901	GGCCTGGATGCCCCAACGGCTCGGACTCCTCGCCACAGGCGCCACCCCCACGGAGGCTG	960
Qy	995	CAGGCGCTTCTGGGGGACCTGCTGGATGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTG	1054
Db	961	CAGGCGCTTCTGGGGGACCTGCTGGATGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTG	1020
Qy	1055	TCGGCCCTGGCCCTGCTACTGCCCCAGGGTGCCTGCACTGGCCGGACCCCCGGACCCCCA	1114
Db	1021	TCGGCCCTGGCCCTGCTACTGCCCCAGGGTGCCTGCACTGGCCGGACCCCCGGACCCCCA	1080
Qy	1115	GCCAGTGGTGCGGGTGGGGCGGCCAATGGCACTGGGGCAGGGGCAGTCATGGGCCCCAAC	1174
Db	1081	GCCAGTGGTGCGGGTGGGGCGGCCAATGGCACTGGGGCAGGGGCAGTCATGGGCCCCAAC	1140
Qy	1175	GCCACCGCTGAGGAGGGCGCACCCTCTGCTGCAGCACTGGCCACCCCGACACGCTGCAG	1234
Db	1141	GCCACCGCTGAGGAGGGCGCACCCTCTGCTGCAGCACTGGCCACCCCGACACGCTGCAG	1200
Qy	1235	GGCCAGTGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAAC	1294
Db	1201	GGCCAGTGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAAC	1260
Qy	1295	AACCGCACCATTGAACCCGAGGCGCTGCGGCGGGGCAACATGAGCTCCCTGGGCTTCACG	1354
Db	1261	AACCGCACCATTGAACCCGAGGCGCTGCGGCGGGGCAACATGAGCTCCCTGGGCTTCACG	1320

Qy	1355	AGCAAGGAGCAGCGGAACCTGGGCCTCCTCGTGCACCTCATGACCAGCAACCCCAAATC	1414
Db	1321	AGCAAGGAGCAGCGGAACCTGGGCCTCCTCGTGCACCTCATGACCAGCAACCCCAAATC	1380
Qy	1415	CTGTACGCGCCTGCGGGCTCTGAGGTCGACCGCGTCATCCTCAAGGCCAACGAGACTTTT	1474
Db	1381	CTGTACGCGCCTGCGGGCTCTGAGGTCGACCGCGTCATCCTCAAGGCCAACGAGACTTTT	1440
Qy	1475	GCTTTTGTGGGCAACGTGACTCACTATGCCCAGGTCTGGCTCAACATCTCGGCGGAGATC	1534
Db	1441	GCTTTTGTGGGCAACGTGACTCACTATGCCCAGGTCTGGCTCAACATCTCGGCGGAGATC	1500
Qy	1535	CGCAGCTTCCTGGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTATGTA	1594
Db	1501	CGCAGCTTCCTGGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTATGTA	1560
Qy	1595	GCAGAGCTGCGGCTGCACCCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCGGCC	1654
Db	1561	GCAGAGCTGCGGCTGCACCCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCGGCC	1620
Qy	1655	CTGAGACAGGACAACCTTCTCGCTGCCCAGTGGCATGGCCCTCCTGCAGCAGCTGGATACC	1714
Db	1621	CTGAGACAGGACAACCTTCTCGCTGCCCAGTGGCATGGCCCTCCTGCAGCAGCTGGATACC	1680
Qy	1715	ATTGACAACGCGGCCTGCGGCTGGATCCAGTTCATGTCCAAGGTGAGCGTGGACATCTTC	1774
Db	1681	ATTGACAACGCGGCCTGCGGCTGGATCCAGTTCATGTCCAAGGTGAGCGTGGACATCTTC	1740
Qy	1775	AAGGGCTTCCCCGACGAGGAGAGCATTTGTCAACTACACCCTCAACCAGGCCTACCAGGAC	1834
Db	1741	AAGGGCTTCCCCGACGAGGAGAGCATTTGTCAACTACACCCTCAACCAGGCCTACCAGGAC	1800
Qy	1835	AACGTCACTGTTTTTGGCAGTGTGATCTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCT	1894
Db	1801	AACGTCACTGTTTTTGGCAGTGTGATCTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCT	1860
Qy	1895	CACGTGCACTACAAGATCCGCCAGAACTCCAGCTTCACCGAGAAAACCAACGAGATCCGC	1954
Db	1861	CACGTGCACTACAAGATCCGCCAGAACTCCAGCTTCACCGAGAAAACCAACGAGATCCGC	1920
Qy	1955	CGCGCCTACTGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCCTCTACGGCTTC	2014
Db	1921	CGCGCCTACTGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCCTCTACGGCTTC	1980
Qy	2015	GTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCACGACGTG	2074
Db	1981	GTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCACGACGTG	2040
Qy	2075	GTGGAGCCAGGCAGCTACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTC	2134
Db	2041	GTGGAGCCAGGCAGCTACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTC	2100
Qy	2135	CTGTTTGTCAATTGAGCACATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTG	2194
Db	2101	CTGTTTGTCAATTGAGCACATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTG	2160

Qy	2195	GCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAG	2254
Db	2161	GCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAG	2220
Qy	2255	ACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAG	2314
Db	2221	ACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAG	2280
Qy	2315	CTGTCCATCTCCGTGACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCAC	2374
Db	2281	CTGTCCATCTCCGTGACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATACAC	2340
Qy	2375	AGCCACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTT	2434
Db	2341	AGCCACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTT	2400
Qy	2435	TGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATC	2494
Db	2401	TGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATC	2460
Qy	2495	ATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCAT	2554
Db	2461	ATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCAT	2520
Qy	2555	GATAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGT	2614
Db	2521	GATAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGT	2580
Qy	2615	CTGGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACC	2674
Db	2581	CTGGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACC	2640
Qy	2675	TTCAGCCAGTCCCCGGTGGAGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTG	2734
Db	2641	TTCAGCCAGTCCCCGGTGGAGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTG	2700
Qy	2735	ATGGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGC	2794
Db	2701	ATGGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGC	2760
Qy	2795	ATGTACGGGCTGCCCCGGCCCTGGTACTTCCCCTGCAGAACTCCTACTGGCTGGGCAGT	2854
Db	2761	ATGTACGGGCTGCCCCGGCCCTGGTACTTCCCCTGCAGAACTCCTACTGGCTGGGCAGT	2820
Qy	2855	GGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTC	2914
Db	2821	GGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTC	2880
Qy	2915	ATGGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATG	2974
Db	2881	ATGGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATG	2940
Qy	2975	GAGGAGGAGCCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAACTCACCAAGGTCTAC	3034
Db	2941	GAGGAGGAGCCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAACTCACCAAGGTCTAC	3000
Qy	3035	AAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTG	3094

Db	3001	 AAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTG	3060
Qy	3095	GTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGC	3154
Db	3061	 GTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGC	3120
Qy	3155	CTGTTCCCTCCAACGTCGGGTTCGCCACCATCTACGGGCACGACATCCGCACGGAGATG	3214
Db	3121	 CTGTTCCCTCCAACGTCGGGTTCGCCACCATCTACGGGCACGACATCCGCACGGAGATG	3180
Qy	3215	GATGAGATCCGCAAGAACCTGGGCATGTGCCCGCAGCACAATGTGCTCTTTGACCGGCTC	3274
Db	3181	 GATGAGATCCGCAAGAACCTGGGCATGTGCCCGCAGCACAATGTGCTCTTTGACCGGCTC	3240
Qy	3275	ACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATC	3334
Db	3241	 ACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATC	3300
Qy	3335	CGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTG	3394
Db	3301	 CGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTG	3360
Qy	3395	GTGCAGACATTGTCGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGC	3454
Db	3361	 GTGCAGACATTGTCGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGC	3420
Qy	3455	GGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGC	3514
Db	3421	 GGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGC	3480
Qy	3515	GCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCAC	3574
Db	3481	 GCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCAC	3540
Qy	3575	CACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTC	3634
Db	3541	 CACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTC	3600
Qy	3635	AAGTGCTGCGGCTCCCCGCTCTTCCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACG	3694
Db	3601	 AAGTGCTGCGGCTCCCCGCTCTTCCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACG	3660
Qy	3695	CTGGTCAAGCGGCCCCGCCGAGCCGGGGGCCCCAAGAGCCAGGGCTGGCATCCAGCCCC	3754
Db	3661	 CTGGTCAAGCGGCCCCGCCGAGCCGGGGGCCCCAAGAGCCAGGGCTGGCATCCAGCCCC	3720
Qy	3755	CCAGGTCGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAG	3814
Db	3721	 CCAGGTCGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAG	3780
Qy	3815	CATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCC	3874
Db	3781	 CATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCC	3840
Qy	3875	AGCGAGGCCGCCAAGAAGGGGGCTTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTG	3934

Db	3841	AGCGAGGCCGCCAAGAAGGGGGCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTG	3900
Qy	3935	GATGCACTGCACCTCAGCAGCTTCGGGGCTGATGGACACGACCCTGGAGGAAGTGTTTCCTC	3994
Db	3901	GATGCACTGCACCTCAGCAGCTTCGGGGCTGATGGACACGACCCTGGAGGAAGTGTTTCCTC	3960
Qy	3995	AAGGTGTCTGGAGGAGGATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGG	4054
Db	3961	AAGGTGTCTGGAGGAGGATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGG	4020
Qy	4055	AAGGATGTGCTCCCTGGGGCGGAGGGCCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTG	4114
Db	4021	AAGGATGTGCTCCCTGGGGCGGAGGGCCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTG	4080
Qy	4115	GCCCCGGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGC	4174
Db	4081	GCCCCGGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGC	4140
Qy	4175	TCTGCCCCGTGGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTC	4234
Db	4141	TCTGCCCCGTGGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTC	4200
Qy	4235	TTTGATAACCCACAGGACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTG	4294
Db	4201	TTTGATAACCCACAGGACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTG	4260
Qy	4295	TCGAGGGTCTGGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTC	4354
Db	4261	TCGAGGGTCTGGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTC	4320
Qy	4355	CACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCC	4414
Db	4321	CACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCC	4380
Qy	4415	CAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGCCATGACCGTGGCCCTGTCCGTCCCG	4474
Db	4381	CAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGCCATGACCGTGGCCCTGTCCGTCCCG	4440
Qy	4475	GAGATTGGTGATCTGCCCCGCTGGTCCTGTACCTTCCCAGTACCACAACCTACACCCAG	4534
Db	4441	GAGATTGGTGATCTGCCCCGCTGGTCCTGTACCTTCCCAGTACCACAACCTACACCCAG	4500
Qy	4535	CCCCGTGGCAATTTTCATCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTA	4594
Db	4501	CCCCGTGGCAATTTTCATCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTA	4560
Qy	4595	TCGCCCCGACGCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGT	4654
Db	4561	TCGCCCCGACGCCAGCCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGT	4620
Qy	4655	GCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCCACGTTGAACCTGAGC	4714
Db	4621	GCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCCACGTTGAACCTGAGC	4680
Qy	4715	AGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTC	4774
Db	4681	AGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTC	4740

Qy	4775	ACACAGGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCGCCCCATCTGAC	4834
Db	4741	ACACAGGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCGCCCCATCTGAC	4800
Qy	4835	TCGCCAGCGTCCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCT	4894
Db	4801	TCGCCAGCGTCCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCT	4860
Qy	4895	GGGCCAGAAATGTGGACGTCGGCACCCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGC	4954
Db	4861	GGGCCAGAAATGTGGACGTCGGCACCCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGC	4920
Qy	4955	TGCACCTGCTCTGCGCAGGGCACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCG	5014
Db	4921	TGCACCTGCTCTGCGCAGGGCACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCG	4980
Qy	5015	CCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCT	5074
Db	4981	CCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCT	5040
Qy	5075	GAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTT	5134
Db	5041	GAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTT	5100
Qy	5135	GGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGG	5194
Db	5101	GGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGG	5160
Qy	5195	AAGATCGCGGTGCGCAGGGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATG	5254
Db	5161	AAGATCGCGGTGCGCAGGGCTGCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATG	5220
Qy	5255	CCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAG	5314
Db	5221	CCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACCTGCCCCAAGAGCAAG	5280
Qy	5315	GGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCC	5374
Db	5281	GGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCC	5340
Qy	5375	AGCCTCTCCCTGGATTACCTGCTGCAGGGCACGGATGTCGTCATCGCCATCTTCATCATC	5434
Db	5341	AGCCTCTCCCTGGATTACCTGCTGCAGGGCACGGATGTCGTCATCGCCATCTTCATCATC	5400
Qy	5435	GTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGCCGAGAAGTCCACC	5494
Db	5401	GTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGCCGAGAAGTCCACC	5460
Qy	5495	AAGGCCAAGCATCTGCAGTTTGTGACGGGCTGCAACCCCATCATCTACTGGCTGGCGAAC	5554
Db	5461	AAGGCCAAGCATCTGCAGTTTGTGACGGGCTGCAACCCCATCATCTACTGGCTGGCGAAC	5520
Qy	5555	TACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCTGCTGTGTGCATCATCCTGTTT	5614
Db	5521	TACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCTGCTGTGTGCATCATCCTGTTT	5580

Qy	5615	GTGTTTCGACCTGCCGGCCTACACGTCGCCCACCAACTTCCCTGCCGTCTCTCCCTCTTC	5674
Db	5581	GTGTTTCGACCTGCCGGCCTACACGTCGCCCACCAACTTCCCTGCCGTCTCTCCCTCTTC	5640
Qy	5675	CTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTC	5734
Db	5641	CTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTC	5700
Qy	5735	CCCAGCTCCGCCTACGTGTTCCCTCATTGTTCATCAATCTCTTCATCGGCATCACCGCCACC	5794
Db	5701	CCCAGCTCCGCCTACGTGTTCCCTCATTGTTCATCAATCTCTTCATCGGCATCACCGCCACC	5760
Qy	5795	GTGGCCACCTTCCTGCTACAGCTCTTCGAGCAGGACAAGGACCTGAAGGTTGTCAACAGT	5854
Db	5761	GTGGCCACCTTCCTGCTACAGCTCTTCGAGCAGGACAAGGACCTGAAGGTTGTCAACAGT	5820
Qy	5855	TACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAG	5914
Db	5821	TACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAG	5880
Qy	5915	ATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATG	5974
Db	5881	ATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATG	5940
Qy	5975	AAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGC	6034
Db	5941	AAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGC	6000
Qy	6035	GTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGC	6094
Db	6001	GTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGC	6060
Qy	6095	ATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGA	6154
Db	6061	ATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGA	6120
Qy	6155	GTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTAC	6214
Db	6121	GTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTAC	6180
Qy	6215	AAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCT	6274
Db	6181	AAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCT	6240
Qy	6275	GGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATG	6334
Db	6241	GGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATG	6300
Qy	6335	CTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCCTTCGTCAATGGACACAGCGTGCTG	6394
Db	6301	CTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCCTTCGTCAATGGACACAGCGTGCTG	6360
Qy	6395	AAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCAGTGTGACGCGCTGTTT	6454
Db	6361	AAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCAGTGTGACGCGCTGTTT	6420
Qy	6455	GACGAGCTCACGGCCCCGGGAGCACCTGCAGCTGTACACGGGCTGCGTGGGATCTCCTGG	6514

Db	6421	 GACGAGCTCACGGCCCGGGAGCACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGG	6480
Qy	6515	AAGGACGAGGCCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCA	6574
Db	6481	 AAGGACGAGGCCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCA	6540
Qy	6575	GACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCC	6634
Db	6541	 GACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCC	6600
Qy	6635	CTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAG	6694
Db	6601	 CTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAG	6660
Qy	6695	GCCCGGCGCTTCTCTGGAACCTCATCCTCGACCTCATCAAGACAGGGCGTTTCAGTGGTG	6754
Db	6661	 GCCCGGCGCTTCTCTGGAACCTCATCCTCGACCTCATCAAGACAGGGCGTTTCAGTGGTG	6720
Qy	6755	CTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTG	6814
Db	6721	 CTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTG	6780
Qy	6815	AACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGC	6874
Db	6781	 AACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGC	6840
Qy	6875	TACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTC	6934
Db	6841	 TACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTC	6900
Qy	6935	AACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAG	6994
Db	6901	 AACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAG	6960
Qy	6995	CTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGC	7054
Db	6961	 CTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGC	7020
Qy	7055	GTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACACTGGACAATGTGTTTCGTGAAC	7114
Db	7021	 GTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACACTGGACAATGTGTTTCGTGAAC	7080
Qy	7115	TTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTG	7174
Db	7081	 TTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTG	7140
Qy	7175	CAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTC	7234
Db	7141	 CAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTC	7200
Qy	7235	CGGGCACTTGTGGCAGACGAGCCCAGGACCTGGACACGGAGGACGAGGGCCTCATCAGC	7294
Db	7201	 CGGGCACTTGTGGCAGACGAGCCCAGGACCTGGACACGGAGGACGAGGGCCTCATCAGC	7260
Qy	7295	TTCGAGGAGGAGCGGGCCCAGCTGTCCTTCAACACGGACACGCTC	7339

Db 7261 TTCGAGGAGGAGCGGGCCCAGCTGTCTTCAACACGGACACGCTC 7305

RESULT 9

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; Publication No. US20030077626A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
; TITLE OF INVENTION: 32613, No. US20030077626A1 Human Transporters
; FILE REFERENCE: 35800/249468
; CURRENT APPLICATION NUMBER: US/10/199,485
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 09/795,693
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 7305
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-199-485-9

Query Match 90.8%; Score 7301.8; DB 15; Length 7305;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7303; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	35	ATGGGCTTCCTGCACCAGCTGCAGCTGCTGCTCTGGAAGAACGTGACGCTCAAACGCCGG	94
Db	1	ATGGGCTTCCTGCACCAGCTGCAGCTGCTGCTCTGGAAGAACGTGACGCTCAAACGCCGG	60
Qy	95	AGCCCGTGGGTCCTGGCCTTCGAGATCTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTG	154
Db	61	AGCCCGTGGGTCCTGGCCTTCGAGATCTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTG	120
Qy	155	GGGCTGCGACAGAAGAAGCCACCATCTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCG	214
Db	121	GGGCTGCGACAGAAGAAGCCACCATCTCCGTGAAGGAAGTCTCCTTCTACACAGCGGCG	180
Qy	215	CCCCTGACGTCTGCCGGCATCCTGCCTGTCATGCAATCGCTGTGCCCGGACGGCCAGCGA	274
Db	181	CCCCTGACGTCTGCCGGCATCCTGCCTGTCATGCAATCGCTGTGCCCGGACGGCCAGCGA	240
Qy	275	GACGAGTTCGGCTTCCTGCAGTACGCCAACTCCACGGTCACGCAGCTGCTTGAGCGCCTG	334
Db	241	GACGAGTTCGGCTTCCTGCAGTACGCCAACTCCACGGTCACGCAGCTGCTTGAGCGCCTG	300
Qy	335	GACCGCGTGGTGGAGGAAGGCAACCTGTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAG	394
Db	301	GACCGCGTGGTGGAGGAAGGCAACCTGTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAG	360
Qy	395	CTCGAGGCCCTACGCCAGCATCTGGAGGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGC	454

Db	361	CTCGAGGCCCTACGCCAGCATCTGGAGGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGC	420
Qy	455	CACCTGGACAGATCCACAGTGTCTTCCTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAG	514
Db	421	CACCTGGACAGATCCACAGTGTCTTCCTTCTCTCTGGACTCGGTGGCCAGAAACCCGCAG	480
Qy	515	GAGCTCTGGCGTTTCCTGACGCAAACTTGTGCTGCCCCAATAGCACGGCCCAAGCACTC	574
Db	481	GAGCTCTGGCGTTTCCTGACGCAAACTTGTGCTGCCCCAATAGCACGGCCCAAGCACTC	540
Qy	575	TTGGCCGCCCCGTGTGGACCCGCCCCGAGGTCTACCACCTGCTCTTTGGTCCCTCATCTGCC	634
Db	541	TTGGCCGCCCCGTGTGGACCCGCCCCGAGGTCTACCACCTGCTCTTTGGTCCCTCATCTGCC	600
Qy	635	CTGGATTACAGTCTGGCCTCCACAAGGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAAT	694
Db	601	CTGGATTACAGTCTGGCCTCCACAAGGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAAT	660
Qy	695	CCCCTGTTCCGGATGGAGGAGCTGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGC	754
Db	661	CCCCTGTTCCGGATGGAGGAGCTGCTGCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGC	720
Qy	755	ACGCCGGGCTCGGGGGAGCTGGGCCGGATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCC	814
Db	721	ACGCCGGGCTCGGGGGAGCTGGGCCGGATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCC	780
Qy	815	CTGCAGGGCTACCGGGATGCTGTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTC	874
Db	781	CTGCAGGGCTACCGGGATGCTGTCTGCAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTC	840
Qy	875	TCTGGGCTGTCTGCTGAGCTCCGGAACCAGCTGGACGTGGCCAAGGTCTCCAGCAGCTG	934
Db	841	TCTGGGCTGTCTGCTGAGCTCCGGAACCAGCTGGACGTGGCCAAGGTCTCCAGCAGCTG	900
Qy	935	GGCCTGGATGCCCCAACGGCTCGGACTCCTCGCCACAGGCGCCACCCCCACGGAGGCTG	994
Db	901	GGCCTGGATGCCCCAACGGCTCGGACTCCTCGCCACAGGCGCCACCCCCACGGAGGCTG	960
Qy	995	CAGGCGCTTCTGGGGGACCTGCTGGATGCCCAGAAAGTTCTGCAGGATGTGGATGTCCTG	1054
Db	961	CAGGCGCTTCTGGGGGACCTGCTGGATGCCCAGAAAGTTCTGCAGGATGTGGATGTCCTG	1020
Qy	1055	TCGGCCCTGGCCCTGCTACTGCCCCAGGGTGCCTGCACTGGCCGGACCCCCGGACCCCCA	1114
Db	1021	TCGGCCCTGGCCCTGCTACTGCCCCAGGGTGCCTGCACTGGCCGGACCCCCGGACCCCCA	1080
Qy	1115	GCCAGTGGTGCGGGTGGGGCGGCCAATGGCACTGGGGCAGGGGCAGTCATGGGGCCCCAAC	1174
Db	1081	GCCAGTGGTGCGGGTGGGGCGGCCAATGGCACTGGGGCAGGGGCAGTCATGGGGCCCCAAC	1140
Qy	1175	GCCACCGCTGAGGAGGGCGCACCTCTGCTGCAGCACTGGCCACCCCGACACGCTGCAG	1234
Db	1141	GCCACCGCTGAGGAGGGCGCACCTCTGCTGCAGCACTGGCCACCCCGACACGCTGCAG	1200
Qy	1235	GGCCAGTGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAAC	1294
Db	1201	GGCCAGTGCTCAGCCTTCGTACAGCTCTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAAC	1260

Qy	1295	AACCGCACCATTTGAACCCGAGGCGCTGCGGCGGGGCAACATGAGCTCCCTGGGCTTCACG	1354
Db	1261	AACCGCACCATTTGAACCCGAGGCGCTGCGGCGGGGCAACATGAGCTCCCTGGGCTTCACG	1320
Qy	1355	AGCAAGGAGCAGCGGAACCTGGGCTCCTCGTGACCTCATGACCAGCAACCCCAAATC	1414
Db	1321	AGCAAGGAGCAGCGGAACCTGGGCTCCTCGTGACCTCATGACCAGCAACCCCAAATC	1380
Qy	1415	CTGTACGCGCCTGCGGGCTCTGAGGTGACCGCGTCATCCTCAAGGCCAACGAGACTTTT	1474
Db	1381	CTGTACGCGCCTGCGGGCTCTGAGGTGACCGCGTCATCCTCAAGGCCAACGAGACTTTT	1440
Qy	1475	GCTTTTGTGGGCAACGTGACTCACTATGCCCAGGTCTGGCTCAACATCTCGGCGGAGATC	1534
Db	1441	GCTTTTGTGGGCAACGTGACTCACTATGCCCAGGTCTGGCTCAACATCTCGGCGGAGATC	1500
Qy	1535	CGCAGCTTCCTGGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTATGTA	1594
Db	1501	CGCAGCTTCCTGGAGCAGGGCAGGCTGCAGCAACACCTGCGCTGGCTGCAGCAGTATGTA	1560
Qy	1595	GCAGAGCTGCGGCTGCACCCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCGGCC	1654
Db	1561	GCAGAGCTGCGGCTGCACCCCGAGGCACTGAACCTGTCACTGGATGAGCTGCCGCCGGCC	1620
Qy	1655	CTGAGACAGGACAACCTTCTCGCTGCCCAGTGGCATGGCCCTCCTGCAGCAGCTGGATACC	1714
Db	1621	CTGAGACAGGACAACCTTCTCGCTGCCCAGTGGCATGGCCCTCCTGCAGCAGCTGGATACC	1680
Qy	1715	ATTGACAACGCGGCCTGCGGCTGGATCCAGTTTCATGTCCAAGGTGAGCGTGGACATCTTC	1774
Db	1681	ATTGACAACGCGGCCTGCGGCTGGATCCAGTTTCATGTCCAAGGTGAGCGTGGACATCTTC	1740
Qy	1775	AAGGGCTTCCCCGACGAGGAGAGCATTGTCAACTACACCCTCAACCAGGCCTACCAGGAC	1834
Db	1741	AAGGGCTTCCCCGACGAGGAGAGCATTGTCAACTACACCCTCAACCAGGCCTACCAGGAC	1800
Qy	1835	AACGTCACTGTTTTTGGCAGTGTGATCTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCT	1894
Db	1801	AACGTCACTGTTTTTGGCAGTGTGATCTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCT	1860
Qy	1895	CACGTGCACTACAAGATCCGCCAGAACTCCAGCTTCACCGAGAAAACCAACGAGATCCGC	1954
Db	1861	CACGTGCACTACAAGATCCGCCAGAACTCCAGCTTCACCGAGAAAACCAACGAGATCCGC	1920
Qy	1955	CGCGCCTACTGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCTCTACGGCTTC	2014
Db	1921	CGCGCCTACTGGCGGCCTGGGCCCAATACTGGCGGCCGCTTCTACTTCTCTACGGCTTC	1980
Qy	2015	GTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCACGACGTG	2074
Db	1981	GTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACACTTTTGTGGGGCACGACGTG	2040
Qy	2075	GTGGAGCCAGGCAGCTACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTC	2134
Db	2041	GTGGAGCCAGGCAGCTACGTGCAGATGTTCCCCTACCCCTGCTACACACGCGATGACTTC	2100

Qy	2135	CTGTTTGTCAATTGAGCACATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTG	2194
Db	2101	CTGTTTGTCAATTGAGCACATGATGCCGCTGTGCATGGTGATCTCCTGGGTCTACTCCGTG	2160
Qy	2195	GCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAG	2254
Db	2161	GCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAG	2220
Qy	2255	ACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAG	2314
Db	2221	ACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAG	2280
Qy	2315	CTGTCCATCTCCGTGACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATGCAC	2374
Db	2281	CTGTCCATCTCCGTGACAGCACTCACCGCCATCCTGAAGTACGGCCAGGTGCTTATACAC	2340
Qy	2375	AGCCACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTT	2434
Db	2341	AGCCACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACGCGGTGGCCACCATCATGTTT	2400
Qy	2435	TGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATC	2494
Db	2401	TGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATC	2460
Qy	2495	ATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCAT	2554
Db	2461	ATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGATCCGAGAGGAGGTGGCGCAT	2520
Qy	2555	GATAAGATCACGGCCTTCGAGAAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGT	2614
Db	2521	GATAAGATCACGGCCTTCGAGAAAGTGCATCGCGTCCCTCATGTCCACGACGGCCTTTGGT	2580
Qy	2615	CTGGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACC	2674
Db	2581	CTGGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCGTGGGCATCCAGTGGCACACC	2640
Qy	2675	TTCAGCCAGTCCCCGGTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTG	2734
Db	2641	TTCAGCCAGTCCCCGGTGGAGGGGGACGACTTCAACTTGCTCCTGGCTGTCACCATGCTG	2700
Qy	2735	ATGGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGC	2794
Db	2701	ATGGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGC	2760
Qy	2795	ATGTACGGGCTGCCCCGGCCCTGGTACTTCCCACCTGCAGAAAGTCCCTACTGGCTGGGCAGT	2854
Db	2761	ATGTACGGGCTGCCCCGGCCCTGGTACTTCCCACCTGCAGAAAGTCCCTACTGGCTGGGCAGT	2820
Qy	2855	GGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTC	2914
Db	2821	GGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTC	2880
Qy	2915	ATGGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATG	2974
Db	2881	ATGGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATG	2940
Qy	2975	GAGGAGGAGCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAACTACCAAGGTCTAC	3034

Db	2941	 GAGGAGGAGCCACCCACCTGCCTCTGGTTGTCTGCGTGGACAAACTCACCAAGGTCTAC	3000
Qy	3035	AAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTG	3094
Db	3001	 AAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTG	3060
Qy	3095	GTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGC	3154
Db	3061	 GTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGC	3120
Qy	3155	CTGTTCCCTCCAACGTCGGGTTCCGCCACCATCTACGGGCACGACATCCGCACGGAGATG	3214
Db	3121	 CTGTTCCCTCCAACGTCGGGTTCCGCCACCATCTACGGGCACGACATCCGCACGGAGATG	3180
Qy	3215	GATGAGATCCGCAAGAACCTGGGCATGTGCCCGCAGCACAATGTGCTCTTTGACCGGCTC	3274
Db	3181	 GATGAGATCCGCAAGAACCTGGGCATGTGCCCGCAGCACAATGTGCTCTTTGACCGGCTC	3240
Qy	3275	ACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATC	3334
Db	3241	 ACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATC	3300
Qy	3335	CGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTG	3394
Db	3301	 CGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTG	3360
Qy	3395	GTGCAGACATTGTCGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGC	3454
Db	3361	 GTGCAGACATTGTCGGGTGGCATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGC	3420
Qy	3455	GGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGC	3514
Db	3421	 GGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGC	3480
Qy	3515	GCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCAC	3574
Db	3481	 GCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGACCATCCTTCTGTCCACCCAC	3540
Qy	3575	CACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTC	3634
Db	3541	 CACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTC	3600
Qy	3635	AAGTGCTGCGGCTCCCCGCTCTTCCTCAAGGGACCTATGGCGACGGGTACCGCCTCACG	3694
Db	3601	 AAGTGCTGCGGCTCCCCGCTCTTCCTCAAGGGACCTATGGCGACGGGTACCGCCTCACG	3660
Qy	3695	CTGGTCAAGCGGCCCCGCCGAGCCGGGGGGCCCCAAGAGCCAGGGCTGGCATCCAGCCCC	3754
Db	3661	 CTGGTCAAGCGGCCCCGCCGAGCCGGGGGGCCCCAAGAGCCAGGGCTGGCATCCAGCCCC	3720
Qy	3755	CCAGGTCGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAG	3814
Db	3721	 CCAGGTCGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAG	3780
Qy	3815	CATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCC	3874

Db	3781	CATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCC	3840
Qy	3875	AGCGAGGCCGCCAAGAAGGGGGCTTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTG	3934
Db	3841	AGCGAGGCCGCCAAGAAGGGGGCTTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTG	3900
Qy	3935	GATGCACTGCACCTCAGCAGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCCCTC	3994
Db	3901	GATGCACTGCACCTCAGCAGCTTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCCCTC	3960
Qy	3995	AAGGTGTGCGGAGGAGGATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGG	4054
Db	3961	AAGGTGTGCGGAGGAGGATCAGTCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGG	4020
Qy	4055	AAGGATGTGCTCCCTGGGGCGGAGGGCCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTG	4114
Db	4021	AAGGATGTGCTCCCTGGGGCGGAGGGCCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTG	4080
Qy	4115	GCCCGGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGC	4174
Db	4081	GCCCGGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGC	4140
Qy	4175	TCTGCCCCGTGGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTC	4234
Db	4141	TCTGCCCCGTGGCGACGAGGGAGCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTC	4200
Qy	4235	TTTGATAACCCACAGGACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTG	4294
Db	4201	TTTGATAACCCACAGGACCCAGACAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTG	4260
Qy	4295	TCGAGGGTCGGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTC	4354
Db	4261	TCGAGGGTCGGCCAGGGCAGCCGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTC	4320
Qy	4355	CACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCCGCCGCAACTCCAAGGCACTCTTCTCC	4414
Db	4321	CACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCCGCCGCAACTCCAAGGCACTCTTCTCC	4380
Qy	4415	CAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCG	4474
Db	4381	CAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCG	4440
Qy	4475	GAGATTGGTGATCTGCCCCCGCTGGTCTGTACCTTCCCAGTACCACAACCTACACCCAG	4534
Db	4441	GAGATTGGTGATCTGCCCCCGCTGGTCTGTACCTTCCCAGTACCACAACCTACACCCAG	4500
Qy	4535	CCCCGTGGCAATTTTCATCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTA	4594
Db	4501	CCCCGTGGCAATTTTCATCCCCTACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTA	4560
Qy	4595	TCGCCCCGACGCCAGCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGT	4654
Db	4561	TCGCCCCGACGCCAGCCCCAGCAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGT	4620
Qy	4655	GCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCACGTTGAACCTGAGC	4714
Db	4621	GCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGGGGCCACGTTGAACCTGAGC	4680

Qy	4715	AGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTC	4774
Db	4681	AGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTC	4740
Qy	4775	ACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCGCCCCATCTGAC	4834
Db	4741	ACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCACCCTCGCCCGCCCCATCTGAC	4800
Qy	4835	TCGCCAGCGTCCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCT	4894
Db	4801	TCGCCAGCGTCCCCGGATGAGGACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCT	4860
Qy	4895	GGGCCAGAAATGTGGACGTGGCACCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGC	4954
Db	4861	GGGCCAGAAATGTGGACGTGGCACCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGC	4920
Qy	4955	TGCACCTGCTCTGCGCAGGGCACC GGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACC CG	5014
Db	4921	TGCACCTGCTCTGCGCAGGGCACC GGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACC CG	4980
Qy	5015	CCCCAGATGCGGGTGGT CACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCT	5074
Db	4981	CCCCAGATGCGGGTGGT CACAGGCGACATCCTGACCGACATCACCGGCCACAATGTCTCT	5040
Qy	5075	GAGTACCTGCTCTT CACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTT	5134
Db	5041	GAGTACCTGCTCTT CACCTCCGACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTT	5100
Qy	5135	GGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGG	5194
Db	5101	GGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGG	5160
Qy	5195	AAGATCGCGGTGCGCAGGGCTGCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATG	5254
Db	5161	AAGATCGCGGTGCGCAGGGCTGCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATG	5220
Qy	5255	CCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACCTGCCAAGAGCAAG	5314
Db	5221	CCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTGCCAACCTGCCAAGAGCAAG	5280
Qy	5315	GGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCC	5374
Db	5281	GGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCC	5340
Qy	5375	AGCCTCTCCCTGGATTACCTGCTGCAGGGCAGGATGTCGTCATCGCCATCTTCATCATC	5434
Db	5341	AGCCTCTCCCTGGATTACCTGCTGCAGGGCAGGATGTCGTCATCGCCATCTTCATCATC	5400
Qy	5435	GTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACC	5494
Db	5401	GTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACC	5460
Qy	5495	AAGGCCAAGCATCTGCAGTTTGT CAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAAC	5554
Db	5461	AAGGCCAAGCATCTGCAGTTTGT CAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAAC	5520

Qy	5555	TACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCTGCTGTGTCATCATCCTGTTT	5614
Db	5521	TACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCTGCTGTGTCATCATCCTGTTT	5580
Qy	5615	GTGTTTCGACCTGCCGGCCTACACGTCGCCCCACCAACTTCCCTGCCGTCTCTCCCTCTTC	5674
Db	5581	GTGTTTCGACCTGCCGGCCTACACGTCGCCCCACCAACTTCCCTGCCGTCTCTCCCTCTTC	5640
Qy	5675	CTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTC	5734
Db	5641	CTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTC	5700
Qy	5735	CCCAGCTCCGCCTACGTGTTCCCTCATTTGTCATCAATCTCTTCATCGGCATCACCGCCACC	5794
Db	5701	CCCAGCTCCGCCTACGTGTTCCCTCATTTGTCATCAATCTCTTCATCGGCATCACCGCCACC	5760
Qy	5795	GTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGT	5854
Db	5761	GTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGT	5820
Qy	5855	TACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAG	5914
Db	5821	TACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAG	5880
Qy	5915	ATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATG	5974
Db	5881	ATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATG	5940
Qy	5975	AAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGC	6034
Db	5941	AAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGC	6000
Qy	6035	GTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGC	6094
Db	6001	GTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGC	6060
Qy	6095	ATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGA	6154
Db	6061	ATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGA	6120
Qy	6155	GTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTAC	6214
Db	6121	GTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTAC	6180
Qy	6215	AAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCT	6274
Db	6181	AAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCT	6240
Qy	6275	GGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATG	6334
Db	6241	GGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATG	6300
Qy	6335	CTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTG	6394
Db	6301	CTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTG	6360
Qy	6395	AAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTT	6454

Db	6361	 AAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTT	6420
Qy	6455	GACGAGCTCACGGCCCCGGGAGCACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGG	6514
Db	6421	 GACGAGCTCACGGCCCCGGGAGCACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGG	6480
Qy	6515	AAGGACGAGGCCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCA	6574
Db	6481	 AAGGACGAGGCCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCA	6540
Qy	6575	GACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCC	6634
Db	6541	 GACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCC	6600
Qy	6635	CTCATTTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCACCACAGGCATGGACCCCCAAG	6694
Db	6601	 CTCATTTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCACCACAGGCATGGACCCCCAAG	6660
Qy	6695	GCCCCGCGCTTCTCTGGAACCTCATCCTCGACCTCATCAAGACAGGGCGTTTCAAGTGGTG	6754
Db	6661	 GCCCCGCGCTTCTCTGGAACCTCATCCTCGACCTCATCAAGACAGGGCGTTTCAAGTGGTG	6720
Qy	6755	CTGACATCACACAGCATGGAGGAGTGCAGGGCGCTGTGCACGCGGCTGGCCATCATGGTG	6814
Db	6721	 CTGACATCACACAGCATGGAGGAGTGCAGGGCGCTGTGCACGCGGCTGGCCATCATGGTG	6780
Qy	6815	AACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGC	6874
Db	6781	 AACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGC	6840
Qy	6875	TACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTC	6934
Db	6841	 TACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTC	6900
Qy	6935	AACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACACACAAAGGTGCAGTACCAG	6994
Db	6901	 AACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACACACAAAGGTGCAGTACCAG	6960
Qy	6995	CTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAAGATGGAGCAGGTGTCTGGC	7054
Db	6961	 CTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTTCAAGATGGAGCAGGTGTCTGGC	7020
Qy	7055	GTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACACTGGACAATGTGTTTCGTGAAC	7114
Db	7021	 GTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACACTGGACAATGTGTTTCGTGAAC	7080
Qy	7115	TTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTG	7174
Db	7081	 TTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTG	7140
Qy	7175	CAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTC	7234
Db	7141	 CAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTC	7200
Qy	7235	CGGGCACTTGTGGCAGACGAGCCCCGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGC	7294

Db 7201 CGGGCACTTGTGGCAGACGAGCCCCGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGC 7260

Qy 7295 TTCGAGGAGGAGCGGGCCCCAGCTGTCCCTTCAACACGGACACGCTC 7339
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Db 7261 TTCGAGGAGGAGCGGGCCCCAGCTGTCCCTTCAACACGGACACGCTC 7305

RESULT 10

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; Sequence 1837, Application US/10152319A
 ; Publication No. US20040072160A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mendrick, Donna
 ; APPLICANT: Porter, Mark
 ; APPLICANT: Johnson, Kory
 ; APPLICANT: Higgs, Brandon
 ; APPLICANT: Castle, Arthur
 ; APPLICANT: Elashoff, Michael
 ; TITLE OF INVENTION: Molecular Toxicology Modeling
 ; FILE REFERENCE: 44921-5089-US
 ; CURRENT APPLICATION NUMBER: US/10/152,319A
 ; CURRENT FILING DATE: 2002-05-22
 ; PRIOR APPLICATION NUMBER: US 60/292,335
 ; PRIOR FILING DATE: 2001-05-22
 ; PRIOR APPLICATION NUMBER: US 60/297,523
 ; PRIOR FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/298,925
 ; PRIOR FILING DATE: 2001-06-19
 ; PRIOR APPLICATION NUMBER: US 60/303,810
 ; PRIOR FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: US 60/303,807
 ; PRIOR FILING DATE: 2001-07-10
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 ; PRIOR APPLICATION NUMBER: US 60/315,047
 ; PRIOR FILING DATE: 2001-08-28
 ; PRIOR APPLICATION NUMBER: US 60/324,928
 ; PRIOR FILING DATE: 2001-09-27
 ; PRIOR APPLICATION NUMBER: US 60/330,867
 ; PRIOR FILING DATE: 2001-11-01
 ; PRIOR APPLICATION NUMBER: US 60/330,462
 ; PRIOR FILING DATE: 2001-10-22
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 2221
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1837
 ; LENGTH: 8040
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; OTHER INFORMATION: Genbank Accession No. NM_024396
 US-10-152-319A-1837

Query Match 72.3%; Score 5810; DB 12; Length 8040;
 Best Local Similarity 84.0%; Pred. No. 0;
 Matches 6768; Conservative 0; Mismatches 1205; Indels 85; Gaps 15;

Qy 1 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 60
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 Db 34 CCGCGGCGCTGAGGCGGCGGAGCGCGGCCCGGCCATGGGCTTCCTGCACCAGCTGCAGCT 93

Qy 61 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTTGGCCTTCGAGAT 120
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 Db 94 GCTGCTCTGGAAGAACGTGACGCTGAAGCGCCGGAGCCCGTGGGTCTTGGCCTTCGAGAT 153

Qy 121 CTTTCATCCCCCTGGTGCTGTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 180
 |||
 Db 154 CTTTCATCCCCCTGTCTCTTCTTCATCCTGTTGGGACTGCGGCAGAAGAAGCCCACCAT 213

Qy 181 CTCCGTGAAGGAAGTCCCCTTCTACACAGCGGCGCCCTGACGTCTGCCGGCATCCTGCC 240
 |||
 Db 214 CTCTGTGAAGGAAG---CTTTCACACGGCAGCACCGCTGACATCGGCCGGCATCCTGCC 270

Qy 241 TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTTCGGCTTCCTGCAGTACGC 300
 |||
 Db 271 TGTCATGCAGTCGCTTTGCCCTGATGGCCAGCGTGATGAGTTTGGCTTCCTGCAGTATGC 330

Qy 301 CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT 360
 |||
 Db 331 CAACTCCACGGTCACCCAGCTTCTGGAACGCCCTCAACCGTGTAGTGGAAGAGAGCAACTT 390

Qy 361 GTTTGACCCAGCGCGGCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA 420
 |||
 Db 391 GTTTGACCCAGAGCGACCTAGCCTGGGCTCAGAGCTTGAGGCACTGCACCAACGTCTGGA 450

Qy 421 GGCCCTCAGTGCGGGCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC 480
 |||
 Db 451 GGCCCTCAGCTCGGGCCCTGGCACCTGGGAGAGCCACTCAGCTAGACCTGCAGTTTCATC 510

Qy 481 CTTCTCTCTGGACTCGGTGGCCAGAAACCCGAGGAGCTCTGGCGTTTCCTGACGCAAAA 540
 |||
 Db 511 CTTCTCTCTGGACTCGGTGGCCAGGGACAAAAGAGAGCTTTGGCGTTTCCTGATGCAGAA 570

Qy 541 CTTGTGCTGCCCCAATAGCACGGCCCAAGCACTCTTGCCCGCCCGTGTGGACCCGCCCCGA 600
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 Db 571 CCTGTCACTGCCCCAACAGCACGGCCAGGCCCTCCTGGCTGCCCCGTGTAGACCTTCTGA 630

Qy 601 GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTACAGTCTGGCCTCCACAA 660
 |||
 Db 631 GGTCTATCGCTTGCTTTTGGTCCCTTACCTGACCTGGATGGAAAGTTGGGGTTCTCAG 690

Qy 661 GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCCTGTTCCGGATGGAGGAGCTGCT 720
 |||
 Db 691 GAAGCAGGAGCCCTGGAGTCACCTGGGTAGCAATCCTCTGTTCCAAATGGAGGAGCTGCT 750

Qy 721 GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG 780
 |||
 Db 751 GCTGGCTCCTGCCCTTTTGGAGCAACTCACATGTGCTCCAGGCTCTGGGGAGCTGGGCCG 810

Qy 781 GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG 840
 |||
 Db 811 GATTCTTACCATGCCTGAGGGTCATCAGGTAGACCTTCAGGGCTACCGGGATGCTGTCTG 870

Qy 841 CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA 900

Db	871		CAGCGGGCAGGCTACAGCTCGTGCCAGCATTTCACTGATCTAGCCACTGAGCTCCGGAA	930
Qy	901		CCAGCTGGACGTGGCCAAGGTCTCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	960
Db	931		CCAGCTGGACATAGCCAAGATTGCCAGCAGCTGGGCTTCAATGTCCCCAACGGCTCAGA	990
Qy	961		CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1020
Db	991		TCCACAGCCGAGGCACCGTCCCCACAGAGTCTGCAGGCACTCTTAGGGGACCTGCTGGA	1050
Qy	1021		TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGCCCTGGCCCTGCTACTGCCCCA	1080
Db	1051		TGTCCAGAAGGTTCTACAGGATGTGGATGTCCTATCAGCCCTTGCCCTGCTGCTGCCTCA	1110
Qy	1081		GGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Db	1111		AGGTGCCTGTGCTGGCCGGGCCCCCGCACCTCAAGCTGGCAGCCCGAGTGGCCCGGCCAA	1170
Qy	1141		TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1200
Db	1171		CAGCACCGGGTAGGGGCAAATACAGTCCCAACACCACCGTTGAGGAGGGCACCCAGTC	1230
Qy	1201		TGCTGCAGCACTGGCCACCCCCGGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
Db	1231		ACCTGTCACCCAGCCTCTCCGGACACTCTGCAAGGCCAGTGCTCAGCCTTTGTGCAGCT	1290
Qy	1261		CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTTGAACCCGAGGCGCT	1320
Db	1291		CTGGGCTGGCTTGCAAGCCATCTTGTGTGGCAACAACCGTACCATTGAGCCTGAAGCACT	1350
Qy	1321		GCGGCGGGGCAACATGAGCTCCCTGGGCTTACAGAGCAAGGAGCAGCGGAACCTGGGCTT	1380
Db	1351		CCGGAGGGGCAACATGAGCTCACTGGGCTTTACAGAGCAAAGAACAACGAACCTGGGCTT	1410
Qy	1381		CCTCGTGCACCTCATGACCAGCAACCCCAAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
Db	1411		TCTTGTGCACCTCATGACCAGCAACCCCAAAATCCTGTATGCACCCGAGGCTCTGAAGC	1470
Qy	1441		CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGTCTTTGTGGGCAACGTGACTCACTA	1500
Db	1471		TGACCATGTTATCCTCAAGGCAAATGAGACCTTTGCCTTTGTGGGCAACGTGACGCACTA	1530
Qy	1501		TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGCAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1531		CGCCAGGTCTGGCTCAACATCTCCGCAGAGATCCGGAGCTTCCTGGAGCAGGGCAGGCT	1590
Qy	1561		GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620
Db	1591		GCAGCAGCATCTGCACTGGCTGCAGCAGTACGTGGCTGACCTCCGGCTACACCCTGAAGC	1650
Qy	1621		ACTGAACCTGTCACTGGATGAGCTGCCGCCGGCCCTGAGACAGGACAACCTTCTCGCTGCC	1680
Db	1651		AATGAACCTGTCACTGGACAGCTGCCCCCTGCTCTGCGCTGGACTACTTTCTCTGCC	1710
Qy	1681		CAGTGGCATGGCCCTCCTGCAGCAGCTGGATACCATTGACAACGCGGCTGCGGCTGGAT	1740

Db	1711	CAATGGCACAGCCCTTCTGCAGCAGCTAGACACAATAGACAATGCAGCCTGTGGCTGGAT	1770
Qy	1741	CCAGTTCATGTCCAAGGTGAGCGTGGACATCTTCAAGGGCTTCCCCGACGAGGAGAGCAT	1800
Db	1771	CCAGTTCATGTCCAAGGTGAGTGTGGACATCTTCAAGGGGTTTCTTGATGAGGAGAGCAT	1830
Qy	1801	TGTCAACTACACCCTCAACCAGGCCTACCAGGACAACGTCACTGTTTTTGCCAGTGTGAT	1860
Db	1831	CGTGAACCTACACTCTCAATCAGGCCTACCAGGACAATGTTACAGTATTTGCCAGCGTGAT	1890
Qy	1861	CTTCCAGACCCGGAAGGACGGCTCGCTCCCGCCTCACGTGCACTACAAGATCCGCCAGAA	1920
Db	1891	TTTCCAGACACGGAAGGATGGTTCCCTCCCCCACCATGTCCATTACAAGATTCGCCAGAA	1950
Qy	1921	CTCCAGCTTCACCGAGAAAAACCAACGAGATCCGCCGCGCCTACTGGCGGCCTGGGGCCAA	1980
Db	1951	CTCAAGCTTCACCGAGAAAAACCAACGAGATCCGTCGTGCTTACTGGCGTCCAGGGCCAA	2010
Qy	1981	TACTGGCGGCCGCTTCTACTTCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCG	2040
Db	2011	CACTGGTGGCCGCTTCTACTTCTCTACGGCTTCGTCTGGATCCAGGACATGATAGAACG	2070
Qy	2041	CGCCATCATCGACACTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGAT	2100
Db	2071	TGCCATCATCAACACGTTTGTGGGGCACGACGTGGTTCGAACCCGGCAACTACGTGCAGAT	2130
Qy	2101	GTTCCCCTACCCCTGCTACACACGCGATGACTTCCTGTTTGTCTATTGAGCACATGATGCC	2160
Db	2131	GTTCCCGTACCCCTGCTACACCCGTGACGACTTCCTGTTTGTCTATTGAGCACATGATGCC	2190
Qy	2161	GCTGTGCATGGTGATCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGC	2220
Db	2191	ACTGTGCATGGTGATCTCCTGGGTTTACTCTGTGGCCATGACCATACAGCACATCGTGGC	2250
Qy	2221	GGAGAAGGAGCACCGGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCA	2280
Db	2251	GGAGAAAGAGCATCGGCTAAAGGAGGTGATGAAGACGATGGGCCTGAACAACGCCGTGCA	2310
Qy	2281	CTGGGTGGCCTGGTTCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCAC	2340
Db	2311	CTGGGTGGCCTGGTTCATCACGGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCCCTGAC	2370
Qy	2341	CGCCATCCTGAAGTACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTT	2400
Db	2371	CGCCATCCTCAAGTATGGCCAGGTCCTCATGCACAGCCACGTGCTCATCATATGGCTCTT	2430
Qy	2401	CCTGGCAGTCTACGCGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2460
Db	2431	CCTTGCTGTCTATGCTGTGGCCACTATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTC	2490
Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Db	2491	TAAGGCCAAGTTGGCCTCGGCCTGCGGCGGCATCATCTACTTCCTGAGCTACGTTCCTA	2550
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
Db	2551	CATGTATGTAGCAATCCGTGAGGAAGTAGCCACGATAAGATCACTGCCTTCGAGAAGTG	2610

Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640
Db	2611	CATTGCGTCCCTGATGTCCACAACAGCCTTCGGCCTGGGTCCAAGTACTTTGCTCTGTA	2670
Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGA	2700
Db	2671	TGAAGTGGCAGGTGTGGGCATCCAGTGGCACACGTTTCAGCCAGTCCCCAGTGGAGGGGA	2730
Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760
Db	2731	TGACTTCAACCTGCTCCTTGCTGTCACCATGCTGATGGTGGACACAGTGGTCTATGGCGT	2790
Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2791	ACTCACTTGGTACATTGAGGCTGTGCACCCAGGTATGTATGGGCTGCCCCGGCCCTGGTA	2850
Qy	2821	CTTCCCACTGCAGAAGTCTTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2851	CTTCCCACTACAGAAGTCTTATTGGCTGGGCAGTGGGCGGACAGAGACCTGGGAGTGGAG	2910
Qy	2881	CTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2911	CTGGCCATGGGCACACGCACCCACGCCTCAGCGTTATGGAGGAGGACCAGGCCTGTGCCAT	2970
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACCCACCTGCCTCT	3000
Db	2971	GGAGAGCCGGCACTTCGAGGAGACTCGCGGTATGGAGGAGGAGCCCACCCACCTGCCTTT	3030
Qy	3001	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3031	GGTCGTCTGCGTGGACAAGCTCACCAAGGTCTATAAAAATGACAAGAAGCTGGCCTTAAA	3090
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3091	CAAACTGAGCCTCAATCTCTACGAGAACCAGGTGGTCTCTTTCCTAGGCCATAACGGGGC	3150
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTGGGGTTCCGC	3180
Db	3151	TGGCAAGACCACTACCATGTCTATCCTGACTGGACTGTTCCCAACCCACGTGGGGCTCAGC	3210
Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3211	CACTATCTATGGCCACGACATCCGCACAGAGATGGATGAGATCCGTAAGAACCTGGGCAT	3270
Qy	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3271	GTGCCCACAGCACAACGTGCTCTTTGACCAGCTCACTGTGGAGGAACACCTCTGGTTCTA	3330
Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3331	CTCACGCCTCAAAAGCATGGCACAAGAGGAGATCCGCAAAGAGATGGACAAGATGATCGA	3390
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGCACTCACTGCTGACAGACATTGTGCGGTGGCATGAA	3420
Db	3391	GGACCTGGAGCTCTCCAACAAGCGCCACTCGCTGGTACAGACGCTGTCTGGAGGCATGAA	3450

Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3480
Db	3451	GCGCAAGCTTTAGTAGCCATTGCCTTCGTGGGTGGCTCTAGAGCCATTATCTTAGATGA	3510
Qy	3481	GCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3540
Db	3511	GCCCACAGCTGGCGTGGACCCCTATGCTCGACGTGCCATCTGGGACCTCATTCTGAAGTA	3570
Qy	3541	CAAGCCAGGCCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3571	CAAGCCGGGTGCGACTATCCTCCTGTCCACCCATCACATGGATGAGGCCGACCTGCTGGG	3630
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCT	3660
Db	3631	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAATGCTGCGGCTCTCCCTCTTCCT	3690
Qy	3661	CAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCGCGAGCCGGG	3720
Db	3691	CAAGGGTGCCTACGGCGATGGCTACCGCCTCACACTGGTCAAGCGGCTGCGGAGCCTGG	3750
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGGCCCCGCTGAGCAGCTG	3780
Db	3751	CACCTCCCAAGAGCCAGGGATGGCTTCCAGCCCCCAGGTGCTCCTCAGCTGAGCAACTG	3810
Qy	3781	CTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3811	CTCAGAGATGCAAGTGTCCAGTTCATCCGCAAGCATGTGGCTTCCTCCCTGCTGGTGTC	3870
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCAAGAAGGGGGCTTT	3900
Db	3871	AGACACGAGCACCGAGCTCTCCTACATCCTGCCCAGCGAGGCTGTCAAGAAAGGGGCCTT	3930
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3931	CGAGCGCCTCTTTCAGCAATTGGAGCACAGCCTGGACGCACTGCATCTGAGCAGTTTTGG	3990
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCTCGGAGGAGGATCAGTCGCT	4020
Db	3991	GCTGATGGACACAACCCTGGAGGAGGTGTTCCTCAAGGTGTCTGAAGAAGACCAGTCACT	4050
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4051	GGAGAATAGTGAGGCCGATGTGAAGGAGTCCCGGAAGGATGCACTGCCTGGGGCAGAGGG	4110
Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCCGTGCTCGGAGCTGACCCAGTC	4140
Db	4111	CCTGACGGCTGTGGAGAGTCAAGCAGGCAACCTGGCTCGGTGCTCAGAGCTGGCACAGTC	4170
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGG	4200
Db	4171	CCAGGCTTCACTGCAGTCTGCATCTTCTGTGGGCTCCGCCCCTGGGGATGAGGGTGTGG	4230
Qy	4201	CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4231	CTACACCGACGGCTACGGTGAATACCGTCCCCCTCTTTGACAACCTGCAGGACCCAGACAG	4290
Qy	4261	TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTTCGGCCAGGGCAGCCGCAA	4320

Db	4291	TGTCAGCTTACAAGAGGCTGAAATGGAGGCCCTGGCTCGGGTAGGCCAGGGCAGCCGCAA	4350
Qy	4321	GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4351	GCTAGAGGGCTGGTGGCTGAAGATGCGGCAGTTCCATGGGCTCCTGGTGAAGCGCTTCCA	4410
Qy	4381	CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4411	CTGTGCTCGCCGGAACTCCAAAGCGCTCTGCTCCCAGATTCTGCTGCCTGCCTTCTTCGT	4470
Qy	4441	CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4471	CTGTGTGGCCATGACTGTGGCATTTGTCTGTCCTGAGATCGGTGACCTGCCTCCACTGGT	4530
Qy	4501	CCTGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4531	CCTGTCGCCTTCTCAGTACCACAACCTATACCCAGCCCCGTGGCAACTTTATCCCCTATGC	4590
Qy	4561	CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCT	4620
Db	4591	CAATGAGGAACGCCGCGAGTACCGATTACGGGTGTACCTGATGCCAGCCCCAGCAGTT	4650
Qy	4621	CGTGAGCACGTTCCGGCTGCCGTCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4651	GGTGAGCACATTCCGGCTGCCCTCTGGTGTGGGTGCCACTTGTGTGCTCAAGTCTCCAGC	4710
Qy	4681	CAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4711	CAACGGCTCCCTGGGGCCCATGCTGAACCTGAGCAGTGGAGAGTCCCGCCTGCTGGCCGC	4770
Qy	4741	TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTACACAGGGGGCTGCCACTGTCCAATTT	4800
Db	4771	ACGGTTCTTCGACAGTATGTGCCTGGAGTCCTTACACAGGGGGCTGCCACTGTCCAATT	4830
Qy	4801	CGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGA---	4857
Db	4831	CGTGCCACCCCCACCCTCGCCCGCCCCCTTCCGACTCACCCCTGTCCCCGGATGAGGATTC	4890
Qy	4858	CCTGCAGGCCTGGAACGTCTCCCTGCCGCCACCGCTGGGCCAGAAATGTGGACGTGCGC	4917
Db	4891	ACTGCTAGCCTGGAATACGTCCCTGCCCCCTACTGCTGGACCAGAGACGTGGACGTGGGC	4950
Qy	4918	ACCTTCCCTGCCCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCAC	4977
Db	4951	GCCTTCTCTGCCACGCCTGGTTACAGAGCCGGTCCGCTGTACCTGCTCTGCACAGGGCAC	5010
Qy	4978	CGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGG	5037
Db	5011	GGGCTTCTCGTGCCCCAGCAGTGTGGGTGGGCACCCACCCAGATGAGAGTGGTCACGGG	5070
Qy	5038	CGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGA	5097
Db	5071	GGACATCCTGACTGACATCACCGGCCACAATGTTTCCGAGTACCTGCTCTTCACCTCTGA	5130
Qy	5098	CCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAGTCCATCCC	5157

Db	5131	CCGTTTTCCGACTGCACCGCTATGGAGCCATCACCTTTGGTAATATCCAGAAGTCCATCCC	5190
Qy	5158	AGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGC	5217
Db	5191	AGCACCCATTGGTACCCGGACCCCTCTCATGGTCCGGAAGATTGCAGTGC GGAGGGTGGC	5250
Qy	5218	CCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAA	5277
Db	5251	CCAGGTGCTCTACAACAACAAGGGCTACCACAGCATGCCCACCTACCTCAACAGCCTCAA	5310
Qy	5278	CAACGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCAT	5337
Db	5311	CAATGCCATTCTGCGTGCAAACCTACCCAAAAGCAAGGGCAATCCAGCAGCCTACGGTAT	5370
Qy	5338	CACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCT	5397
Db	5371	CACCGTCACCAACCACCCCATGAACAAGACCAGTGCTAGCCTCTCCCTGGATTACCTACT	5430
Qy	5398	GCAGGGCACGGATGTCGTATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGC	5457
Db	5431	GCAGGGCACAGACGTGGTCATCGCCATCTTCATCATTGTGGCCATGTCCTTCGTGCCGGC	5490
Qy	5458	CAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGT	5517
Db	5491	CAGCTTCGTGGTCTTCCTTGTTGGCCGAGAAATCCACCAAGGCCAAACACCTGCAGTTCGT	5550
Qy	5518	CAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTA	5577
Db	5551	CAGCGGGTGCAACCCTGTCATCTACTGGCTAGCCAACCTACGTGTGGGACATGCTCAATTA	5610
Qy	5578	CCTGGTCCCCGCTACCTGCTGTGTATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACAC	5637
Db	5611	CCTGGTCCCCGGCCACCTGCTGCATCATCATCCTCTTCGTGTTTGACTTGCCGGCCTACAC	5670
Qy	5638	GTCGCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCAC	5697
Db	5671	GTCACCCACCAACTTCCCCGCGGTGCTCTCCTTGTTCTTCCTGCTCTATGGATGGTCCATCAC	5730
Qy	5698	GCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGTCCCCAGCTCCGCCTACGTGTTCCCT	5757
Db	5731	ACCCATCATGTACCCGGCCTCCTTCTGGTTTGAGGTCCCTAGCTCAGCCTACGTGTTCCCT	5790
Qy	5758	CATTGTCATCAATCTCTTCATCGGCATCACGCCACCGTGGCCACCTTCCTGCTACAGCT	5817
Db	5791	CATCGTCATCAACCTCTTCATTGGCATCACGGCCACAGTGGCCACCTTCCTTCTGCAGCT	5850
Qy	5818	CTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCAT	5877
Db	5851	CTTTGAGCATGACAAGGATCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCAT	5910
Qy	5878	TTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAA	5937
Db	5911	CTTCCCCAACTACAACCTGGGCCACGGACTCATGGAGATAGCCTACAACGAATACATCAA	5970
Qy	5938	CGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACAT	5997
Db	5971	CGAATACTATGCCAAGATCGGCCAGTTTGACAAGATGAAGTCCCCGTTTGAGTGGGACAT	6030

Qy	5998	TGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTTCGTGGGCTTCCTCCTGACCAT	6057
Db	6031	TGTCACACGTGGACTGGTGGCCATGACAGTCGAGGGCTTCGTGGGATTCTTTCTCACCAT	6090
Qy	6058	CATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGT	6117
Db	6091	CATGTGTCAATATAACTTCCTACGGCAGCCACAGCGTCTGCCTGTGTCTACTAAACCTGT	6150
Qy	6118	GGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAA	6177
Db	6151	GGAAGACGATGTAGACGTGGCCAGTGAGCGGCAAAGAGTGCTCCGTGGCGATGCTGACAA	6210
Qy	6178	TGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTAT	6237
Db	6211	TGACATGGTCAAGATCGAGAACCTGACTAAGGTGTACAAGTCTCGGAAGATCGGCCGCAT	6270
Qy	6238	CCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGG	6297
Db	6271	CCTGGCAGTGACCGCCTTTGCCTGGGTGTGCGCCCCGAGAGTGCTTTGGGCTCCTCGG	6330
Qy	6298	CGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGAC	6357
Db	6331	GGTCAATGGTGCCGGGAAGACCAGCACCTTCAAGATGTTGACTGGAGATGAGAGCACAAC	6390
Qy	6358	GGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCA	6417
Db	6391	AGGGGGCGAGGCCTTTGTCAATGGACACAGTGCTGAAGGACCTGCTCCAGGTTGAGCA	6450
Qy	6418	GAGCCTCGGCTACTGCCCCGAGTGACGCGCTGTTGACGAGCTCACGGCCCCGGGAGCA	6477
Db	6451	GAGCCTTGCTACTGCCCCAGTTGACGCCCCGTTCGATGAGCTCACGGCTCGGAACA	6510
Qy	6478	CCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAA	6537
Db	6511	CCTGCAGCTGTATACTCGGCTTCGAGGCATCCCCTGGAAGGATGAGGCGCAGGTGGTGAG	6570
Qy	6538	GTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAG	6597
Db	6571	GTGGGCCCTGGAGAAGCTGGAGCTGACGAAGTGTGCAGACAAGCCAGCCGGTAGCTACAG	6630
Qy	6598	CGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTTGGGTACCCAGCCTTCAT	6657
Db	6631	TGGGGGCAACAAACGGAACTTTCCACAGCCATCGCTCTCATTTGGGTACCCTGCCTTCAT	6690
Qy	6658	CTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCT	6717
Db	6691	CTTTCTAGACGAGCCCACCCTGGCATGGACCCTAAGGCCCGGCGCTTCCTGTGGAACCT	6750
Qy	6718	CATCCTCGACCTCATCAAGACAGGGCGTTTCAAGTGGTGCTGACATCACACAGCATGGAGGA	6777
Db	6751	CATTCTGGACCTCATCAAGACAGGACGTTTCAAGTGGTGCTGACCTCACACAGCATGGAGGA	6810
Qy	6778	GTGCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGG	6837
Db	6811	ATGCGAGGCTGTGTGCACACGGCTGGCCATCATGGTGAATGGACGGCTGCGCTGCCTGGG	6870

Qy 6838 CAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAA 6897
 || ||||| ||||| ||||| || ||||| ||||| || |||||

Db 6871 GAGTATCCAGCACCTCAAGAACAGGTTTGGGGACGGCTACATGATCACTGTAAGGACCAA 6930

Qy 6898 GAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCAT 6957
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 6931 AAGCAGCCAGAACGTGAAGGATGTGGTGCGGTTCTTCAACCGCAACTTCCCGAGAGGCCAT 6990

Qy 6958 GCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCT 7017
 ||||| || ||||| || ||||| ||||| ||||| ||||| |||||

Db 6991 GCTCAAGGAACGCCACCATAACGAAGGTGCAGTATCAGCTCAAGTCGGAGCACATCTCGCT 7050

Qy 7018 GGCCCAGGTGTTTCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTC 7077
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7051 GGCTCAGGTGTTTCAAGATGGAGCACGTGGTGGTGTACTGGGCATCGAGGACTACTC 7110

Qy 7078 GGTCAAGCAGACCACACTGGACAATGTGTTGCTGAACTTTGCCAAGAAGCAGAGTGACAA 7137
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7111 AGTCAGCCAGACCCTCTGGATAACGTGTTTGTGAACTTCGCCAAGAAGCAAAGTGACAA 7170

Qy 7138 CCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCCTCTCGGCTGCTTGCT 7197
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7171 TGTGGAGCAGCAAGAGGCTGA---GCCATCCACCTTGCCGTCCCCCTTG---GACTACT 7224

Qy 7198 CAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCC 7257
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7225 TAGCCTGCTGCGGCCCGCCCTGCACCCACAGAGCTCCGGGCACTGGTGGCCGATGAGCC 7284

Qy 7258 CGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCAGCT 7317
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7285 TGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAAGAGCGGGCCAGCT 7344

Qy 7318 GTCCTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTC 7377
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7345 CTCCTTCAACACCGATACGCTCTGCTGACGTTCAAGAGTCACATCAGGGATG----- 7396

Qy 7378 CACTGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCC 7437
 ||| | | || | || | || | || | || |

Db 7397 -----CAGCTGTTTGGGGCAGAAAGTCAGGCGGTGGCCGTAGCCCCAGTCACACA 7445

Qy 7438 TGCCAGGGCCTGGAGTGG-AGGTTCAAGACCAAGGGGCTTCTGGTCTCCAGCCCCTGTA 7496
 ||||| ||||| || ||||| ||||| ||||| ||||| |||||

Db 7446 TGCCAGGCCCTGGAAAGGCAGGTTCAAGACCAAGGGCTCCCGCCCTCC----- 7494

Qy 7497 CTCGGCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAAAGGCTGACCCG 7556
 || | | || | || | || | || | || | || | || |

Db 7495 -----TCCCAACTACCATCCTCCCCGATCGTGCCAAAGGCTGGGCTG 7536

Qy 7557 GCCC-GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCC 7615
 |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 7537 GCCCTGGGCTGCACACACCCTCACCTGCTTTGCCTTAAAGCCTTGGGTCTTGCCCGAGC 7596

Qy 7616 CCTCGCCCCTGCCTGGCACTGCTCACC-GCCCAAGGCGACCGGCTGGACCAGGCA-CT 7673
 || ||||| |||| |||| |||| |||| |||| |||| ||||

Db 7597 CCCTTACCCTGCCAGCACCATCCACCTTCCAGGGTGACATGGGCTGCCCAAGTATCC 7656

Qy 7674 GCTGGCCTTTCTCCTGCCCGGCCCTCGGAACCAGCTTTTCTCTTACGATGAAGGCTGAT 7733

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      || || |||||      ||||| |      | | |      | | |      ||      |
Db      7657 TGTGACCCTTCTCTGCAGCGGCCACCAGTCTACCCAGGCCAGCATCTTGCACAGATGTCT 7716

Qy      7734 GCCGAGAGCGGGCTGTGGGCGGAGCTGGGTGAG-TCCCGTATTTATTTTGCTTTGAGAAG 7792
      | ||      | ||| | || | | || | | || | ||||| |||
Db      7717 TTCATGAAAAGACTGCAGTTGGGGAGGTGGCAGCTTGCCTACTTATTTTGCTTTAAGA-- 7774

Qy      7793 AGGCTCCTCTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCT 7852
      |||| | || || || || || || || ||||| ||
Db      7775 ----GCCTCCCTCACTCTGCTGTTGTGAAGAAGTTAGGCTACCATGGGAAGCCATGAATG 7830

Qy      7853 TGGGCCAGCTGGCAGG-----TGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCA 7905
      |||      ||      ||||| ||||| || ||||| |||
Db      7831 TGGCTGCCTCAGCCCTGGTGAATGGCAGGAACGGAGAAGCTGGGCTTGCTGGCTAGGTG 7890

Qy      7906 AGGGGGCCA-----GACCCCCCCCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGC 7960
      ||||| || || | || | ||||| | ||||| | |||||
Db      7891 AGGGGGCCACTGCTCCCTCCCTGCCCCCTCAAGCTGCCTTTGCTCTCCCGCTCAGCTTGG- 7949

Qy      7961 CCCCTGCCCCGCCCCACCTCCCTGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTGTTT 8020
      |||| || || || || || || | |||| ||||| ||||| |||||
Db      7950 -CCCTTCCTGCCACCCATGTGGGAGTAGGACCTTGTATATAGCACACAGATGTTTGTGTTT 8008

Qy      8021 AAATAAATAAAACAAAATG 8038
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Db      8009 CAATAAATAAGCAAAAAG 8026

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RESULT 11

US-10-191-803-169

; Sequence 169, Application US/10191803

; Publication No. US20040014040A1

; GENERAL INFORMATION:

; APPLICANT: MENDRICK, Donna

; APPLICANT: PORTER, Mark

; APPLICANT: JOHNSON, Kory

; APPLICANT: HIGGS, Brandon

; APPLICANT: CASTLE, Arthur

; APPLICANT: ELASHOFF, Michael

; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling

; FILE REFERENCE: 44921-5090US

; CURRENT APPLICATION NUMBER: US/10/191,803

; CURRENT FILING DATE: 2002-07-10

; PRIOR APPLICATION NUMBER: US 60/303,819

; PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: US 60/305,623

; PRIOR FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: US 60/369,351

; PRIOR FILING DATE: 2002-04-03

; PRIOR APPLICATION NUMBER: US 60/377,611

; PRIOR FILING DATE: 2002-05-06

; NUMBER OF SEQ ID NOS: 1140

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 169

; LENGTH: 8040

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_024396
US-10-191-803-169

Query Match 72.3%; Score 5810; DB 16; Length 8040;
Best Local Similarity 84.0%; Pred. No. 0;
Matches 6768; Conservative 0; Mismatches 1205; Indels 85; Gaps 15;

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Qy      1 CCGCGGCGCTGAGGCGGCGGAGCGTGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 60
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Db      34 CCGCGGCGCTGAGGCGGCGGAGCGCGGCCCCGCCATGGGCTTCCTGCACCAGCTGCAGCT 93

Qy      61 GCTGCTCTGGAAGAACGTGACGCTCAAACGCCGGAGCCCGTGGGTCTGGCCTTCGAGAT 120
          |||
Db      94 GCTGCTCTGGAAGAACGTGACGCTGAAGCGCCGGAGCCCGTGGGTCTGGCCTTCGAGAT 153

Qy     121 CTTTCATCCCCCTGGTGTCTTCTTTATCCTGCTGGGGCTGCGACAGAAGAAGCCCACCAT 180
          |||
Db     154 CTTTCATCCCCCTTGTCTCTTCTTCATCCTGTTGGGACTGCGGCAGAAGAAGCCCACCAT 213

Qy     181 CTCCGTGAAGGAAGTCCCCCTTCTACACAGCGGCGCCCCCTGACGTCTGCCGGCATCCTGCC 240
          |||
Db     214 CTCTGTGAAGGAAG---CTTTCTACACGGCAGCACCGCTGACATCGGCCGGCATCCTGCC 270

Qy     241 TGTCATGCAATCGCTGTGCCCCGACGGCCAGCGAGACGAGTTCGGCTTCCTGCAGTACGC 300
          |||
Db     271 TGTCATGCAGTCGCTTTGCCCTGATGGCCAGCGTGATGAGTTTGGCTTCCTGCAGTATGC 330

Qy     301 CAACTCCACGGTCACGCAGCTGCTTGAGCGCCTGGACCGCGTGGTGGAGGAAGGCAACCT 360
          |||
Db     331 CAACTCCACGGTCACCCAGCTTCTGGAACGCCTCAACCGTGAGTGGAAGAGAGCAACTT 390

Qy     361 GTTTGACCCAGCGCGGCCCAGCCTGGGCTCAGAGCTCGAGGCCCTACGCCAGCATCTGGA 420
          |||
Db     391 GTTTGACCCAGAGCGACCTAGCCTGGGCTCAGAGCTTGAGGCACTGCACCAACGTCTGGA 450

Qy     421 GGCCCTCAGTGCGGGCCCCGGGCACCTCGGGGAGCCACCTGGACAGATCCACAGTGTCTTC 480
          |||
Db     451 GGCCCTCAGCTCGGGCCCTGGCACCTGGGAGAGCCACTCAGCTAGACCTGCAGTTTCATC 510

Qy     481 CTTCTCTCTGGACTCGGTGGCCAGAAACCCGCGAGAGCTCTGGCGTTTCCTGACGCAAAA 540
          |||
Db     511 CTTCTCTCTGGACTCGGTGGCCAGGACAAAAGAGAGCTTTGGCGTTTCCTGATGCAGAA 570

Qy     541 CTTGTGCGTGCCCAATAGCACGGCCCAAGCACTCTTGGCCGCCCGTGTGGACCCGCCCGA 600
          |||
Db     571 CCTGTCACTGCCCAACAGCACGGCCAGGCCCTCCTGGCTGCCCGTGTAGACCCCTCTGA 630

Qy     601 GGTCTACCACCTGCTCTTTGGTCCCTCATCTGCCCTGGATTTCACAGTCTGGCCTCCACAA 660
          |||
Db     631 GGTCTATCGCTTGCTTTTTTGGTCTTTTACCTGACCTGGATGGAAAGTTGGGGTTCCTCAG 690

Qy     661 GGGTCAGGAGCCCTGGAGCCGCCTAGGGGGCAATCCCTGTTCCGGATGGAGGAGCTGCT 720
          |||
Db     691 GAAGCAGGAGCCCTGGAGTCACCTGGGTAGCAATCCTCTGTTCCAAATGGAGGAGCTGCT 750

Qy     721 GCTGGCTCCTGCCCTCCTGGAGCAGCTCACCTGCACGCCGGGCTCGGGGGAGCTGGGCCG 780
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Db	751	 GCTGGCTCCTGCCCTTTTGGAGCAACTCACATGTGCTCCAGGCTCTGGGGAGCTGGGCCG	810
Qy	781	GATCCTCACTGTGCCTGAGAGTCAGAAGGGAGCCCTGCAGGGCTACCGGGATGCTGTCTG	840
Db	811	 GATTCTTACCATGCCTGAGGGTCATCAGGTAGACCTTCAGGGCTACCGGGATGCTGTCTG	870
Qy	841	CAGTGGGCAGGCTGCTGCGCGTGCCAGGCGCTTCTCTGGGCTGTCTGCTGAGCTCCGGAA	900
Db	871	 CAGCGGGCAGGCTACAGCTCGTGCCAGCATTTCAGTGATCTAGCCACTGAGCTCCGGAA	930
Qy	901	CCAGCTGGACGTGGCCAAGGTCTCCAGCAGCTGGGCCTGGATGCCCCAACGGCTCGGA	960
Db	931	 CCAGCTGGACATAGCCAAGATTGCCAGCAGCTGGGCTTCAATGTCCCCAACGGCTCAGA	990
Qy	961	CTCCTCGCCACAGGCGCCACCCCCACGGAGGCTGCAGGCGCTTCTGGGGGACCTGCTGGA	1020
Db	991	 TCCACAGCCGAGGCACCGTCCCCACAGAGTCTGCAGGCACTCTTAGGGGACCTGCTGGA	1050
Qy	1021	TGCCCAGAAGGTTCTGCAGGATGTGGATGTCCTGTGCGGCCCTGGCCCTGCTACTGCCCCA	1080
Db	1051	 TGTCCAGAAGGTTCTACAGGATGTGGATGTCCTATCAGCCCTTGCCCTGCTGCTGCCTCA	1110
Qy	1081	GGGTGCCTGCACTGGCCGGACCCCCGGACCCCCAGCCAGTGGTGCGGGTGGGGCGGCCAA	1140
Db	1111	 AGGTGCCTGTGCTGGCCGGGCCCCCGCACCTCAAGCTGGCAGCCCGAGTGGCCCGGCCAA	1170
Qy	1141	TGGCACTGGGGCAGGGGCAGTCATGGGCCCCAACGCCACCGCTGAGGAGGGCGCACCCCTC	1200
Db	1171	 CAGCACCGGGGTAGGGGCAAATACAGGTCCCAACACCACCGTTGAGGAGGGCACCCAGTC	1230
Qy	1201	TGCTGCAGCACTGGCCACCCCGACACGCTGCAGGGCCAGTGCTCAGCCTTCGTACAGCT	1260
Db	1231	 ACCTGTCACCCCAGCCTCTCCGGACACTCTGCAAGGCCAGTGCTCAGCCTTTGTGCAGCT	1290
Qy	1261	CTGGGCCGGCCTGCAGCCCATCTTGTGTGGCAACAACCGCACCATTGAACCCGAGGCGCT	1320
Db	1291	 CTGGGCTGGCTTGCAGCCCATCTTGTGTGGCAACAACCGTACCATTGAGCCTGAAGCACT	1350
Qy	1321	GCGGCGGGGCAACATGAGCTCCCTGGGCTTCACGAGCAAGGAGCAGCGGAACCTGGGCCT	1380
Db	1351	 CCGGAGGGGCAACATGAGCTCACTGGGCTTTACGAGCAAAGAACAACGGAACCTGGGCCT	1410
Qy	1381	CCTCGTGCACCTCATGACCAGCAACCCCAAATCCTGTACGCGCCTGCGGGCTCTGAGGT	1440
Db	1411	 TCTTGTGCACCTCATGACCAGCAACCCCAAATCCTGTATGCACCCGCAGGCTCTGAAGC	1470
Qy	1441	CGACCGCGTCATCCTCAAGGCCAACGAGACTTTTGCTTTTGTGGGCAACGTGACTCACTA	1500
Db	1471	 TGACCATGTTATCCTCAAGGCAAATGAGACCTTTGCCTTTGTGGGCAACGTGACGCACTA	1530
Qy	1501	TGCCCAGGTCTGGCTCAACATCTCGGCGGAGATCCGAGCTTCCTGGAGCAGGGCAGGCT	1560
Db	1531	 CGCCCAGGTCTGGCTCAACATCTCCGAGAGATCCGAGCTTCCTGGAGCAGGGCAGGCT	1590
Qy	1561	GCAGCAACACCTGCGCTGGCTGCAGCAGTATGTAGCAGAGCTGCGGCTGCACCCCGAGGC	1620

[illegible]

Qy	2461	CAAGGCCAAGCTGGCCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTA	2520
Db	2491	TAAGGCCAAGTTGGCCTCGGCCTGCGGCGGCATCATCTACTTCCTGAGCTACGTTCCCTA	2550
Qy	2521	CATGTACGTGGCGATCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTG	2580
Db	2551	CATGTATGTAGCAATCCGTGAGGAAGTAGCCACGATAAGATCACTGCCTTCGAGAAGTG	2610
Qy	2581	CATCGCGTCCCTCATGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTA	2640
Db	2611	CATTGCGTCCCTGATGTCCACAACAGCCTTCGGCCTGGGTTCCAAGTACTTTGCTCTGTA	2670
Qy	2641	TGAGGTGGCCGGCGTGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGA	2700
Db	2671	TGAAGTGGCAGGTGTGGGCATCCAGTGGCACACGTTCAAGTCCCCAGTGGAAAGGGGA	2730
Qy	2701	CGACTTCAACTTGCTCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCAT	2760
Db	2731	TGACTTCAACCTGCTCCTTGCTGTCACCATGCTGATGGTGGACACAGTGGTCTATGGCGT	2790
Qy	2761	CCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTA	2820
Db	2791	ACTCACTTGGTACATTGAGGCTGTGCACCCAGGTATGTATGGGCTGCCCCGGCCCTGGTA	2850
Qy	2821	CTTCCCACTGCAGAAGTCCTACTGGCTGGGCGAGTGGGCGGACAGAAGCCTGGGAGTGGAG	2880
Db	2851	CTTCCCACTACAGAAGTCCTATTGGCTGGGCGAGTGGGCGGACAGAGACCTGGGAGTGGAG	2910
Qy	2881	CTGGCCGTGGGCACGCACCCCCGCCTCAGTGTCATGGAGGAGGACCAGGCCTGTGCCAT	2940
Db	2911	CTGGCCATGGGCACACGCACCACGCCTCAGCGTTATGGAGGAGGACCAGGCCTGTGCCAT	2970
Qy	2941	GGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCT	3000
Db	2971	GGAGAGCCGGCACTTCGAGGAGACTCGCGGTATGGAGGAGGAGCCACCCACCTGCCTTT	3030
Qy	3001	GGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAA	3060
Db	3031	GGTCGTCTGCGTGGACAAGCTCACCAAGGTCTATAAAATGACAAGAAGCTGGCCCTAAA	3090
Qy	3061	CAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGC	3120
Db	3091	CAAAGTGAAGCCTCAATCTCTACGAGAACCAGGTGGTCTCTTTCCTAGGCCATAACGGGGC	3150
Qy	3121	GGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCGCG	3180
Db	3151	TGGCAAGACCACTACCATGTCTATCCTGACTGGACTGTTCCACCCACGTCGGGCTCAGC	3210
Qy	3181	CACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCAT	3240
Db	3211	CACTATCTATGGCCACGACATCCGCACAGAGATGGATGAGATCCGTAAGAACCTGGGCAT	3270
Qy	3241	GTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTA	3300
Db	3271	GTGCCCCACAGCACAACGTGCTCTTTGACAGCTCACTGTGGAGGAACACCTCTGGTTCTA	3330

Qy	3301	CTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGA	3360
Db	3331	CTCACGCCTCAAAAAGCATGGCACAAAGAGGAGATCCGCAAAGAGATGGACAAGATGATCGA	3390
Qy	3361	GGACCTGGAGCTCTCCAACAAACGGGCACTCACTGGTGCAGACATTGTCTGGGTGGCATGAA	3420
Db	3391	GGACCTGGAGCTCTCCAACAAGCGCCACTCGCTGGTACAGACGCTGTCTGGAGGCATGAA	3450
Qy	3421	GCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGA	3480
Db	3451	GCGCAAGCTTTTCAGTAGCCATTGCCTTCGTGGGTGGCTCTAGAGCCATTATCTTAGATGA	3510
Qy	3481	GCCACAGCGGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTA	3540
Db	3511	GCCACAGCTGGCGTGGACCCCTATGCTCGACGTGCCATCTGGGACCTCATCTGAAGTA	3570
Qy	3541	CAAGCCAGGCCGCGACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGG	3600
Db	3571	CAAGCCGGGTGCGACTATCCTCCTGTCCACCCATCACATGGATGAGGCCGACCTGCTGGG	3630
Qy	3601	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGTGCGGCTCCCCGCTCTTCCT	3660
Db	3631	GGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAATGCTGCGGCTCTCCCTCTTCCT	3690
Qy	3661	CAAGGGCACCTATGGCGACGGGTACGCGCTCACGCTGGTCAAGCGGCCCGCCGAGCCGGG	3720
Db	3691	CAAGGGTGCCTACGGCGATGGCTACGCGCTCACACTGGTCAAGCGGCCTGCGGAGCCTGG	3750
Qy	3721	GGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTG	3780
Db	3751	CACCTCCCAAGAGCCAGGGATGGCTTCCAGCCCCCTCAGGTCGTCTCAGCTGAGCAACTG	3810
Qy	3781	CTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTC	3840
Db	3811	CTCAGAGATGCAAGTGTCCCAGTTCATCCGCAAGCATGTGGCTTCCTCCCTGCTGGTGTG	3870
Qy	3841	AGACACAAGCACGGAGCTCTCCTACATCCTGCCAGCGAGGCCGCCAAGAAGGGGGCTTT	3900
Db	3871	AGACACGAGCACCGAGCTCTCCTACATCCTGCCAGCGAGGCTGTCAAGAAAGGGGCCTT	3930
Qy	3901	CGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGG	3960
Db	3931	CGAGCGCCTCTTTCAGCAATTGGAGCACAGCCTGGACGCACTGCATCTGAGCAGTTTGG	3990
Qy	3961	GCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCTGAGGAGGATCAGTCGCT	4020
Db	3991	GCTGATGGACACAACCCTGGAGGAGGTGTTCCTCAAGGTGTCTGAAGAAGACCAGTCACT	4050
Qy	4021	GGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGG	4080
Db	4051	GGAGAATAGTGAGGCCGATGTGAAGGAGTCCCGGAAGGATGCACTGCCTGGGGCAGAGGG	4110
Qy	4081	CCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTC	4140
Db	4111	CCTGACGGCTGTGGAGAGTCAAGCAGGCAACCTGGCTCGGTGCTCAGAGCTGGCACAGTC	4170
Qy	4141	GCAGGCATCGCTGCAGTCGGCGTTCATCTGTGGGCTCTGCCCCGTGGCGACGAGGGAGCTGG	4200

Db	4171		CCAGGCTTCACTGCAGTCTGCATCTTCTGTGGGCTCCGCCCGTGGGGATGAGGGTGCTGG	4230
Qy	4201		CTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAA	4260
Db	4231		CTACACCGACGGCTACGGTGACTACCGTCCCCTCTTTGACAACTTGACAGGACCCAGACAG	4290
Qy	4261		TGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAA	4320
Db	4291		TGTCAGCTTACAAGAGGCTGAAATGGAGGCCCTGGCTCGGGTAGGCCAGGGCAGCCGCAA	4350
Qy	4321		GCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCA	4380
Db	4351		GCTAGAGGGCTGGTGGCTGAAGATGCGGCAGTTCCATGGGCTCCTGGTGAAGCGCTTCCA	4410
Qy	4381		CTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGT	4440
Db	4411		CTGTGCTCGCCGGAACCTCAAAGCGCTCTGCTCCCAGATTCTGCTGCCTGCCTTCTTCGT	4470
Qy	4441		CTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGT	4500
Db	4471		CTGTGTGGCCATGACTGTGGCATTGTCTGTCCCTGAGATCGGTGACCTGCCTCCACTGGT	4530
Qy	4501		CCTGTACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCTACGC	4560
Db	4531		CCTGTGCTTCTCAGTACCACAACCTATACCCAGCCCCGTGGCAACTTTATCCCCTATGC	4590
Qy	4561		CAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCAGCAGCT	4620
Db	4591		CAATGAGGAACGCCGCGAGTACCGATTACGGCTGTCACCTGATGCCAGCCCCAGCAGTT	4650
Qy	4621		CGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGC	4680
Db	4651		GGTGAGCACATTCCGGCTGCCCTCTGGTGTGGGTGCCACTTGTGTGCTCAAGTCTCCAGC	4710
Qy	4681		CAACGGCTCGTGGGGCCACGTTGAACCTGAGCAGCGGGAGTCGCGCCTGCTGGCGGC	4740
Db	4711		CAACGGCTCCCTGGGGCCCATGCTGAACCTTGAGCAGTGGAGAGTCCCGCCTGCTGGCCGC	4770
Qy	4741		TCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATTT	4800
Db	4771		ACGGTTCCTTCGACAGTATGTGCCTGGAGTCCTTCACACAGGGGCTGCCACTGTCCAATT	4830
Qy	4801		CGTGCCACCCCCACCCTCGCCCGCCCATCTGACTCGCCAGCGTCCCCGGATGAGGA---	4857
Db	4831		CGTGCCACCCCCACCCTCGCCCGCCCTTCCGACTCACCCCTGTCCCCGGATGAGGATTC	4890
Qy	4858		CCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCGGC	4917
Db	4891		ACTGCTAGCCTGGAATACGTCCCTGCCCCCTACTGCTGGACCAGAGACGTGGACGTTGGC	4950
Qy	4918		ACCCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCAC	4977
Db	4951		GCCTTCTCTGCCACGCCTGGTTACAGAGCCGGTCCGCTGTACCTGCTCTGCACAGGGCAC	5010
Qy	4978		CGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACAGG	5037

Db 5011 GGGCTTCTCGTGCCCCAGCAGTGTGGGTGGGCACCCACCCCAGATGAGAGTGGTCACGGG 5070
 Qy 5038 CGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGA 5097
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 Db 5071 GGACATCCTGACTGACATCACCGGCCACAATGTTTCCGAGTACCTGCTCTTCACCTCTGA 5130
 Qy 5098 CCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAGTCCATCCC 5157
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 Db 5131 CCGTTTCCGACTGCACCGCTATGGAGCCATCACCTTTGGTAATATCCAGAAGTCCATCCC 5190
 Qy 5158 AGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGC 5217
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 Db 5191 AGCACCCATTGGTACCCGGACCCCTCTCATGGTCCGGAAGATTGCAGTGCAGGAGGGTGGC 5250
 Qy 5218 CCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTCAA 5277
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 Db 5251 CCAGGTGCTCTACAACAACAAGGGCTACCACAGCATGCCACCTACCTCAACAGCCTCAA 5310
 Qy 5278 CAACGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCAT 5337
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 Db 5311 CAATGCCATTCTGCGTGCAAACCTACCCAAAAGCAAGGGCAATCCAGCAGCCTACGGTAT 5370
 Qy 5338 CACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCT 5397
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 Db 5371 CACCGTCACCAACCACCCCATGAACAAGACCAGTGCTAGCCTCTCCCTGGATTACCTACT 5430
 Qy 5398 GCAGGGCACGGATGTGCGTCATCGCCATCTTCATCATCGTGGCCATGTCTTCGTGCCGGC 5457
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 Db 5431 GCAGGGCACAGACGTGGTCATCGCCATCTTCATCATTGTGGCCATGTCTTCGTGCCGGC 5490
 Qy 5458 CAGCTTCGTTGTCTTCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGT 5517
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 Db 5491 CAGCTTCGTGGTCTTCTTGTGGCCGAGAAATCCACCAAGGCCAAACACCTGCAGTTCGT 5550
 Qy 5518 CAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTA 5577
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 Db 5551 CAGCGGTGCAACCCCTGTCATCTACTGGCTAGCCAACTACGTGTGGGACATGCTCAATTA 5610
 Qy 5578 CCTGGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTGACCTGCCGGCCTACAC 5637
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 Db 5611 CCTGGTCCCCGGCCACCTGCTGCATCATCCTCTTCGTGTTTGACTTGCCGGCCTACAC 5670
 Qy 5638 GTCGCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCAC 5697
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 Db 5671 GTCACCCACCAACTTCCCCGCGGTGCTCTCCTTGTTCCTGCTCTATGGATGGTCCATCAC 5730
 Qy 5698 GCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCAGCTCCGCCTACGTGTTCCCT 5757
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 Db 5731 ACCCATCATGTACCCGGCCTCCTTCTGGTTTGAGGTCCCTAGCTCAGCCTACGTGTTCCCT 5790
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 Db 5791 CATCGTCATCAACCTCTTCATTGGCATCACGGCCACAGTGGCCACCTTCTTCTGCAGCT 5850
 Qy 5818 CTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCAT 5877
 |||
 Db 5851 CTTTGAGCATGACAAGGATCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCAT 5910

QY	5878	TTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAA	5937
Db	5911	CTTCCCCAACTACAACCTGGGCCACGGACTCATGGAGATAGCCTACAACGAATACATCAA	5970
QY	5938	CGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACAT	5997
Db	5971	CGAATACTATGCCAAGATCGGCCAGTTTGACAAGATGAAGTCCCCGTTTGAGTGGGACAT	6030
QY	5998	TGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCAT	6057
Db	6031	TGTCACACGTGGACTGGTGGCCATGACAGTCGAGGGCTTCGTGGGATTCTTTCTCACCAT	6090
QY	6058	CATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGT	6117
Db	6091	CATGTGTCAATATAACTTCCTACGGCAGCCACAGCGTCTGCCTGTGTCTACTAAACCTGT	6150
QY	6118	GGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAA	6177
Db	6151	GGAAGACGATGTAGACGTGGCCAGTGAGCGGCAAAGAGTGCTCCGTGGCGATGCTGACAA	6210
QY	6178	TGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTAT	6237
Db	6211	TGACATGGTCAAGATCGAGAACCTGACTAAGGTGTACAAGTCTCGGAAGATCGGCCGCAT	6270
QY	6238	CCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCTGGCGAGTGCTTCGGGCTCCTGGG	6297
Db	6271	CCTGGCAGTGGACCGCCTTTGCCTGGGTGTGCGCCCCGGAGAGTGCTTTGGGCTCCTCGG	6330
QY	6298	CGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGAC	6357
Db	6331	GGTCAATGGTGCCGGAAGACCAGCACCTTCAAGATGTTGACTGGAGATGAGAGCACAAC	6390
QY	6358	GGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCA	6417
Db	6391	AGGGGGCGAGGCCTTTGTCAATGGACACAGTGTGCTCAAGGACCTGCTCCAGGTTGAGCA	6450
QY	6418	GAGCCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGAGCA	6477
Db	6451	GAGCCTTGCTACTGCCCCAGTTCGACGCCCTGTTTCGATGAGCTCACGGCTCGCGAACA	6510
QY	6478	CCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAA	6537
Db	6511	CCTGCAGCTGTATACTCGGCTTCGAGGCATCCCCTGGAAGGATGAGGCGCAGGTGGTGAG	6570
QY	6538	GTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAG	6597
Db	6571	GTGGGCCCTGGAGAAGCTGGAGCTGACGAAGTGTGCAGACAAGCCAGCCGGTAGCTACAG	6630
QY	6598	CGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCAT	6657
Db	6631	TGGGGGCAACAAACGGAACTTTCCACAGCCATCGCTCTCATTGGGTACCTGCCTTCAT	6690
QY	6658	CTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCT	6717
Db	6691	CTTTCTAGACGAGCCCACCACTGGCATGGACCCTAAGGCCCGGCGCTTCCTGTGGAACCT	6750

QY	6718	CATCCTCGACCTCATCAAGACAGGGCGTTTCAGTGGTGCTGACATCACACAGCATGGAGGA	6777
Db	6751	CATTCTGGACCTCATCAAGACAGGACGTTTCAGTGGTGCTGACCTCACACAGCATGGAGGA	6810
QY	6778	GTGCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGG	6837
Db	6811	ATGCGAGGCTGTGTGCACACGGCTGGCCATCATGGTGAATGGACGGCTGCGCTGCCTGGG	6870
QY	6838	CAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAA	6897
Db	6871	GAGTATCCAGCACCTCAAGAACAGGTTTGGGGACGGCTACATGATCACTGTAAGGACCAA	6930
QY	6898	GAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCAT	6957
Db	6931	AAGCAGCCAGAACGTGAAGGATGTGGTGCGGTTCTTCAACCGCAACTTCCCGAGAGGCCAT	6990
QY	6958	GCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCT	7017
Db	6991	GCTCAAGGAACGCCACCATACGAAGGTGCAGTATCAGCTCAAGTCGGAGCACATCTCGCT	7050
QY	7018	GGCCCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTC	7077
Db	7051	GGCTCAGGTGTTTCAGCAAGATGGAGCACGTGGTCGGTGTACTGGGCATCGAGGACTACTC	7110
QY	7078	GGTCAGCCAGACCACACTGGACAATGTGTTTCGTGAACCTTGCCTAAGAAGCAGAGTGACAA	7137
Db	7111	AGTCAGCCAGACCCTCTGGATAACGTGTTTGTGAACCTTCGCTAAGAAGCAAAGTGACAA	7170
QY	7138	CCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCT	7197
Db	7171	TGTGGAGCAGCAAGAGGCTGA---GCCATCCACCTTGCCGTCCCCCCTTG---GACTACT	7224
QY	7198	CAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACCTGTGGCAGACGAGCC	7257
Db	7225	TAGCCTGCTGCGGCCCCGCCCTGCACCCACAGAGCTCCGGGCACCTGGTGGCCGATGAGCC	7284
QY	7258	CGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCT	7317
Db	7285	TGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAAGAGCGGGCCCAGCT	7344
QY	7318	GTCTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTC	7377
Db	7345	CTCTTCAACACCGATACGCTCTGCTGACGTTCAAGAGTCACATCAGGGATG-----	7396
QY	7378	CACTGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCC	7437
Db	7397	-----CAGCTGTTTGGGGCAGAAGTCAGGCGGTGGCCGTAGCCCCAGTCACACA	7445
QY	7438	TGCCAGGGCCTGGAGTGG-AGGTTTCAGGACCAAGGGGCTTCTGGTCTCCAGCCCCTGTA	7496
Db	7446	TGCCAGGCCCTGGAAAGGCAGGTTTCAGGACCAAGGGGCTCCCGCCCTCC-----	7494
QY	7497	CTCGGCCATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCG	7556
Db	7495	-----TCCCAACTACCATCCTCCCCGATCGTGCCAAAGGCTGGGCTG	7536
QY	7557	GCCC-GGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCGGCC	7615


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; APPLICANT: YANG, Junming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: SANJANWALA, Madhu S.
; APPLICANT: RAUMANN, Brigitte E.
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; APPLICANT: KHAN, Farrah A.
; APPLICANT: KEARNEY, Liam
; APPLICANT: ELLIOTT, Vicky S.
; APPLICANT: SEILHAMER, Jeffrey J.
; APPLICANT: POLICKY, Jennifer L.
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: BURFORD, Neil
; APPLICANT: DING, Li
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: HILLMAN, Jennifer L.
; TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
; FILE REFERENCE: PI-0109 PCT
; CURRENT APPLICATION NUMBER: US/10/297,022
; CURRENT FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/208,424; 60/209,001; 60/210,588; 60/212,335;
60/213,747; 60/215,391
; PRIOR FILING DATE: 2000-05-26; 2000-06-01; 2000-06-08; 2000-06-16; 2000-06-
22; 2000-06-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PERL Program
; SEQ ID NO 45
; LENGTH: 5540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030216310A1 2311751CB1
US-10-297-022-45

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Query Match          68.9%; Score 5536.8; DB 16; Length 5540;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5538; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy      1995 TCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACA 2054
          |||
Db      1 TCTACTTCCTCTACGGCTTCGTCTGGATCCAGGACATGATGGAGCGCGCCATCATCGACA 60

Qy      2055 CTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGATGTTCCCCTACCCCT 2114
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Db      61 CTTTTGTGGGGCACGACGTGGTGGAGCCAGGCAGCTACGTGCAGATGTTCCCCTACCCCT 120

Qy      2115 GCTACACACGCGATGACTTCCTGTTTGTCATTGAGCACATGATGCCGCTGTGCATGGTGA 2174
          |||
Db      121 GCTACACACGCGATGACTTCCTGTTTGTCATTGAGCACATGATGCCGCTGTGCATGGTGA 180

Qy      2175 TCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACC 2234
          |||
Db      181 TCTCCTGGGTCTACTCCGTGGCCATGACCATCCAGCACATCGTGGCGGAGAAGGAGCACC 240

Qy      2235 GGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGT 2294

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Db	241	 GGCTCAAGGAGGTGATGAAGACCATGGGCCTGAACAACGCGGTGCACTGGGTGGCCTGGT	300
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Db	301	 TCATCACCGGCTTTGTGCAGCTGTCCATCTCCGTGACAGCACTCACCGCCATCCTGAAGT	360
Qy	2355	ACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACG	2414
Db	361	 ACGGCCAGGTGCTTATGCACAGCCACGTGGTCATCATCTGGCTCTTCCTGGCAGTCTACG	420
Qy	2415	CGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGG	2474
Db	421	 CGGTGGCCACCATCATGTTCTGCTTCCTGGTGTCTGTGCTGTACTCCAAGGCCAAGCTGG	480
Qy	2475	CCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGA	2534
Db	481	 CCTCGGCCTGCGGTGGCATCATCTACTTCCTGAGCTACGTGCCCTACATGTACGTGGCGA	540
Qy	2535	TCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCA	2594
Db	541	 TCCGAGAGGAGGTGGCGCATGATAAGATCACGGCCTTCGAGAAGTGCATCGCGTCCCTCA	600
Qy	2595	TGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCG	2654
Db	601	 TGTCCACGACGGCCTTTGGTCTGGGCTCTAAGTACTTCGCGCTGTATGAGGTGGCCGGCG	660
Qy	2655	TGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGACGACTTCAACTTGC	2714
Db	661	 TGGGCATCCAGTGGCACACCTTCAGCCAGTCCCCGGTGGAGGGGGACGACTTCAACTTGC	720
Qy	2715	TCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACA	2774
Db	721	 TCCTGGCTGTCACCATGCTGATGGTGGACGCCGTGGTCTATGGCATCCTCACGTGGTACA	780
Qy	2775	TTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTACTTCCCACTGCAGA	2834
Db	781	 TTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCCTGGTACTTCCCACTGCAGA	840
Qy	2835	AGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCAC	2894
Db	841	 AGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAGTGGAGCTGGCCGTGGGCAC	900
Qy	2895	GCACCCCCCGCCTCAGTGTGTCATGGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCT	2954
Db	901	 GCACCCCCCGCCTCAGTGTGTCATGGAGGAGGACCAGGCCTGTGCCATGGAGAGCCGGCGCT	960
Qy	2955	TTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCTGGTTGTCTGCGTGG	3014
Db	961	 TTGAGGAGACCCGTGGCATGGAGGAGGAGCCACCCACCTGCCTCTGGTTGTCTGCGTGG	1020
Qy	3015	ACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGA	3074
Db	1021	 ACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCCCTGAACAAGCTGAGCCTGA	1080
Qy	3075	ACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCA	3134

Db	1081	ACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAACGGGGCGGGCAAGACCACCA	1140
Qy	3135	CCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCCGCCACCATCTACGGGC	3194
Db	1141	CCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGTTCCGCCACCATCTACGGGC	1200
Qy	3195	ACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCATGTGCCCCGAGCACA	3254
Db	1201	ACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTGGGCATGTGCCCCGAGCACA	1260
Qy	3255	ATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGA	3314
Db	1261	ATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGGTTCTACTCACGGCTCAAGA	1320
Qy	3315	GCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCT	3374
Db	1321	GCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATGATCGAGGACCTGGAGCTCT	1380
Qy	3375	CCAACAAACGGCACTCACTGGTGCAGACATTGTGGGTGGCATGAAGCGCAAGCTGTCCG	3434
Db	1381	CCAACAAACGGCACTCACTGGTGCAGACATTGTGGGTGGCATGAAGCGCAAGCTGTCCG	1440
Qy	3435	TGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGGCG	3494
Db	1441	TGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTGGACGAGCCACGGCGGGCG	1500
Qy	3495	TGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGCA	3554
Db	1501	TGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTGAAGTACAAGCCAGGCCGCA	1560
Qy	3555	CCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCA	3614
Db	1561	CCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTGCTTGGGGACCGCATTGCCA	1620
Qy	3615	TCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCTCAAGGGCACCTATG	3674
Db	1621	TCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTCTTCCTCAAGGGCACCTATG	1680
Qy	3675	GCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCCGAGCCGGGGGGGGCCCCAAGAGC	3734
Db	1681	GCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCCGAGCCGGGGGGGGCCCCAAGAGC	1740
Qy	3735	CAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGG	3794
Db	1741	CAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGCAGCTGCTCCGAGCTCCAGG	1800
Qy	3795	TGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGG	3854
Db	1801	TGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTGGTCTCAGACACAAGCACGG	1860
Qy	3855	AGCTCTCCTACATCCTGCCAGCGAGGCCGCCAAGAAGGGGGCTTTCGAGCGCCTCTTCC	3914
Db	1861	AGCTCTCCTACATCCTGCCAGCGAGGCCGCCAAGAAGGGGGCTTTCGAGCGCCTCTTCC	1920
Qy	3915	AGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGGGCTGATGGACACGA	3974
Db	1921	AGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGCTTCGGGCTGATGGACACGA	1980

Qy	3975	CCCTGGAGGAAGTGTTCCTCAAGGTGTCGGAGGAGGATCAGTCGCTGGAGAACAGTGAGG	4034
Db	1981	CCCTGGAGGAAGTGTTCCTCAAGGTGTCGGAGGAGGATCAGTCGCTGGAGAACAGTGAGG	2040
Qy	4035	CCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGGCCCGGCGTCTGGGG	4094
Db	2041	CCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCGGAGGGCCCGGCGTCTGGGG	2100
Qy	4095	AGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGC	4154
Db	2101	AGGGTCACGCTGGCAATCTGGCCCGGTGCTCGGAGCTGACCCAGTCGCAGGCATCGCTGC	2160
Qy	4155	AGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGGCTACACCGACGTCT	4214
Db	2161	AGTCGGCGTCATCTGTGGGCTCTGCCCCTGGCGACGAGGGAGCTGGCTACACCGACGTCT	2220
Qy	4215	ATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAATGTCAGCCTGCAAG	4274
Db	2221	ATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCAGACAATGTCAGCCTGCAAG	2280
Qy	4275	AGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAAGCTGGACGGCGGGT	4334
Db	2281	AGGTGGAGGCAGAGGCCCTGTGAGGGTCGGCCAGGGCAGCCGCAAGCTGGACGGCGGGT	2340
Qy	4335	GGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCGCCGCA	4394
Db	2341	GGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGCTTCCACTGCGCCCGCCGCA	2400
Qy	4395	ACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGGCCATGA	4454
Db	2401	ACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTCTTCGTCTGCGTGGCCATGA	2460
Qy	4455	CCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGTCCTGTACCTTCCC	4514
Db	2461	CCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCGCTGGTCCTGTACCTTCCC	2520
Qy	4515	AGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCCTACGCCAACGAGGAGCGCC	4574
Db	2521	AGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCCCTACGCCAACGAGGAGCGCC	2580
Qy	4575	GCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCCAGCAGCTCGTGAGCACGTTCC	4634
Db	2581	GCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCCAGCAGCTCGTGAGCACGTTCC	2640
Qy	4635	GGCTGCCGTCGGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGG	4694
Db	2641	GGCTGCCGTCGGGGGTGGGTGCCACCTGCGTGCTCAAGTCTCCCGCCAACGGCTCGCTGG	2700
Qy	4695	GGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACA	4754
Db	2701	GGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTGGCGGCTCGGTTCTTCGACA	2760
Qy	4755	GCATGTGTCTGGAGTCTTTCACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCAC	4814
Db	2761	GCATGTGTCTGGAGTCTTTCACACAGGGGCTGCCACTGTCCAATTTTCGTGCCACCCCCAC	2820

Qy	4815	CCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCTGCAGGCCTGGAACG	4874
Db	2821	CCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAGGACCTGCAGGCCTGGAACG	2880
Qy	4875	TCTCCCTGCCGCCCCACCGCTGGGCCAGAAATGTGGACGTCCGGCACCCTCCCTGCCGCGCC	4934
Db	2881	TCTCCCTGCCGCCCCACCGCTGGGCCAGAAATGTGGACGTCCGGCACCCTCCCTGCCGCGCC	2940
Qy	4935	TGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GGCTTCTCCTGCCCCA	4994
Db	2941	TGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGCACC GGCTTCTCCTGCCCCA	3000
Qy	4995	GCAGTGTGGGCGGGCACC CGCCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACA	5054
Db	3001	GCAGTGTGGGCGGGCACC CGCCCCAGATGCGGGTGGTCACAGGCGACATCCTGACCGACA	3060
Qy	5055	TCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACC	5114
Db	3061	TCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCCGACCGCTTCCGACTGCACC	3120
Qy	5115	GGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCA	5174
Db	3121	GGTATGGGGCCATCACCTTTGGAAACGTCCTGAAGTCCATCCCAGCCTCATTTGGCACCA	3180
Qy	5175	GGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCAGGTTTTCTACAACA	5234
Db	3181	GGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCTGCCCAGGTTTTCTACAACA	3240
Qy	5235	ACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTG	5294
Db	3241	ACAAGGGCTATCACAGCATGCCCACCTACCTCAACAGCCTCAACAACGCCATCCTGCGTG	3300
Qy	5295	CCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACC	5354
Db	3301	CCAACCTGCCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACC	3360
Qy	5355	CCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGGGCAGGATGTCG	5414
Db	3361	CCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGGGCAGGATGTCG	3420
Qy	5415	TCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCC	5474
Db	3421	TCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCC	3480
Qy	5475	TCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGACGGCTGCAACCCCA	5534
Db	3481	TCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTGACGGCTGCAACCCCA	3540
Qy	5535	TCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCT	5594
Db	3541	TCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCT	3600
Qy	5595	GCTGTGTCATCATCTGTTTGTGTTTCGACCTGCCGGCCTACACGTCGCCCACCAACTTCC	5654
Db	3601	GCTGTGTCATCATCTGTTTGTGTTTCGACCTGCCGGCCTACACGTCGCCCACCAACTTCC	3660
Qy	5655	CTGCCGTCCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGG	5714

Db	3661	 CTGCCGTCCTCTCCCTCTTCTGCTCTATGGGTGGTCCATCACGCCCATCATGTACCCGG	3720
Qy	5715	CCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCATTGTCATCAATCTCT	5774
Db	3721	 CCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCCCTCATTGTCATCAATCTCT	3780
Qy	5775	TCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGG	5834
Db	3781	 TCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGG	3840
Qy	5835	ACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACC	5894
Db	3841	 ACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACC	3900
Qy	5895	TGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGA	5954
Db	3901	 TGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGA	3960
Qy	5955	TTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGG	6014
Db	3961	 TTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGG	4020
Qy	6015	TGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAAC	6074
Db	4021	 TGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAAC	4080
Qy	6075	TCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACG	6134
Db	4081	 TCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACG	4140
Qy	6135	TGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTG	6194
Db	4141	 TGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTG	4200
Qy	6195	AGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCC	6254
Db	4201	 AGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCC	4260
Qy	6255	TGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCA	6314
Db	4261	 TGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCA	4320
Qy	6315	AGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTCG	6374
Db	4321	 AGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGGCGAGGCCTTCG	4380
Qy	6375	TCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCC	6434
Db	4381	 TCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCC	4440
Qy	6435	CGCAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCTGCAGCTGTACACGC	6494
Db	4441	 CGCAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAGCACCTGCAGCTGTACACGC	4500
Qy	6495	GGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGC	6554

Db	4501	GGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGC	4560
Qy	6555	TGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGA	6614
Db	4561	TGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGA	4620
Qy	6615	AGCTCTCCACGGCCATCGCCCTCATTTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCA	6674
Db	4621	AGCTCTCCACGGCCATCGCCCTCATTTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCA	4680
Qy	6675	CCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCCTCGACCTCATCA	6734
Db	4681	CCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCCTCGACCTCATCA	4740
Qy	6735	AGACAGGGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCA	6794
Db	4741	AGACAGGGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCA	4800
Qy	6795	CGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGA	6854
Db	4801	CGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGA	4860
Qy	6855	AGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTGA	6914
Db	4861	AGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTGA	4920
Qy	6915	AGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACC	6974
Db	4921	AGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACC	4980
Qy	6975	ACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTACAGCA	7034
Db	4981	ACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTACAGCA	5040
Qy	7035	AGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACAC	7094
Db	5041	AGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACAC	5100
Qy	7095	TGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGA	7154
Db	5101	TGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGA	5160
Qy	7155	CGGAGCCGCCATCCGCACTGCAGTCCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCC	7214
Db	5161	CGGAGCCGCCATCCGCACTGCAGTCCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCC	5220
Qy	7215	GGTCTGCCCCACGGAGCTCCGGGCACCTTGTGGCAGACGAGCCCAGGACCTGGACACGG	7274
Db	5221	GGTCTGCCCCACGGAGCTCCGGGCACCTTGTGGCAGACGAGCCCAGGACCTGGACACGG	5280
Qy	7275	AGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCTTCAACACGGACA	7334
Db	5281	AGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCTTCAACACGGACA	5340
Qy	7335	CGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTGACCACCCAGAGC	7394
Db	5341	CGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTGACCACCCAGAGC	5400

Qy 7395 TGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGCCAGGGCCTGGAGTG 7454
 |||
 Db 5401 TGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGCCAGGGCCTGGAGTG 5460
 Qy 7455 GAGGTTTCAGGACCAAGGGGCTTCTGGTCTCCAGCCCCTGTACTCGGCCATGCCCTGCGG 7514
 |||
 Db 5461 GAGGTTTCAGGACCAAGGGGCTTCTGGTCTCCAGCCCCTGTACTCGGCCATGTCCTGCGG 5520
 Qy 7515 TCACTGCGGTTGCCGCCCCCT 7534
 |||
 Db 5521 TCACTGCGGTTGCCGCCCCCT 5540

RESULT 13

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; GENERAL INFORMATION:

; APPLICANT: Dai, Hongyue

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; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients

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; SEQ ID NO 47

; LENGTH: 5285

; TYPE: DNA

; ORGANISM: Homo sapiens

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Query Match 65.7%; Score 5285; DB 13; Length 5285;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2756 GGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCC 2815
 |||
 Db 1 GGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCC 60
 Qy 2816 TGGTACTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAG 2875
 |||
 Db 61 TGGTACTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAG 120
 Qy 2876 TGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTTCATGGAGGAGGACCAGGCCTGT 2935

Db	121	 TGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCATGGAGGAGGACCAGGCCTGT	180
Qy	2936	GCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACCCACCTG	2995
Db	181	 GCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACCCACCTG	240
Qy	2996	CCTCTGGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCC	3055
Db	241	 CCTCTGGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCC	300
Qy	3056	CTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAAC	3115
Db	301	 CTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAAC	360
Qy	3116	GGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGT	3175
Db	361	 GGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGT	420
Qy	3176	TCCGCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTG	3235
Db	421	 TCCGCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTG	480
Qy	3236	GGCATGTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGG	3295
Db	481	 GGCATGTGCCCCGAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGG	540
Qy	3296	TTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATG	3355
Db	541	 TTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATG	600
Qy	3356	ATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTGCGGTGGC	3415
Db	601	 ATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTGCGGTGGC	660
Qy	3416	ATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTG	3475
Db	661	 ATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTG	720
Qy	3476	GACGAGCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTG	3535
Db	721	 GACGAGCCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTG	780
Qy	3536	AAGTACAAGCCAGGCCGCACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTG	3595
Db	781	 AAGTACAAGCCAGGCCGCACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTG	840
Qy	3596	CTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTC	3655
Db	841	 CTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTC	900
Qy	3656	TTCCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCCGAG	3715
Db	901	 TTCCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCCGAG	960
Qy	3716	CCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCGGGCCCCGCTGAGC	3775

Db	961	CCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTCTGGGCCCCGCTGAGC	1020
Qy	3776	AGCTGCTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTG	3835
Db	1021	AGCTGCTCCGAGCTCCAGGTGTCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTG	1080
Qy	3836	GTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGG	3895
Db	1081	GTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGG	1140
Qy	3896	GCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGC	3955
Db	1141	GCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGC	1200
Qy	3956	TTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCTGGAGGAGGATCAG	4015
Db	1201	TTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCCTCAAGGTGTCTGGAGGAGGATCAG	1260
Qy	4016	TCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCG	4075
Db	1261	TCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCG	1320
Qy	4076	GAGGGCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCCGGTGCTCGGAGCTGACC	4135
Db	1321	GAGGGCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCCGGTGCTCGGAGCTGACC	1380
Qy	4136	CAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCGTGGCGACGAGGGA	4195
Db	1381	CAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCCGTGGCGACGAGGGA	1440
Qy	4196	GCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCA	4255
Db	1441	GCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCA	1500
Qy	4256	GACAATGTCTAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCTGAGGGTCTGGCCAGGGCAGC	4315
Db	1501	GACAATGTCTAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCTGAGGGTCTGGCCAGGGCAGC	1560
Qy	4316	CGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGC	4375
Db	1561	CGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGC	1620
Qy	4376	TTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTC	4435
Db	1621	TTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTC	1680
Qy	4436	TTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCCG	4495
Db	1681	TTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCCG	1740
Qy	4496	CTGGTCCTGTCTACCTTCCCAGTACCACAACTACACCCAGCCCCGTGGCAATTTTCATCCCC	4555
Db	1741	CTGGTCCTGTCTACCTTCCCAGTACCACAACTACACCCAGCCCCGTGGCAATTTTCATCCCC	1800
Qy	4556	TACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCCGACGCCAGCCCCCAG	4615
Db	1801	TACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCCGACGCCAGCCCCCAG	1860

Qy	4616	CAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCT	4675
Db	1861	CAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCT	1920
Qy	4676	CCCGCCAACGGCTCGCTGGGGCCCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTG	4735
Db	1921	CCCGCCAACGGCTCGCTGGGGCCCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTG	1980
Qy	4736	GCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCC	4795
Db	1981	GCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCC	2040
Qy	4796	AATTTTCGTGCCACCCCCACCTCGCCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAG	4855
Db	2041	AATTTTCGTGCCACCCCCACCTCGCCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAG	2100
Qy	4856	GACCTGCAGGCCTGGAACGTCTCCCTGCCGCCACCGCTGGGCCAGAAATGTGGACGTCG	4915
Db	2101	GACCTGCAGGCCTGGAACGTCTCCCTGCCGCCACCGCTGGGCCAGAAATGTGGACGTCG	2160
Qy	4916	GCACCTCCCTGCCGCGCCTGGTACGGGAGCCCCGTCCGCTGCACCTGCTCTGCGCAGGGC	4975
Db	2161	GCACCTCCCTGCCGCGCCTGGTACGGGAGCCCCGTCCGCTGCACCTGCTCTGCGCAGGGC	2220
Qy	4976	ACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACA	5035
Db	2221	ACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACA	2280
Qy	5036	GGCGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCC	5095
Db	2281	GGCGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCC	2340
Qy	5096	GACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAGTCCATC	5155
Db	2341	GACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAGTCCATC	2400
Qy	5156	CCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCT	5215
Db	2401	CCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCT	2460
Qy	5216	GCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTC	5275
Db	2461	GCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTC	2520
Qy	5276	AACAACGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGC	5335
Db	2521	AACAACGCCATCCTGCGTGCCAACCTGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGC	2580
Qy	5336	ATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTG	5395
Db	2581	ATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTG	2640
Qy	5396	CTGCAGGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCG	5455
Db	2641	CTGCAGGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCG	2700

Qy	5456	GCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTT	5515
Db	2701	GCCAGCTTCGTTGTCTTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTT	2760
Qy	5516	GTCAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAAC	5575
Db	2761	GTCAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAAC	2820
Qy	5576	TACCTGGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTAC	5635
Db	2821	TACCTGGTCCCCGCTACCTGCTGTGTCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTAC	2880
Qy	5636	ACGTCGCCCACCAACTTCCCTGCCGTCCCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATC	5695
Db	2881	ACGTCGCCCACCAACTTCCCTGCCGTCCCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATC	2940
Qy	5696	ACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCCTACGTGTTT	5755
Db	2941	ACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCCTACGTGTTT	3000
Qy	5756	CTCATGTGCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAG	5815
Db	3001	CTCATGTGCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAG	3060
Qy	5816	CTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTC	5875
Db	3061	CTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTC	3120
Qy	5876	ATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATC	5935
Db	3121	ATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCCTACAACGAGTACATC	3180
Qy	5936	AACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGAC	5995
Db	3181	AACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGAC	3240
Qy	5996	ATTGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACC	6055
Db	3241	ATTGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACC	3300
Qy	6056	ATCATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCT	6115
Db	3301	ATCATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCT	3360
Qy	6116	GTGGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGAC	6175
Db	3361	GTGGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGAC	3420
Qy	6176	AATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGT	6235
Db	3421	AATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGT	3480
Qy	6236	ATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTG	6295
Db	3481	ATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTG	3540
Qy	6296	GGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGGCGACGAGAGCACG	6355

Db	3541	 GGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACG	3600
Qy	6356	ACGGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAG	6415
Db	3601	 ACGGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAG	3660
Qy	6416	CAGAGCCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCGGGAG	6475
Db	3661	 CAGAGCCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTGACGAGCTCACGGCCCGGGAG	3720
Qy	6476	CACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTG	6535
Db	3721	 CACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTG	3780
Qy	6536	AAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTAC	6595
Db	3781	 AAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTAC	3840
Qy	6596	AGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTTGGGTACCCAGCCTTC	6655
Db	3841	 AGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTTGGGTACCCAGCCTTC	3900
Qy	6656	ATCTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAAC	6715
Db	3901	 ATCTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAAC	3960
Qy	6716	CTCATCCTCGACCTCATCAAGACAGGGCGTTAGTGGTGCTGACATCACACAGCATGGAG	6775
Db	3961	 CTCATCCTCGACCTCATCAAGACAGGGCGTTAGTGGTGCTGACATCACACAGCATGGAG	4020
Qy	6776	GAGTGCAGGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTG	6835
Db	4021	 GAGTGCAGGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTG	4080
Qy	6836	GGCAGCATCCAGCACCTGAAGAACCGGTTTGAGATGGCTACATGATCACGGTGCGGACC	6895
Db	4081	 GGCAGCATCCAGCACCTGAAGAACCGGTTTGAGATGGCTACATGATCACGGTGCGGACC	4140
Qy	6896	AAGAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCC	6955
Db	4141	 AAGAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCC	4200
Qy	6956	ATGCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCG	7015
Db	4201	 ATGCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCG	4260
Qy	7016	CTGGCCCAGGTGTTTCTAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTAC	7075
Db	4261	 CTGGCCCAGGTGTTTCTAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTAC	4320
Qy	7076	TCGGTCAGCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGAC	7135
Db	4321	 TCGGTCAGCCAGACCACACTGGACAATGTGTTTCGTGAACCTTTGCCAAGAAGCAGAGTGAC	4380
Qy	7136	AACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTG	7195

Db	4381	AACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCCTCTCGGCTGCTTG	4440
Qy	7196	CTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAG	7255
Db	4441	CTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAG	4500
Qy	7256	CCCGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAG	7315
Db	4501	CCCGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAG	4560
Qy	7316	CTGTCCTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGC	7375
Db	4561	CTGTCCTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGC	4620
Qy	7376	TCCACTGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTG	7435
Db	4621	TCCACTGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTG	4680
Qy	7436	CCTGCCAGGGCCTGGAGTGGAGGTTCAGGACCAAGGGGCTTCTGGTCTCCAGCCCCCTGT	7495
Db	4681	CCTGCCAGGGCCTGGAGTGGAGGTTCAGGACCAAGGGGCTTCTGGTCTCCAGCCCCCTGT	4740
Qy	7496	ACTCGGCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAAAGGCTGACCC	7555
Db	4741	ACTCGGCCATGCCCTGCGGTCACTGCGGTTGCCGCCCTAATTGTGCCAAAGGCTGACCC	4800
Qy	7556	GGCCCCGGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCCGCC	7615
Db	4801	GGCCCCGGGCTGCGTACACCCTTGCCCTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCCGCC	4860
Qy	7616	CCTCGCCCCTGCCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGC	7675
Db	4861	CCTCGCCCCTGCCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGC	4920
Qy	7676	TGGCCTTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTTTACGATGAAGGCTGATGC	7735
Db	4921	TGGCCTTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTTTACGATGAAGGCTGATGC	4980
Qy	7736	CGAGAGCGGGCTGTGGGCGGAGCTGGGTCACTCCCGTATTTATTTTGCTTTGAGAAGAGG	7795
Db	4981	CGAGAGCGGGCTGTGGGCGGAGCTGGGTCACTCCCGTATTTATTTTGCTTTGAGAAGAGG	5040
Qy	7796	CTCCTCTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGG	7855
Db	5041	CTCCTCTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGG	5100
Qy	7856	GCCAGCTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGA	7915
Db	5101	GCCAGCTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGA	5160
Qy	7916	CCCCCCCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGCCCCCTGCCCGCCAC	7975
Db	5161	CCCCCCCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGCCCCCTGCCCGCCAC	5220
Qy	7976	CTCCCTGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAAA	8035
Db	5221	CTCCCTGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAAA	5280

Qy 8036 ATGTC 8040
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Db 5281 ATGTC 5285

RESULT 14

US-10-172-118-47

; Sequence 47, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 47
; LENGTH: 5285
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AB028985
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-47

Query Match 65.7%; Score 5285; DB 13; Length 5285;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2756 GGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCC 2815
|||||
Db 1 GGCATCCTCACGTGGTACATTGAGGCTGTGCACCCAGGCATGTACGGGCTGCCCCGGCCC 60

Qy 2816 TGGTACTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAG 2875
|||||
Db 61 TGGTACTTCCCACTGCAGAAGTCCTACTGGCTGGGCAGTGGGCGGACAGAAGCCTGGGAG 120

Qy 2876 TGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCATGGAGGAGGACCAGGCCTGT 2935
|||||
Db 121 TGGAGCTGGCCGTGGGCACGCACCCCCCGCCTCAGTGTCATGGAGGAGGACCAGGCCTGT 180

Qy 2936 GCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACCCACCTG 2995
|||||
Db 181 GCCATGGAGAGCCGGCGCTTTGAGGAGACCCGTGGCATGGAGGAGGAGCCCACCCACCTG 240

Qy 2996 CCTCTGGTTGTCTGCGTGGACAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCC 3055
|||||

Db	241	CCTCTGGTTGTCTGCGTGGACAAACTCACCAAGGTCTACAAGGACGACAAGAAGCTGGCC	300
Qy	3056	CTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAAC	3115
Db	301	CTGAACAAGCTGAGCCTGAACCTCTACGAGAACCAGGTGGTCTCCTTCTTGGGCCACAAC	360
Qy	3116	GGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGT	3175
Db	361	GGGGCGGGCAAGACCACCACCATGTCCATCCTGACCGGCCTGTTCCCTCCAACGTCGGGT	420
Qy	3176	TCCGCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTG	3235
Db	421	TCCGCCACCATCTACGGGCACGACATCCGCACGGAGATGGATGAGATCCGCAAGAACCTG	480
Qy	3236	GGCATGTGCCCAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGG	3295
Db	481	GGCATGTGCCCAGCACAATGTGCTCTTTGACCGGCTCACGGTGGAGGAACACCTCTGG	540
Qy	3296	TTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATG	3355
Db	541	TTCTACTCACGGCTCAAGAGCATGGCTCAGGAGGAGATCCGCAGAGAGATGGACAAGATG	600
Qy	3356	ATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGC	3415
Db	601	ATCGAGGACCTGGAGCTCTCCAACAAACGGCACTCACTGGTGCAGACATTGTCGGGTGGC	660
Qy	3416	ATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTG	3475
Db	661	ATGAAGCGCAAGCTGTCCGTGGCCATCGCCTTCGTGGGCGGCTCTCGCGCCATCATCCTG	720
Qy	3476	GACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTG	3535
Db	721	GACGAGCCACGGCGGGCGTGGACCCCTACGCGCGCCGCGCCATCTGGGACCTCATCCTG	780
Qy	3536	AAGTACAAGCCAGGCCGCACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTG	3595
Db	781	AAGTACAAGCCAGGCCGCACCATCCTTCTGTCCACCCACCACATGGATGAGGCTGACCTG	840
Qy	3596	CTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTC	3655
Db	841	CTTGGGGACCGCATTGCCATCATCTCCCATGGGAAGCTCAAGTGCTGCGGCTCCCCGCTC	900
Qy	3656	TTCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCGAG	3715
Db	901	TTCTCAAGGGCACCTATGGCGACGGGTACCGCCTCACGCTGGTCAAGCGGCCCCGCGAG	960
Qy	3716	CCGGGGGGCCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGGCCCCGCTGAGC	3775
Db	961	CCGGGGGGGGCCCCAAGAGCCAGGGCTGGCATCCAGCCCCCAGGTGCGGGCCCCGCTGAGC	1020
Qy	3776	AGCTGCTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTG	3835
Db	1021	AGCTGCTCCGAGCTCCAGGTGTCCCAGTTCATCCGCAAGCATGTGGCCTCCTGCCTGCTG	1080
Qy	3836	GTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGG	3895
Db	1081	GTCTCAGACACAAGCACGGAGCTCTCCTACATCCTGCCCAGCGAGGCCGCCAAGAAGGGG	1140

Qy	3896	GCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGC	3955
Db	1141	GCTTTCGAGCGCCTCTTCCAGCACCTGGAGCGCAGCCTGGATGCACTGCACCTCAGCAGC	1200
Qy	3956	TTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCCCTCAAGGTGTCGGAGGAGGATCAG	4015
Db	1201	TTCGGGCTGATGGACACGACCCTGGAGGAAGTGTTCCCTCAAGGTGTCGGAGGAGGATCAG	1260
Qy	4016	TCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCG	4075
Db	1261	TCGCTGGAGAACAGTGAGGCCGATGTGAAGGAGTCCAGGAAGGATGTGCTCCCTGGGGCG	1320
Qy	4076	GAGGGCCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCCGGTGCTCGGAGCTGACC	4135
Db	1321	GAGGGCCCCGGCGTCTGGGGAGGGTCACGCTGGCAATCTGGCCCCGGTGCTCGGAGCTGACC	1380
Qy	4136	CAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCGTGGCGACGAGGGA	4195
Db	1381	CAGTCGCAGGCATCGCTGCAGTCGGCGTCATCTGTGGGCTCTGCCCGTGGCGACGAGGGA	1440
Qy	4196	GCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCA	4255
Db	1441	GCTGGCTACACCGACGTCTATGGCGACTACCGCCCCCTCTTTGATAACCCACAGGACCCA	1500
Qy	4256	GACAAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTCGGCCAGGGCAGC	4315
Db	1501	GACAAATGTCAGCCTGCAAGAGGTGGAGGCAGAGGCCCTGTCGAGGGTCGGCCAGGGCAGC	1560
Qy	4316	CGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGC	4375
Db	1561	CGCAAGCTGGACGGCGGGTGGCTGAAGGTGCGCCAGTTCCACGGGCTGCTGGTCAAACGC	1620
Qy	4376	TTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTC	4435
Db	1621	TTCCACTGCGCCCGCCGCAACTCCAAGGCACTCTTCTCCCAGATCTTGCTGCCAGCCTTC	1680
Qy	4436	TTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCCG	4495
Db	1681	TTCGTCTGCGTGGCCATGACCGTGGCCCTGTCCGTCCCGGAGATTGGTGATCTGCCCCCG	1740
Qy	4496	CTGGTCCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCC	4555
Db	1741	CTGGTCCTGTCACCTTCCCAGTACCACAACCTACACCCAGCCCCGTGGCAATTTTCATCCCC	1800
Qy	4556	TACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCCAG	4615
Db	1801	TACGCCAACGAGGAGCGCCGCGAGTACCGGCTGCGGCTATCGCCCGACGCCAGCCCCCAG	1860
Qy	4616	CAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCT	4675
Db	1861	CAGCTCGTGAGCACGTTCCGGCTGCCGTGCGGGGTGGGTGCCACCTGCGTGCTCAAGTCT	1920
Qy	4676	CCCGCCAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTG	4735
Db	1921	CCCGCCAACGGCTCGCTGGGGCCACGTTGAACCTGAGCAGCGGGGAGTCGCGCCTGCTG	1980

Qy	4736	GCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCC	4795
Db	1981	GCGGCTCGGTTCTTCGACAGCATGTGTCTGGAGTCCTTCACACAGGGGCTGCCACTGTCC	2040
Qy	4796	AATTTTCGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAG	4855
Db	2041	AATTTTCGTGCCACCCCCACCCTCGCCCGCCCCATCTGACTCGCCAGCGTCCCCGGATGAG	2100
Qy	4856	GACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCG	4915
Db	2101	GACCTGCAGGCCTGGAACGTCTCCCTGCCGCCCACCGCTGGGCCAGAAATGTGGACGTCG	2160
Qy	4916	GCACCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGC	4975
Db	2161	GCACCTCCCTGCCGCGCCTGGTACGGGAGCCCGTCCGCTGCACCTGCTCTGCGCAGGGC	2220
Qy	4976	ACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACA	5035
Db	2221	ACCGGCTTCTCCTGCCCCAGCAGTGTGGGCGGGCACCCGCCCCAGATGCGGGTGGTCACA	2280
Qy	5036	GGCGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCC	5095
Db	2281	GGCGACATCCTGACCGACATCACCGGCCACAATGTCTCTGAGTACCTGCTCTTCACCTCC	2340
Qy	5096	GACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAGTCCATC	5155
Db	2341	GACCGCTTCCGACTGCACCGGTATGGGGCCATCACCTTTGGAAACGTCTGAAGTCCATC	2400
Qy	5156	CCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCT	5215
Db	2401	CCAGCCTCATTTGGCACCAGGGCCCCACCCATGGTGCGGAAGATCGCGGTGCGCAGGGCT	2460
Qy	5216	GCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTC	5275
Db	2461	GCCCAGGTTTTCTACAACAACAAGGGCTATCACAGCATGCCACCTACCTCAACAGCCTC	2520
Qy	5276	AACAACGCCATCCTGCGTGCCAACCTGCCAAGAGCAAGGGCAACCCGGCGGCTTACGGC	5335
Db	2521	AACAACGCCATCCTGCGTGCCAACCTGCCAAGAGCAAGGGCAACCCGGCGGCTTACGGC	2580
Qy	5336	ATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTG	5395
Db	2581	ATCACCGTCACCAACCACCCCATGAATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTG	2640
Qy	5396	CTGCAGGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCG	5455
Db	2641	CTGCAGGGCACGGATGTCGTCATCGCCATCTTCATCATCGTGGCCATGTCCTTCGTGCCG	2700
Qy	5456	GCCAGCTTCGTTGTCTTCTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTT	5515
Db	2701	GCCAGCTTCGTTGTCTTCTCCTCGTGGCCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTT	2760
Qy	5516	GTCAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAAC	5575
Db	2761	GTCAGCGGCTGCAACCCCATCATCTACTGGCTGGCGAACTACGTGTGGGACATGCTCAAC	2820
Qy	5576	TACCTGGTCCCCGCTACCTGCTGTGTGCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTAC	5635

Db	2821	 TACCTGGTCCCCGCTACCTGCTGTGTTCATCATCTGTTTGTGTTTCGACCTGCCGGCCTAC	2880
Qy	5636	ACGTCGCCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATC	5695
Db	2881	 ACGTCGCCCCACCAACTTCCCTGCCGTCTCTCCCTCTTCCTGCTCTATGGGTGGTCCATC	2940
Qy	5696	ACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTT	5755
Db	2941	 ACGCCCATCATGTACCCGGCCTCCTTCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTT	3000
Qy	5756	CTCATTTGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAG	5815
Db	3001	 CTCATTTGTCATCAATCTCTTCATCGGCATCACCGCCACCGTGGCCACCTTCCTGCTACAG	3060
Qy	5816	CTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTC	5875
Db	3061	 CTCTTCGAGCACGACAAGGACCTGAAGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTC	3120
Qy	5876	ATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCTTACAACGAGTACATC	5935
Db	3121	 ATTTTCCCCAACTACAACCTGGGCCACGGGCTCATGGAGATGGCTTACAACGAGTACATC	3180
Qy	5936	AACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGAC	5995
Db	3181	 AACGAGTACTACGCCAAGATTGGCCAGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGAC	3240
Qy	5996	ATTGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACC	6055
Db	3241	 ATTGTCACCCGCGGACTGGTGGCCATGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACC	3300
Qy	6056	ATCATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCT	6115
Db	3301	 ATCATGTGCCAGTACAACCTTCCTGCGGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCT	3360
Qy	6116	GTGGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGAC	6175
Db	3361	 GTGGAGGATGATGTGGACGTGGCCAGTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGAC	3420
Qy	6176	AATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGT	6235
Db	3421	 AATGACATGGTCAAGATTGAGAACCTGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGT	3480
Qy	6236	ATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTG	6295
Db	3481	 ATCCTGGCCGTTGACCGCCTGTGCCTGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTG	3540
Qy	6296	GGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACG	6355
Db	3541	 GGCGTCAACGGTGCGGGCAAGACCAGCACCTTCAAGATGCTGACCGGCGACGAGAGCACG	3600
Qy	6356	ACGGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAG	6415
Db	3601	 ACGGGGGGCGAGGCCTTCGTCAATGGACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAG	3660
Qy	6416	CAGAGCCTCGGCTACTGCCCGCAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAG	6475

Db	3661	CAGAGCCTCGGCTACTGCCCCGAGTGTGACGCGCTGTTTCGACGAGCTCACGGCCCCGGGAG	3720
Qy	6476	CACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTG	6535
Db	3721	CACCTGCAGCTGTACACGCGGCTGCGTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTG	3780
Qy	6536	AAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTAC	6595
Db	3781	AAGTGGGCTCTGGAGAAGCTGGAGCTGACCAAGTACGCAGACAAGCCGGCTGGCACCTAC	3840
Qy	6596	AGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTC	6655
Db	3841	AGCGGCGGCAACAAGCGGAAGCTCTCCACGGCCATCGCCCTCATTGGGTACCCAGCCTTC	3900
Qy	6656	ATCTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAAC	6715
Db	3901	ATCTTCCTGGACGAGCCCACCACAGGCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAAC	3960
Qy	6716	CTCATCCTCGACCTCATCAAGACAGGGCGTTCAGTGGTGCTGACATCACACAGCATGGAG	6775
Db	3961	CTCATCCTCGACCTCATCAAGACAGGGCGTTCAGTGGTGCTGACATCACACAGCATGGAG	4020
Qy	6776	GAGTGCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTG	6835
Db	4021	GAGTGCGAGGCGCTGTGCACGCGGCTGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTG	4080
Qy	6836	GGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACC	6895
Db	4081	GGCAGCATCCAGCACCTGAAGAACCGGTTTGGAGATGGCTACATGATCACGGTGCGGACC	4140
Qy	6896	AAGAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCC	6955
Db	4141	AAGAGCAGCCAGAGTGTGAAGGACGTGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCC	4200
Qy	6956	ATGCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCG	7015
Db	4201	ATGCTCAAGGAGCGGCACCACACAAAGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCG	4260
Qy	7016	CTGGCCCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTAC	7075
Db	4261	CTGGCCCAGGTGTTTCAGCAAGATGGAGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTAC	4320
Qy	7076	TCGGTCAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGAC	7135
Db	4321	TCGGTCAGCCAGACCACACTGGACAATGTGTTTCGTGAACTTTGCCAAGAAGCAGAGTGAC	4380
Qy	7136	AACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTG	7195
Db	4381	AACCTGGAGCAGCAGGAGACGGAGCCGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTG	4440
Qy	7196	CTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAG	7255
Db	4441	CTCAGCCTGCTCCGGCCCCGGTCTGCCCCACGGAGCTCCGGGCACTTGTGGCAGACGAG	4500
Qy	7256	CCCGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCAG	7315
Db	4501	CCCGAGGACCTGGACACGGAGGACGAGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCAG	4560

Qy	7316	CTGTCCTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGC	7375
Db	4561	CTGTCCTTCAACACGGACACGCTCTGCTGACCACCCAGAGCTGGGCCAGGGAGGACACGC	4620
Qy	7376	TCCACTGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTG	7435
Db	4621	TCCACTGACCACCCAGAGCTGGGCCAGGGACTCAACAATGGGGACAGAAGTCCCCCAGTG	4680
Qy	7436	CCTGCCAGGGCCTGGAGTGGAGGTTCAAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCCTGT	7495
Db	4681	CCTGCCAGGGCCTGGAGTGGAGGTTCAAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCCTGT	4740
Qy	7496	ACTCGGCCATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCC	7555
Db	4741	ACTCGGCCATGCCCTGCGGTCACTGCGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCC	4800
Qy	7556	GGCCCGGGCTGCGTACACCCTTGCCCTGCTTTGCCCTTAAAGCCTCGGGGTCTGCCCGGCC	7615
Db	4801	GGCCCGGGCTGCGTACACCCTTGCCCTGCTTTGCCCTTAAAGCCTCGGGGTCTGCCCGGCC	4860
Qy	7616	CCTCGCCCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGC	7675
Db	4861	CCTCGCCCCCTGCCTGGCACTGCTCACCGCCCAAGGCGACGCCGGCTGGACCAGGCACTGC	4920
Qy	7676	TGGCCTTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGC	7735
Db	4921	TGGCCTTTCTCCTGCCCCGGCCTCGGAACCAGCTTTTCTCTCTTACGATGAAGGCTGATGC	4980
Qy	7736	CGAGAGCGGGCTGTGGGCGGAGCTGGGTCACTCCCGTATTTATTTTGCTTTGAGAAGAGG	7795
Db	4981	CGAGAGCGGGCTGTGGGCGGAGCTGGGTCACTCCCGTATTTATTTTGCTTTGAGAAGAGG	5040
Qy	7796	CTCCTCTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGG	7855
Db	5041	CTCCTCTGGCCCTGCTCTCCTGCAGGGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGG	5100
Qy	7856	GCCAGCTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGA	7915
Db	5101	GCCAGCTGGCAGGTGGCAGGAATGGAGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGA	5160
Qy	7916	CCCCCCCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCAC	7975
Db	5161	CCCCCCCCAACCCCCAGCTGCCATCGCTCTCCACCCAGCTTGGCCCCCTGCCCGCCAC	5220
Qy	7976	CTCCCTGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAAA	8035
Db	5221	CTCCCTGGGAGCCGGGCCTGTACATAGCGCACAGATGTTTGTTTTAAATAAATAAACAAA	5280
Qy	8036	ATGTC	8040
Db	5281	ATGTC	5285

RESULT 15

US-09-822-830A-36

; Sequence 36, Application US/09822830A

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; Patent No. US20020142952A1
; GENERAL INFORMATION:
; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
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; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 2740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-36

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Query Match          34.0%;  Score 2736.8;  DB 9;  Length 2740;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 2738;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

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Qy      5301 TGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGA 5360
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Db        1 TGCCCAAGAGCAAGGGCAACCCGGCGGCTTACGGCATCACCGTCACCAACCACCCCATGA 60

Qy      5361 ATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGGGCAGCGATGTCGTCATCG 5420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 ATAAGACCAGCGCCAGCCTCTCCCTGGATTACCTGCTGCAGGGCAGCGATGTCGTCATCG 120

Qy      5421 CCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGG 5480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 CCATCTTCATCATCGTGGCCATGTCCTTCGTGCCGGCCAGCTTCGTTGTCTTCCTCGTGG 180

Qy      5481 CCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTTCAGCGGCTGCAACCCCATCATCT 5540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CCGAGAAGTCCACCAAGGCCAAGCATCTGCAGTTTGTTCAGCGGCTGCAACCCCATCATCT 240

Qy      5541 ACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCTGCTGTG 5600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 ACTGGCTGGCGAACTACGTGTGGGACATGCTCAACTACCTGGTCCCCGCTACCTGCTGTG 300

Qy      5601 TCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTCGCCCACCAACTTCCCTGCCG 5660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TCATCATCCTGTTTGTGTTTCGACCTGCCGGCCTACACGTCGCCCACCAACTTCCCTGCCG 360

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy	5721	TCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCTTCATTGTCATCAATCTCTTCATCG	5780
Db	421	TCTGGTTCGAGGTCCCCAGCTCCGCCTACGTGTTCTTCATTGTCATCAATCTCTTCATCG	480
Qy	5781	GCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGGACCTGA	5840
Db	481	GCATCACCGCCACCGTGGCCACCTTCCTGCTACAGCTCTTCGAGCACGACAAGGACCTGA	540
Qy	5841	AGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTGGGCC	5900
Db	541	AGGTTGTCAACAGTTACCTGAAAAGCTGCTTCCTCATTTTCCCCAACTACAACCTGGGCC	600
Qy	5901	ACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATTGGCC	5960
Db	601	ACGGGCTCATGGAGATGGCCTACAACGAGTACATCAACGAGTACTACGCCAAGATTGGCC	660
Qy	5961	AGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGGTGGCCA	6020
Db	661	AGTTTGACAAGATGAAGTCCCCGTTTCGAGTGGGACATTGTCACCCGCGGACTGGTGGCCA	720
Qy	6021	TGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTCCTGC	6080
Db	721	TGGCGGTTGAGGGCGTCGTGGGCTTCCTCCTGACCATCATGTGCCAGTACAACCTCCTGC	780
Qy	6081	GGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTGGCCA	6140
Db	781	GGCGGCCACAGCGCATGCCTGTGTCTACCAAGCCTGTGGAGGATGATGTGGACGTGGCCA	840
Qy	6141	GTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAGAACC	6200
Db	841	GTGAGCGGCAGCGAGTGCTCCGGGGAGACGCCGACAATGACATGGTCAAGATTGAGAACC	900
Qy	6201	TGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCC	6260
Db	901	TGACCAAGGTCTACAAGTCCCGGAAGATTGGCCGTATCCTGGCCGTTGACCGCCTGTGCC	960
Qy	6261	TGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCA	6320
Db	961	TGGGTGTGCGTCCTGGCGAGTGCTTCGGGCTCCTGGGCGTCAACGGTGCGGGCAAGACCA	1020
Qy	6321	GCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGCGAGGCCTTCGTCAATG	6380
Db	1021	GCACCTTCAAGATGCTGACCGGCGACGAGAGCACGACGGGGGCGAGGCCTTCGTCAATG	1080
Qy	6381	GACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCGAGT	6440
Db	1081	GACACAGCGTGCTGAAGGAGCTGCTCCAGGTGCAGCAGAGCCTCGGCTACTGCCCCGAGT	1140
Qy	6441	GTGACGCGCTGTTTCGACGAGCTCACGGCCCGGGAGCACCTGCAGCTGTACACGCGGCTGC	6500
Db	1141	GTGACGCGCTGTTTCGACGAGCTCACGGCCCGGGAGCACCTGCAGCTGTACACGCGGCTGC	1200
Qy	6501	GTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGC	6560
Db	1201	GTGGGATCTCCTGGAAGGACGAGGCCCGGGTGGTGAAGTGGGCTCTGGAGAAGCTGGAGC	1260
Qy	6561	TGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGCGGCAACAAGCGGAAGCTCT	6620

Db	1261	 TGACCAAGTACGCAGACAAGCCGGCTGGCACCTACAGCGGCGGCAACAAGCGGAAGCTCT	1320
Qy	6621	CCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCACCACAG	6680
Db	1321	 CCACGGCCATCGCCCTCATTGGGTACCCAGCCTTCATCTTCCTGGACGAGCCCACCACAG	1380
Qy	6681	GCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCCTCGACCTCATCAAGACAG	6740
Db	1381	 GCATGGACCCCAAGGCCCGGCGCTTCCTCTGGAACCTCATCCTCGACCTCATCAAGACAG	1440
Qy	6741	GGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCACGCGGC	6800
Db	1441	 GGCGTTCAGTGGTGCTGACATCACACAGCATGGAGGAGTGCGAGGCGCTGTGCACGCGGC	1500
Qy	6801	TGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACC	6860
Db	1501	 TGGCCATCATGGTGAACGGTCGCCTGCGGTGCCTGGGCAGCATCCAGCACCTGAAGAACC	1560
Qy	6861	GGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTGAAGGACG	6920
Db	1561	 GGTTTGGAGATGGCTACATGATCACGGTGCGGACCAAGAGCAGCCAGAGTGTGAAGGACG	1620
Qy	6921	TGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACCACACAA	6980
Db	1621	 TGGTGCGGTTCTTCAACCGCAACTTCCCGGAAGCCATGCTCAAGGAGCGGCACCACACAA	1680
Qy	6981	AGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTCAAGATGG	7040
Db	1681	 AGGTGCAGTACCAGCTCAAGTCGGAGCACATCTCGCTGGCCCAGGTGTTCAAGATGG	1740
Qy	7041	AGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACACTGGACA	7100
Db	1741	 AGCAGGTGTCTGGCGTGCTGGGCATCGAGGACTACTCGGTGAGCCAGACCACACTGGACA	1800
Qy	7101	ATGTGTTCTGTAACCTTTCGAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGC	7160
Db	1801	 ATGTGTTCTGTAACCTTTCGAAGAAGCAGAGTGACAACCTGGAGCAGCAGGAGACGGAGC	1860
Qy	7161	CGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTG	7220
Db	1861	 CGCCATCCGCACTGCAGTCCCCTCTCGGCTGCTTGCTCAGCCTGCTCCGGCCCCGGTCTG	1920
Qy	7221	CCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGAGGACCTGGACACGGAGGACG	7280
Db	1921	 CCCCACGGAGCTCCGGGCACTTGTGGCAGACGAGCCCGAGGACCTGGACACGGAGGACG	1980
Qy	7281	AGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCCTTCAACACGGACACGCTCT	7340
Db	1981	 AGGGCCTCATCAGCTTCGAGGAGGAGCGGGCCCAGCTGTCCTTCAACACGGACACGCTCT	2040
Qy	7341	GCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTGACCACCCAGAGCTGGGCC	7400
Db	2041	 GCTGACCACCCAGAGCTGGGCCAGGGAGGACACGCTCCACTGACCACCCAGAGCTGGGCC	2100
Qy	7401	AGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGCCAGGGCCTGGAGTGGAGGTT	7460

Db	2101	AGGGACTCAACAATGGGGACAGAAGTCCCCCAGTGCCTGCCAGGGCCTGGAGTGGAGGTT	2160
Qy	7461	CAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCGGCCATGCCCTGCGGTCACTG	7520
Db	2161	CAGGACCAAGGGGCTTCTGGTCCTCCAGCCCCTGTACTCGGCCATGCCCTGCGGTCACTG	2220
Qy	7521	CGGTTGCCGCCCCCTAATTGTGCCAAAGGCTGACCCGGCCCCGGGCTGCGTACACCCTTGCC	7580
Db	2221	CGGTTGCCGCCCCCTAATTGTGCCAAAGGTTGACCCGGCCCCGGGCTGCGTACACCCTTGCC	2280
Qy	7581	CTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCCGGCCCCCTCGCCCCTGCCTGGCACTGCTCA	7640
Db	2281	CTGCTTTGCCTTAAAGCCTCGGGGTCTGCCCCGGCCCCCTCGCCCATGCCTGGCACTGCTCA	2340
Qy	7641	CCGCCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCCTTTCTCCTGCCCGGCCTCGG	7700
Db	2341	CCGCCCCAAGGCGACGCCGGCTGGACCAGGCACTGCTGGCCTTTCTCCTGCCCGGCCTCGG	2400
Qy	7701	AACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGAGCGGGCTGTGGGCGGAGCTG	7760
Db	2401	AACCAGCTTTTCTCTCTTACGATGAAGGCTGATGCCGAGAGCGGGCTGTGGGCGGAGCTG	2460
Qy	7761	GGTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCTCTGGCCCTGCTCTCCTGCAG	7820
Db	2461	GGTCAGTCCCGTATTTATTTTGCTTTGAGAAGAGGCTCCTCTGGCCCTGCTCTCCTGCAG	2520
Qy	7821	GGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAGCTGGCAGGTGGCAGGAATGG	7880
Db	2521	GGAGGTGGCTGTCCCGCGGGAAGCCATCAGCTTGGGCCAGCTGGCAGGTGGCAGGAATGG	2580
Qy	7881	AGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCCCCCCAACCCCCAGCTGCCATC	7940
Db	2581	AGAAGCTGACCCTGCTGGCCAGGCAAGGGGCCAGACCCCCCCCCAACCCCCAGCTGCCATC	2640
Qy	7941	GCTCTCCCACCCAGCTTGGCCCCCTGCCCGCCACCTCCCTGGGAGCCGGGCCTGTACAT	8000
Db	2641	GCTCTCCCACCCAGCTTGGCCCCCTGCCCGCCACCTCCCTGGGAGCCGGGCCTGTACAT	2700
Qy	8001	AGCGCACAGATGTTTGTTTTAAATAAAATAAACAAAATGTC	8040
Db	2701	AGCGCACAGATGTTTGTTTTAAATAAAATAAACAAAATGTC	2740

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 Job time : 3606 secs